



Program and Abstracts



Welcome

Welcome to Bento Gonçalves, we hope that your stay in Brazil will impress you not only because of rich scientific discussions during the Meeting, but also because of the friendly nature of the Brazilian people. Have a productive and excellent week!

**Antonio Costa
de Oliveira, Chair**



ICSS Board Members

Suk-Ha Lee
President ICSS

Ronald Phillips
Vice-President ICSC
Crop Science Society of America

Sui K. Yau
Africa and West Asia

John R. Porter
Europe

Antonio Costa de Oliveira
South America

Usha Zehr
South and Central Asia

Jane Ininda
Africa

Tony Fischer
International Crop Science Agency





Local Organizing Committee

Adriana Hemerly (Universidade Federal do Rio de Janeiro - RJ)

Aluizio Borem (Universidade Federal de Viçosa - MG)

Antonio V. O. Figueira (Universidade de São Paulo - SP)

Ariano Magalhães Jr. (Embrapa Clima Temperado - RS)

Carlos Roberto Riede (Instituto Agrônômico do Paraná - PR)

Eduardo Alano Vieira (Embrapa Cerrados - GO)

Elizabeth Fontes (Universidade Federal de Viçosa - MG)

Janette Fett (Universidade Federal do Rio Grande do Sul - RS)

José Baldin Pinheiro (Universidade de São Paulo - SP)

José Fernandes Barbosa Neto (Universidade Federal do Rio Grande do Sul - RS)

Luiz Federizzi (Universidade Federal do Rio Grande do Sul - RS)

Marcelo Menossi (Universidade de Campinas - SP)

Marcia Margis (Universidade Federal do Rio Grande do Sul - RS)

Marcio Alves Ferreira (Universidade Federal do Rio de Janeiro - RJ)

Moacir Pasqual (Universidade Federal de Lavras - MG)

Rogério Margis (Universidade Federal do Rio Grande do Sul - RS)

Rosa Lía Barbieri (Embrapa Clima Temperado - RS)

Silmar Peske (Universidade Federal de Pelotas - RS)





Table of Contents

General Information.....	05
Copyright and Citation.....	06
Speakers.....	07
Program.....	08
Poster Session Program.....	25
Tourism.....	50
Abstracts.....	53
Oral Presentation.....	54
Plenary Talks.....	110
Poster Session.....	118
Agricultural Extension and Economics.....	119
Agronomy.....	121
Biomedical, Health-Beneficial and Nutritionally Enhanced Plants.....	200
Crop Breeding & Genetics.....	206
Crop Ecology, Management & Quality.....	273
Crop Physiology and metabolism.....	294
Forage & Grazing Lands.....	347
Genomics, Molecular Genetics and Biotechnology.....	360
Plant Genetic Resources.....	421
Seed Physiology, Production & Technology.....	430
Workshops.....	447





General Information

Date and Venue

Schedule - The 6th ICSC will be held between August 10 to 6 in the E Pavillion of Fundaparque Events Center. On August ,8 will not have Scientific Activities in the Events center. The day is free for sightseeing. Find tour options in the RotaSul Both.

Secretariat

Located in the Exposition Area

Business Hours

August 06, 07 and 09 – From 8:00 am to 7:00 pm

August 08 – Closed

August 10 – From 8:00 am to 1:00 pm

Technical Visits (* Limited vacancies)

Technical Visit to EMBRAPA Grape and Wine (Brazilian Company of Agricultural Research)

Date: August 08, 2012

Visit Programme

- Departure from main Hotel (Conference Shuttle)
- Reception at EMBRAPA with presentation of an Institutional Video (subtitles in english)
- Lecture: Brazilian Wine Regions and Embrapa Support
- Break
- Visit to the experimental areas of grapevine at experimental fields
- Tasting of research products at sensory analysis laboratory
- Closing of the visit

Schedule - (limited vacancies)

Option A - From 08:30 to 12h00 am

Option B - From 01:30 to 05:00 pm

Cost – US\$ 40.00

Purchasing in the Congress Secretariat up to August 07.

Media Desk - Located in the mezzanine inside E Pavillion

Badge - To access the Exhibition Area and Auditoriums is mandatory to use your badge.

Certificate - Congress and Posters

From August 9 up to August 10

- **Speakers** - Delivered to the speaker after each lecture. Include Abstract Oral Presentation.

Simultaneous Translation - Not available

Abstracts - During the conference you will receive a pendrive with the abstracts of Oral Presentation, Posters and Workshops in PDF format. It will be available from August, 9.

Travel Agency - Trips

The RotaSul Travel Agency is located in the Exhibition Area. For information about tickets (receipts and/or changes in flights), lodging, tours and shuttle contact them.

Companion persons registered in the conference must withdraw the Vineyards Valley Tour Voucher in the RotaSul both (included in the registration cost), scheduled to be held on 08 August.

Social activities

Typical Dinner - Laço Velho Traditional Gaucho's Center (walking distance from Dall'Onder Grande Hotel)

August 8 – (wednesday) starts at 8:00 pm

US\$ 40,00 – tickets available at Conference's Secretariat up to August 7

* water and soft drinks included (alcoholic drinks must be paid separately)

Typical fair - Along the Exhibition Area –Typical Products

Meal - Lunch next to the Exhibition Area, the restaurant will cater all registered participants (including companions). Lunch no charge.

Mobile Phones - For the proper progress of activities of the Conference, please be kind enough and turn off or put in silent mode your cell phones, pagers and beepers.



Copyright and Citation

Copyright © 2012. Individual authors retain copyright in the papers published in HTML and PDF on flash drive and the Internet for the 6th International Crop Science Congress. The editors retains the non-exclusive right to publish the proceedings from the 6th International Crop Science Congress in electronic format in perpetuity.

Reproduction and the making available of this material for personal or non-commercial purposes is authorised, on condition that:

- attribution is given to the copyright owner;
- no official connection is claimed;
- the material is made available without charge or at cost; and
- the material is not subject to inaccurate, misleading or derogatory treatment.

This publication may be of assistance to you but the publisher, editors and authors do not guarantee that the publication is without flaw of any kind or is wholly appropriate for your particular purposes and therefore disclaim all liability for any error, loss or other consequence, which may arise from you relying on any information in this publication.

First Published 2012

6th International Crop Science Congress
Bento Gonçalves - RS, Brazil, 06 to 10 August 2012

Editor

PhD Antonio Costa de Oliveira

Graphic design and publishing

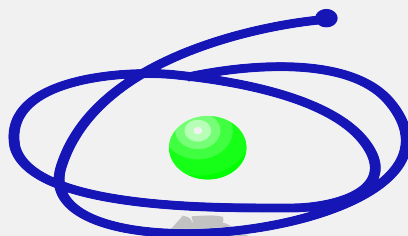
Carlos Busanello

ISBN X XXXXXX XX X

These proceedings may be cited as

Antonio Costa de Oliveira (2012). 6th International Crop Science Congress: Program and abstracts. Bento Gonçalves - RS, Brazil, 6 to 10 August 2012.

Sponsors





Speakers

Abdel Ismail	Philippines	Julio Cesar Bogiani	Brazil
Ademir Capelaro	Brazil	Jurandir Vieira Magalhães	Brazil
Adriana Silva Hemerly	Brazil	Karine Chenu	Australia
Alexander Johnson	Australia	Kenneth G. Cassman	USA
Ana Clara Pontaroli	Argentina	Kevin Smith	USA
Ana Gabriela Monnerat Carvalho Bassa	Brazil	Luiz Carlos Federizzi	Brazil
André Abreu	Brazil	Luiz Joaquim Castelo Branco Carvalho	Brazil
André Comeau	Canada	Lynn E. Sollenberger	USA
Antonio Augusto Franco Garcia	Brazil	Mai Komatsu	USA
Antonio Costa de Oliveira	Brazil	Maité Vaslin de Freitas Silva	Brazil
Antonio Domingos Padula	Brazil	Manoel Abilio de Queiróz	Brazil
Antonio J. Hall	Argentina	Manuela Chaves	Portugal
Antonio Vargas de Oliveira Figueira	Brazil	Marcelo Menossi	Brazil
Bertrand Joël Bernard Hirel	France	Marcia Margis	Brazil
Cacilda Borges do Valle	Brazil	Marcio Alves-Ferreira	Brazil
Carlos Alberto da Silva Ledo	Brazil	Marcos Antonio Machado	Brazil
Chikelu Mba	Italy	Marie-Anne Van Sluys	Brazil
Chittaranjan Kole	USA	Mark Sorrells	USA
Clive James	Canada	Maurício Antônio Lopes	Brazil
Cristian Chaparro	Brazil	Michael A. Grusak	USA
Dale Loussaert	USA	Michel Vincentz	Brazil
David John Bertoli	Brazil	Nils Berding	Australia
David Peter Jackson	USA	Pablo Antonio Calviño	Argentina
David Somers	USA	Patrícia Silva Ritschel	Brazil
Decio Zylbersztajn	Brazil	Patricio Grassini	USA
Diana Marais	South Africa	Paul Moore	USA
Diran Makinde	Burkina Faso	Paulo Cavalcanti Gomes Ferreira	Brazil
Durval Dourado Neto	Brazil	Paulo Cesar Sentelhas	Brazil
Eberson Sanches Calvo	Brazil	Pedro Luiz Scheeren	Brazil
Edward C. A. Runge	USA	Perry Gustafson	USA
Eliseu Binneck	Brazil	Peter M Gresshoff	Australia
Fernando Héctor Andrade	Argentina	Prakash Lakshmanan	Australia
Fernando Irajá Félix de Carvalho	Brazil	Qifa Zhang	China
Fernando Salvagioti	Argentina	Rajeev Kumar Varshney	India
Francisco Carlos Krzyzanowski	Brazil	Ray Ming	USA
Francisco José Becker Reifschneider	Brazil	Régis Lopes Correa	Brazil
Fred van Eeuwijk	Netherlands	Renato Vicentini	Brazil
Gary Stacey	USA	Ricardo Abdelnoor	Brazil
Gea Galluzzi	Colombia	Richard Mkandawire	South Africa
Geraldo Ubirajara Berger	Brazil	Robert Henry	Australia
Grover Shannon	USA	Roberto Tuberosa	Italy
Hans-Joachim Braun	Germany	Rogério Margis	Brazil
Henry T. Nguyen	USA	Ronald L. Phillips	USA
Humberto Prieto	Chile	Rosa Lía Barbieri	Brazil
Igor Rezende Coelho	Brazil	Rouf Mian	USA
Ivan Ortiz-Monasterio	México	Rubens Onofre Nodari	Brazil
Jacques Le Gouis	France	Samuel Ribeiro Giordano	Brazil
Jane Ininda	Kenya	Schuyler S. Korban	USA
Janette Palma Fett	Brazil	Scott Allen Jackson	USA
Jerry C. Nelson	USA	Sidney Netto Parentoni	Brazil
Jill Cairns	Zimbabwe	Silmar Teichert Peske	Brazil
João Carlos Garcia	Brazil	Siu Mui Tsai	Brazil
John Jifon	USA	Songbi Chen	China
Jose A. Bressiani	Brazil	Steven J. Clough	USA
José de Barros França Neto	Brazil	Suk-Ha Lee	Korea
José Eloir Denardin	Brazil	Thomas R Sinclair	USA
José Fernandes Barbosa Neto	Brazil	Usha Barwale Zehr	India
José Francisco Montenegro Valls	Brazil	Vera Maria Quecini	Brazil
José Guillermo Seijo	Argentina	Victor Oscar Sadras	Australia
Judson Ferreira Valentim	Brazil	Yunbi Xu	China



Program



Program

06th

August, 2012 - Monday

8:30 am - 9:30 am - Registration

9:30 am - 10:20 am

YELLOW AUDITORIUM

Plenary Talk 01 - Development of a Science-Based, Advanced Tropical Agriculture in Brazil

Mauricio Lopes (Brazil)

Chair: Antonio Costa de Oliveira (Brazil)

10:30 am - 11:00 am - Coffee Break

11:00 am - 12:30 am

YELLOW AUDITORIUM

Workshop 1 - Training Plant Scientists: Present Opportunities and Future Needs

Chair: Ed Runge (USA)

Keynote: Ron Phillips (USA) - "The Path to Discovery"

Speaker 1: Mba Chikelu (Nigeria) - Global Partnership Initiative for Plant Breeding Capacity Building (GIPB): The Crop Improvement Coalition

Speaker 2: Jerry Nelson (USA) - Meeting Education Needs in SouthEast Asia and Africa

Speaker 3: Ed Runge (USA) - Training Agricultural Scientists in a More Globalized World

GREEN AUDITORIUM

Workshop 2 - Soybean Breeding and Genetics

Chair: José Baldin Pinheiro (Brazil)

Keynote: Eberson Sanches Calvo (Brazil) - Tropical soybean: Improvement and production

Speaker 1: Steven J. Clough (USA) - Gene expression associated with soybean resistance to stink bug complex

Speaker 2: Vera Quecini (Brazil) - "Photoperception and photoperiod genes in soybean"

BLUE AUDITORIUM

Workshop 3 - Forage Production

Chair: Miguel Dall' Agnol (Brazil)

Keynote: Lynn E. Sollenberger (USA) - Opportunities and Constraints for Animal Production on Warm-Climate Grasslands

Speaker 1: Cacilda Borges do Valle (Brazil) - Animal Production on Tropical Pastures in Brazil

Speaker 2: José F. M. Valls (Brazil) - The Potential of Native Germplasm for Forage Production

Speaker 3: Judson F. Valentim (Brazil) - The Role of Legumes in Forage Production Systems in Tropical Latin America

RED AUDITORIUM

Workshop 4 - Nutritionally Enhanced Crops

Chair: Janette Fett (Brazil)

Keynote: Ivan Ortiz-Monasterio (México) - Alleviating malnutrition with biofortified crops: Development and delivery of nutritious maize and wheat varieties

Speaker 1: Alexander Johnson (Australia) - Development of high-iron rice to improve global health

Speaker 2: Michael A. Grusak (USA) - Getting more from our foods: Assessing and targeting nutrient bioavailability in our food crops

Speaker 3: Janette Palma Fett (Brazil) - "Iron biofortification in rice: what have we learned so far"

12:30 am - 1:30 pm - Break - Lunch



Program

06th

August, 2012 - Monday

ORAL PRESENTATION

1:30 pm - 2:30 pm - BLUE AUDITORIUM

TITLE	PRESENTER
GENETIC STRUCTURE OF POTATO BREEDING GERMPLASM FROM EMBRAPA	Angela Rohr
SOIL ENVIRONMENT EFFECT ANALYSIS ABOUT DOUBLE-ZERO-TILLAGE-CROPPING WITH WINTER WHEAT-RICE ROTATION SYSTEM IN YELLOW RIVER NINGXIA BASIN, CHINA	Angela Rohr
INTERSPECIFIC CROSSES IN POTATO AND THE UTILIZATION OF THE 2,4-D AUXIN	Joana Liska Bock
UNDERUTILIZED CAPSICUM PEPPER DIVERSITY IN ITS ANDEAN CENTRE OF ORIGIN: ADVANCES IN HIGH VALUE DIFFERENTIATION	Maarten van Zonneveld

1:30 pm - 2:30 pm - GREEN AUDITORIUM

TITLE	PRESENTER
INFLUENCE OF EXCESS SOIL WATER DURING EARLY GROWTH STAGE ON GROWTH, NUTRIENT UPTAKE, AND YIELD OF SOYBEAN AND AM COLONIZATION AND BIOMASS	Rintaro Hattori
POST-FLOWERING PHOTOPERIODIC EFFECT ON SOYBEAN REPRODUCTIVE EFFICIENCY	Adriana Graciela Kantolic
DECOMPOSITION AND CARBON CYCLING OF HEVEA LEAVES IN THAILAND	Dr. Pisamai Chantuma
PHYTOHORMONES EFFECT ON THE YIELD, QUALITY AND SOURCE-SINK RELATIONSHIP OF SUPER HYBRID RICE (ORYZA SATIVA L.)	Fahd Rasul
PHYTOHORMONES EFFECT ON THE YIELD, QUALITY AND SOURCE-SINK RELATIONSHIP OF SUPER HYBRID RICE (ORYZA SATIVA L.)	Fahd Rasul

1:30 pm - 2:30 pm - RED AUDITORIUM

TITLE	PRESENTER
RICE CROP UNDER SPRINKLER IRRIGATION	Ariano Martins de Magalhães Júnior
COVER CROPS IN IRRIGATED POTATO ROTATION SYSTEMS IN THE US NORTHWEST	Ashok K. Alva
HERBAGE MASS AND MORPHOLOGICAL COMPOSITION OF ELEPHANT GRASS SUBJECTED TO STRATEGIES OF ROTATIONAL STOCKING MANAGEMENT	Eliana Vera Geremia
WHICH IS THE LOWEST LATITUDE FOR CANOLA PRODUCTION ?	Gilberto Omar Tamm





Program

06th

August, 2012 - Monday

ORAL PRESENTATION

1:30 pm - 2:30 pm - YELLOW AUDITORIUM

TITLE	PRESENTER
EVALUATING OF DISTINCTNESS, UNIFORMITY AND STABILITY FOR WHEAT (TRITICUM AESTIVUM L.) CULTIVARS BASED ON MOLECULAR MARKERS	Lixin Wang
ROOT TRAITS ANALYSIS OF RECOMBINANT INBRED LINES TO IMPROVE PHOSPHORUS ACQUISITION EFFICIENCY IN MAIZE	Bárbara França Negri
CLASSIFICATION OF RESISTANCE TO PHAKOPSORA PACHYRHIZI IN SOYBEAN POPULATIONS POTENCIALLY SEGREGATING TWO RPP GENES	Renan Milagres Lage Novaes
SOYBEAN KNOWLEDGE BASE (SOYKB) FOR SOYBEAN TRANSLATIONAL GENOMICS AND BREEDING	Dong Xu

2:30 pm - 4:00 pm

YELLOW AUDITORIUM

Workshop 5 - Soybean Physiology and Production

Chair: Norman Neumaier (Brazil)

Keynote: Thomas R Sinclair (USA) - Physiological Improvement in Soybean Water Use to Increase Yields

Speaker 1: Paulo Sentelhas (Brazil) - Soybean Yield Gaps in Southern Brazil - Their Importance, Magnitude, and Causes

Speaker 2: Durval Dourado Neto (Brazil) - Advances in water use and transport in soybean

GREEN AUDITORIUM

Workshop 6 - Maize production

Chair: Newton Carneiro (Brazil)

Keynote: Sidney Parentoni (Brazil) - Challenges and opportunities for maize in Brasil: a view from public sector

Speaker 1: João Carlos Garcia (Brazil) - Maize production in Brazil: Past and Future Perspectives

Speaker 2: José Eloir Denardin (Brazil) - Maize as no-till system success

Speaker 3: Ademir Capelaro (Brazil) - Maize in Brazil: a view from a private company

BLUE AUDITORIUM

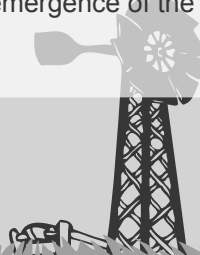
Workshop 7 - Advances in Agribusiness

Chair: Paulo Rigatto (Brazil)

Keynote: Decio Zylbersztajn (Brazil) - Role of Institutions in Reshaping the Global Agricultural Landscape: Perspectives from Brazil

Speaker 1: Samuel Ribeiro Giordano (Brasil) - Overview of Brazilian advances in Agrichains

Speaker 2: Antonio Domingos Padula (Brazil) - The emergence of the biodiesel industry in Brasil: current figures and future prospects





Program

06th

August, 2012 - Monday

2:30 pm - 4:00 pm

RED AUDITORIUM

Workshop 8 - Applications of Physiology in Crop Management and Breeding

Chair: Ana Pontaroli (Argentina)

Keynote: Fernando Andrade (Argentina) - Our research on ecophysiological bases for maize management

Speaker 1: Fernando Salvagiotti (Argentina) - Nutrient management and fertilization in soybean: a perspective from the crop

Speaker 2: Pablo Calviño (Argentina) - Sunflower yield differences as related to environmental variables. Comparison with maize and soybean

Speaker 3: Ana Clara Pontaroli (Argentina) - Wheat spike fertility: genetics and breeding applications of a key ecophysiological yield component

4:00 pm - 4:30 pm - Coffee Break

4:30 pm - 6:00 pm

YELLOW AUDITORIUM

Workshop 9 - Conservation and use of genetic resources of Cucurbitaceae and neglected crops

Chair: Rosa Lia Barbieri (Brazil)

Keynote: Manoel Abilio de Queiróz (Brazil) - Conservation and use of genetic resources of watermelon

Speaker 1: Gea Galluzzi (Colombia) - Conservation and use of underutilized genetic resources in Latin America and policy aspects

Speaker 2: Rosa Lía Barbieri (Brazil) - Co+A1:E43nservation and use of genetic resources of Cucurbita in Brazil

GREEN AUDITORIUM

Workshop 10 - Challenges to sustainable Wheat production

Chair: Pedro Scheeren (Brazil)

Keynote: André Comeau (Canada) - A systemic approach to genetics and crop management, leading to a sustainable wheat revolution

Speaker 1: Hans-Joachim Braun (Germany) - CIMMYT's breeding strategies for raising yield potential of wheat

Speaker 2: Pedro Luiz Scheeren (Brazil) - Co-evolution of breeding strategies and cropping systems for raising wheat yield potential on stressful environments

BLUE AUDITORIUM

Workshop 11 - The role of Seed Associations on Crop Production: How to Globalize Brazil in the World Seed Market?

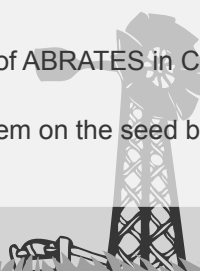
Chair: Silmar Peske (Brazil)

Keynote: Geraldo Berger (Brazil) -Seed and Sustainable Agriculture In Brazil

Speaker 1: TBA

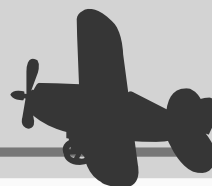
Speaker 2: José B. França-Neto (Brazil) - The Role of ABRATES in Conveying Seed Science to the Production Sector

Speaker 3: Silmar Peske (Brazil) - The role of Abrasem on the seed business





Program



06th

August, 2012 - Monday

4:00 pm - 6:00 pm

RED AUDITORIUM

Workshop 12 - Crop Physiology and Metabolism

Chair: Bertrand Hirel (France)

Keynote: Bertrand Hirel (France) - Improving Nitrogen Use Efficiency in Crops for Sustainable Agriculture

Speaker 1: Jacques LE GOUIS (France) - Traits and Tools to Improve Wheat Nitrogen Use efficiency

Speaker 2: Dale Loussaert (USA) - Maize Reproductive Response to Nitrogen"

6:00 pm - 7:00 pm - Opening session





Program

07th

August, 2012 - Tuesday

YELLOW AUDITORIUM - (2000 PAX)

8:30 am - 9:20 am

Plenary Talk 02 - Breeding Crops for Acid Soils - Perry Gustafson (USA)

Chair: Marcelo Menossi (Brazil)

9:30 am - 10:20 am

Plenary Talk 03 - Sustainability and Nitrogen Fixation - Peter Gresshoff (Australia)

Chair: Adriana Hemerly (Brazil)

10:30 am - 11:00 am - Coffee Break

11:00 am - 12:30 am

YELLOW AUDITORIUM

Workshop 13 - Climate Genomics and Breeding of Climate Resilient Crops for Future Food Security

Chair: Chittaranjan Kole (USA)

Keynote: Robert Henry (Australia) - Emerging opportunities for genomics-based breeding of climate resilient crop varieties for future food security

Speaker 1: Perry Gustafson (USA) - Breeding crops for boron deficiency: A case study of wheat breeding in Bangladesh

Speaker 2: Suk-Ha Lee (Korea) - Climate change adaptation strategy for crop improvement employing genomics

Speaker 3: Henry Nguyen (USA) - Exploiting the root system to improve crop adaptation to climate change

GREEN AUDITORIUM

Workshop 14 - Statistical Genetics in Crops

Chair: Antonio Augusto F. Garcia (Brazil)

Keynote: Fred van Eeuwijk (Netherlands) - Multi-trait QTL modelling for sets of physiologically related traits

Speaker 1: Kevin Smith (USA) - Implementing Genomic Selection in Barley

Speaker 2: Mark Sorrells (USA) - Genomic Selection in Plants: Empirical Results and Implications for Plant Breeding

Speaker 3: Antonio Augusto F. Garcia (Brazil) - "Genetic Mapping in Polyploids"

11:00 am - 12:30 am - RED AUDITORIUM

TITLE

PRESENTER

BREEDING FOR LOW NITROGEN TOLERANCE IN SOUTHERN AND EASTERN AFRICA: WHAT'S NEW?

Biswanath Das

BREEDING BIOFORTIFIED WHEAT CULTIVARS AT IAPAR – BRAZIL

Carlos Roberto Riede

GAS EXCHANGE AND RELATIVE CHLOROPHYLL CONTENT AS SELECTION CRITERIA IN SPRING WHEAT POPULATIONS

Cristiano Lemes da Silva

TROPICAL BARLEY: CHALLENGES AND PERSPECTIVES IN BRAZIL

Euclydes Minella

RECIPROCAL RECURRENT SELECTION: A STRATEGY TO OBTAIN SUPERIOR APOMICTIC HYBRIDS IN BRACHIARIA DECUMBENS

Sanzio Carvalho Lima Barrios

TESTCROSS PERFORMANCE AND GENETIC DISTANCE AMONG DOUBLED HAPLOID INBRED LINES DERIVED FROM TROPICAL BACKCROSS MAIZE POPULATIONS

Yoseph Beyene Aydağ



Program

07th

August, 2012 - Tuesday

12:30 am - 1:30 pm - Break - Lunch - Poster presentation

ORAL PRESENTATION

1:30 pm - 2:30 pm - BLUE AUDITORIUM

TITLE	PRESENTER
EFFECTS OF TWO ORGANIC SUPPLEMENTS ON IN VITRO GERMINATION OF ENDANGERED NATIVE ORCHIDS IN COLOMBIA, SOUTH AMERICA	Giovanni Orlando Cancino Escalante
ASSESSING THE EFFECT OF SOIL PH AND NUTRIENT AVAILABILITY ON THE GROWTH OF SUGARCANE (SACCHARUM SPP.) BRAZILIAN GERMPLASM	Rodrigo Gazaffi
OUTCROSSING/QTL: A NEW SOFTWARE TO PERFORM QTL MAPPING STUDIES IN OUTBRED SPECIES	Karina Elizabeth D'Andrea
GENETIC VARIATION IN A MAIZE POPULATION OF RILS: I- HERITABILITY STUDY OF THE ECO-PHYSIOLOGICAL AND NUMERICAL DETERMINANTS OF GRAIN YIELD	

1:30 pm - 2:30 pm - GREEN AUDITORIUM

TITLE	PRESENTER
SOIL ENVIRONMENT EFFECT ANALYSIS ABOUT DOUBLE-ZERO-TILLAGE-CROPPING WITH WINTER WHEAT-RICE ROTATION SYSTEM IN YELLOW RIVER NINGXIA BASIN, CHINA	Hanmin Yuan
COMPARISON OF NITROGEN FERTILIZERS, INDUCE AND ZINC ADDITION ON GLYPHOSATE EFFICACY ON THREE DIFFERENT WEED SPECIES	Hussein Fawzy Hussein Abouziena
AGRICULTURAL PROJECT MANAGEMENT: SUGARCANE FARMING OPERATIONS CASE STUDY	Marcelo Sans Dodson
GILL GROWING SEASON RAINFALL INFLUENCES THE YIELD BENEFITS ASSOCIATED WITH SUBSOIL MANURING	Jaikirat Singh

1:30 pm - 2:30 pm - RED AUDITORIUM

TITLE	PRESENTER
MPG1 PROTEIN IMMUNODETECTION IN GENETICALLY MODIFIED MELON	Camila Pegoraro
COUPLING ARABIDOPSIS HETEROLOGOUS EXPRESSION, IONOMICS PROFILING AND SYNCHROTRON RADIATION-BASED TECHNIQUES FOR RAPID CHARACTERIZATION OF METAL-RELATED GENES FROM RICE (ORYZA SATIVA)	Felipe Klein Ricachenevsky
EVOLUTION OF VACUOLAR IRON TRANSPORTER 1 (VIT1) PROTEINS IN PLANTS AND FUNCTIONAL CHARACTERIZATION OF RICE PARALOGS	Felipe Klein Ricachenevsky
ISOLATION AND CHARACTERIZATION OF FLOWERS TISSUE SPECIFIC PROMOTERS IN GOSSYPIMUM HIRSUTUM FOR CONTROL OF THE COTTON BOLL WEEVIL (ANTHONOMUS GRANDIS)	Sinara Artico



Program

07th

August, 2012 - Tuesday

ORAL PRESENTATION

1:30 pm - 2:30 pm - YELLOW AUDITORIUM

TITLE

PRESENTER

MORPHOLOGICAL, PHYSIOLOGICAL AND PHENOLOGICAL TRAITS ASSOCIATED WITH CULTIVAR EVOLUTION AND CROP IMPROVEMENT IN CALIFORNIA PROCESSING TOMATOES

Felipe H. Barrios Masias

NIGHTTIME TEMPERATURE INCREMENT REDUCES GRAIN YIELD IN WHEAT AND BARLEY: A FIELD STUDY

Guillermo Ariel García

IS FLORET DEATH TRIGGERED BY THE DEVELOPMENTAL STAGE OF THE MOST ADVANCED FLORETS IN DURUM WHEAT?

Gustavo Ariel SLAFER LAGO

TOWARDS AN UNDERSTANDING OF THE ROLE OF STARCH PHOSPHORYLATION IN CEREALS

Jean-Philippe Ral

2:30 pm - 4:00 pm

YELLOW AUDITORIUM

Workshop 15 - Conservation of Regional Crop Wild Relatives

Chair: José F. M. Valls (Brazil)

Keynote: José F. M. Valls (Brazil) - Integrated conservation and sustainable use of regional Crop Wild Relatives

Speaker 1: Guillermo Seijo (Argentina) - Novel diversity in wild peanut relatives and the importance of their conservation in South America

Speaker 2: TBA

Speaker 3: Francisco J. B. Reifschneider (Brazil) - "Diversity of Capsicum in Brazil and its genetic and agronomic potential"

GREEN AUDITORIUM

Workshop 16 - Marker-Assisted Selection

Chair: Yunbi Xu (China)

Keynote: Henry T. Nguyen (USA) - Marker-assisted selection in the era of whole genome sequencing

Speaker 1: Mai Komatsu (USA) - Maize genome diversity and its use in marker-assisted selection

Speaker 2: Rajeev Varshney (India) - Success story of MAS for drought tolerance traits in chickpea

Speaker 3: Yunbi Xu (China) - Environmental assaying or e-typing as a key component for marker-assisted breeding platform

BLUE AUDITORIUM

Workshop 17 - Plant development

Chair: Marcio Alves Ferreira (Brazil)

Keynote: Dave Jackson (USA) - Understanding inflorescence architecture in maize: genetics and systems approaches

Speaker 1: Michel Vincentz (Brazil) - A glimpse into energetic homeostasis and growth in Arabidopsis thaliana

Speaker 2: Marcio Alves-Ferreira (Brazil) - Isolation and characterization flower specific promoters in cotton and their potential as a tool for biotechnology

4:00 pm - 4:30 pm - Coffee Break



Program

07th

August, 2012 - Tuesday

4:30 pm - 6:00 pm

YELLOW AUDITORIUM

Workshop 18 - Cassava Production

Chair: Luiz J. Castelo Branco Carvalho (Brazil)

Keynote: Luiz J. C. B. Carvalho (Brazil) - Cassava Germplasm Biotechnologies: enhancing nutritional and starch quality of storage root

Speaker 1: Chikelu Mba (Italy) - Cassava Breeding Technology: Constraints, solutions and opportunities to enhance root yield and quality for industrial utilization

Speaker 2: Songbi Chen (China) - Cassava PROTEOME Technologies: approaches and strategies to increase starch yield and nutritional quality varieties

GREEN AUDITORIUM

Workshop 19 - Genomics for Soybean Crop Improvement

Chair: Suk-Ha Lee (Korea)

Keynote: Scott A. Jackson (USA) - "Leveraging Genomics for Soybean Improvement

Speaker 1: Suk-Ha Lee (Korea) - Genomic resources of Glycine soja for soybean crop improvement

Speaker 2: Ricardo Abdelnoor (Brazil) - "Allelic Variation on Brazilian Soybean Cultivars"

Speaker 3: M.A. Rouf Mian (USA) - DNA based breeding for improvement of pest resistance and quality traits of food-grade soybeans

BLUE AUDITORIUM

Workshop 20 - Genomics of root development and environmental interactions

Chair: Adriana Hemerly (Brazil)

Keynote: Gary Stacey (USA) - Soybean Root Hair: a single cell model for plant systems biology

Speaker 1: Antonio C. de Oliveira (Brazil) - Regulatory elements linking genes co-regulated in response to abiotic stresses

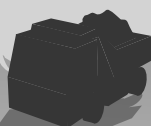
Speaker 2: Adriana S. Hemerly (Brazil) - Transcriptome analysis of genetic and environmental factors controlling sugarcane root development

YELLOW AUDITORIUM

6:30 pm - 6:50 pm

Plenary Talk 04 - Crop Science Research to Assure Global Food Security - Part 2 - Kenneth G. Cassman (USA)

Chair: Marcio Alves-Ferreira (Brazil)





Program

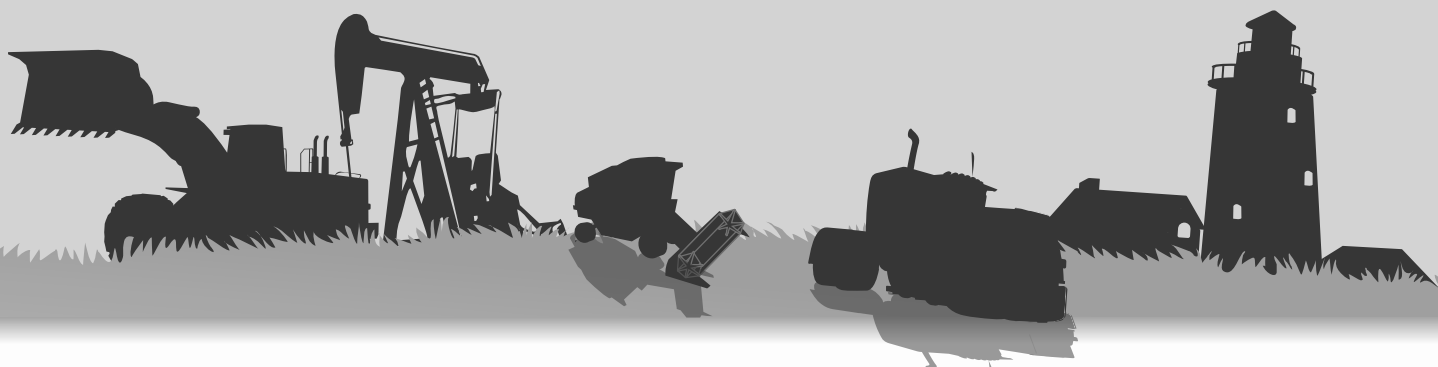
08th

August, 2012 - Wednesday

Day with no scientific activities

SIGHTSEEING TOURS* and TECHNICAL VISITS

* The tours should be booked and paid by the participant





Program

09th

August, 2012 - Thursday

YELLOW AUDITORIUM

8:30 am - 9:20 am

Plenary Talk 05 - Rice genomics, biotechnology and Breeding – Feeding Billions - Qifa Zhang (China)

Chair: Márcia Regis (Brazil)

9:30 am - 10:20 am

Plenary Talk 06 - Drought, the New (old?) Challenge for Agriculture: What Role for Genomics-Assisted Breeding?

Roberto Tuberosa (Italy)

Chair: Jose Barbosa Neto (Brazil)

* 10:20 am - Launching of the book "Plant Breeding for Abiotic Stress Tolerance"

10:30 am - 11:00 am - Coffee Break



11:00 am - 12:30 am

YELLOW AUDITORIUM

Workshop 21 - RNA silencing

Chair: Rogerio Margis (Brazil)

Speaker 1: Maité Vaslin de Freitas Silva (Brazil) - Global alteration of microRNAs and transposon-derived small RNAs in cotton (*Gossypium hirsutum*) during virus infection

Speaker 2: Régis Lopes Correa (Brazil) - Suppressors of Gene Silencing in the Plant Viral Family Luteoviridae

Speaker 3: Rogério Margis (Brazil) - "Comparative analysis of microRNA edition by nucleotide addition in dicots and monocots"

GREEN AUDITORIUM

Workshop 22 - Bioinformatics and Crop Breeding

Chair: Luciano Maia (Brazil)

Keynote: Cristian Chaparro (Brazil) - State of the art and challenges in NGS mapping and assembly: the hunt for structural variants in rice

Speaker 1: Renato Vicentini (Brazil) - From genotype to phenotype in sugarcane: a systems biology approach to understanding the sucrose synthesis and accumulation

Speaker 2: Eliseu Binneck (Brazil) - Web-based platform for RNA-Seq data analysis and storage: a case study on soybean gene expression experiments

BLUE AUDITORIUM

Workshop 23 - Transgenic crops

Chair: Aluizio Borém (Brazil)

Keynote: David Somers (USA) - GM varieties: what the market can expect

Speaker 1: Gabriela Bassa (Brazil) - GM Trees

Speaker 2: André Abreu (Brazil) - GM Crops for sustainable agriculture

RED AUDITORIUM

Workshop 24 - Breeding for Abiotic Stress Tolerance

Chair: Henry Nguyen (USA)

Keynote: Jill Cairns (Zimbabwe) - Progress in breeding for drought stress tolerant maize in Eastern and Southern Africa

Speaker 1: Abdel Ismail (Philippines) - Progress in breeding for submergence tolerance in rice

Speaker 2: J. Grover Shannon (USA) - Progress in breeding for drought and flooding tolerance in soybean

Speaker 3: Jurandir Magalhães (Brazil) - Molecular breeding for aluminum tolerance in sorghum based on the AltSB locus





Program

09th

August, 2012 - Thursday

12:30 am - 1:30 pm - Break - Lunch - Poster presentation

ORAL PRESENTATION

1:30 pm - 2:30 pm - BLUE AUDITORIUM

TITLE

PRESENTER

DORMANT CANOLA SEED – STILL A SLEEPING BEAST?

Sabine Gruber

THE AGMIP WHEAT PILOT STUDY: A SENSITIVITY ANALYSIS WITH 27 CROP MODELS

Senthold Asseng

EARLY PLANTING MITIGATES THE LEVEL OF DEOXYNIVALENOL CONTAMINATION OF BARLEY IN EASTERN CANADA

Thin Meiw Choo

A LOT MORE WITH LESS: IMPROVING PROFITABILITY OF THE WHEAT-MAIZE PRODUCTION IN THE NORTH CHINA PLAIN WITH BETTER FIELD MANAGEMENT AND RATIONAL INPUT

Wei-li LIANG

1:30 pm - 2:30 pm - GREEN AUDITORIUM

TITLE

PRESENTER

GRAIN NITROGEN PERCENTAGE IN WHEAT AND BARLEY GROWN UNDER A WIDE RANGE OF YIELDING CONDITIONS AND IN RESPONSE TO POST FLOWERING DEGRAINING

Ignacio Alzueta

DYNAMICS OF AMMONIA VOLATILIZATION FROM APPLIED UREA EVALUATED BY ADJUSTED PARAMETERS OF A LOGISTIC FUNCTION

Marcos Lima
Campos do Vale

MAKORI PLASTICITY IN ROOT DEVELOPMENT AND ITS CONTRIBUTION TO SHOOT DRY MATTER PRODUCTION AS AFFECTED BY NITROGEN APPLICATION IN NERICA (NEW RICE FOR AFRICA)

Menge Daniel

MODELLING PREDICTS THAT HEAT STRESS, NOT DROUGHT, WILL INCREASE VULNERABILITY OF WHEAT IN EUROPE

Mikhail Semenov

1:30 pm - RED AUDITORIUM

TITLE

PRESENTER

MODELLING PREDICTS THAT HEAT STRESS, NOT DROUGHT, WILL INCREASE VULNERABILITY OF WHEAT IN EUROPE

Emanoella Lima
Soares

PROTEOMIC ANALYSIS OF DIFFERENT REGIONS IN THE INNER INTEGUMENT OF JATROPHA CURCAS L. SEEDS

Emanoella Lima
Soares

PHYSIOLOGICAL REASONS OF SALINITY TOLERANCE AND SODICITY TOLERANCE

Emi Kaburagi

EVALUATION OF RICE PRODUCTIVITY WITH RICE GROWTH SIMULATION MODEL IN SANKER RIVER BASIN, CAMBODIA

Koki Homma

TRANSGENIC SWEETPOTATO WITH ENHANCED CONTENT OF CAROTENOID

Sang-Soo Kwak



Program

09th

August, 2012 - Thursday

ORAL PRESENTATION

1:30 pm - 2:30 pm - YELLOW AUDITORIUM

TITLE	PRESENTER
THE RELATIONSHIP OF DEVELOPMENTAL GENES, GROWTH HABIT AND SEEDLING VIGOUR OF WHEAT	Felicity Harris
USE OF CLIMATE DATA TO PREDICT YIELD OF MISCANTHUS IN SOUTH AMERICA	kwang soo kim
GENETIC VARIATION FOR RETROTRANSPOSON DERIVED SMALL INTERFERING RNAS	Wesley T Barber
GROWTH AND GENETIC DIVERSITY ANALYSIS OF GENUS TARAXACUM ACCESSIONS COLLECTED IN KOREA	Chang Hyu Bae

2:30 pm - 4:00 pm

YELLOW AUDITORIUM

Workshop 25 - Advancing the frontiers of crop science through physiological understanding" a Special Symposium, honoring Prof. A. J. Hall

Chair: Gustavo Slafer (Spain)

Opening: Gustavo A Slafer (Spain) - Advancing the frontiers of crop science through physiological understanding

Keynote 1: Fernando H. Andrade (Argentina) - Crop physiology contributions to crop productivity

Keynote 2: Patricio Grassini (USA) - "Yield gap closure through identifying ways to improve resource use efficiency

GREEN AUDITORIUM

Workshop 26 - Weed management and stalks control in herbicide tolerant cotton fields

Chair: Lúcia Vieira Hoffmann (Brazil)

Keynote: Julio Cesar Bogiani (Brazil) - Weed management and stalks control in herbicide tolerant cotton fields

Speaker 1: Igor Rezende Coelho (Brazil) - Management System for weeds and stalk control in Glyphosate Tolerant Cotton Fields

Speaker 2: André Abreu (Brazil) - Alternatives and rotation of technologies for the management of resistant weeds and spontaneous cotton plants"

BLUE AUDITORIUM

Workshop 27 - Experiences in Crop Improvement in Africa

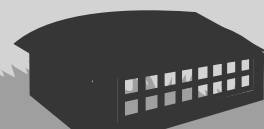
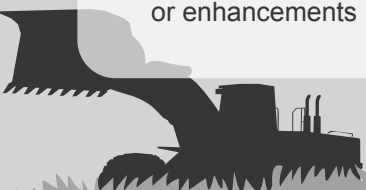
Chair: Jane Ininda (Kenya)

Keynote: Richard Mkandawire (South Africa) - Achieving a green revolution in Africa in the 21st Century-Lessons for Transforming Africa's Agriculture

Speaker 1: Jane Ininda (Kenya) - Developing Farmer Driven Seed Systems in Africa

Speaker 2: Diana Marais (South Africa) - The role of Biotechnology in food security for Africa

Speaker 3: Diran Makinde (Burkina Faso) - Agricultural policies and Food Security issues in Africa-Deterrents or enhancements





Program

09th

August, 2012 - Thursday

2:30 pm - 4:00 pm

RED AUDITORIUM

Workshop 28 - Sugarcane Production

Chair: Jorge da Silva (Brazil)

Keynote: Nils Berding (Australia) - Improving sugarcane productivity: The challenge for traditional crop improvement

Speaker 1: Paul H. Moore (USA) - Physiological Constraints to Sugarcane Yield Potential

Speaker 2: Jose A. Bressiani (Brazil) - Potential use of sugarcane and relatives as a feedstock for BioEnergy production

Speaker 3: John Jifon (USA) - Energy Canes and Related Grasses as Bioenergy Feedstocks for Texas

4:00 pm - 4:30 pm - Coffee Break

4:30 pm - 6:00 pm

YELLOW AUDITORIUM

Continuation Workshop 25 - Advancing the frontiers of crop science through physiological understanding" a Special Symposium, honoring Prof. A. J. Hall

Keynote 3: Karine Chenu (Australia) - Modelling genotype, environment and genotype x environment interactions to aid crop improvement

Keynote 4: Victor Oscar Sadras (Australia) - Phenotypic Plasticity of Crop Traits

Closing: Antonio J. Hall (Argentina) "Tour guides, discoverers or team players?"

GREEN AUDITORIUM

Workshop 29 - Sugarcane Genomics

Chair: Antonio Figueira (Brazil)

Keynote: Ray Ming (USA) - Applications of RNA-seq in sugarcane genomic research

Speaker 1: Marie-Anne Van Sluys (Brazil) - Sugarcane mobile genome landscape: how to translate information to cultivar assessment?

Speaker 2: Paulo Ferreira (Brazil) - Epigenetics and small RNAs in sugarcane

Speaker 3: Antonio Figueira (Brazil) - Large-scale transcriptomic analyses in sugarcane: searching for genes associated with drought tolerance

BLUE AUDITORIUM

Workshop 30 - Honor to Prof. Fernando Carvalho - From Genetics to Plant Breeding: Scientific Advances and Training of Students

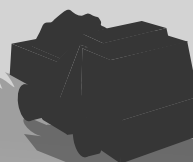
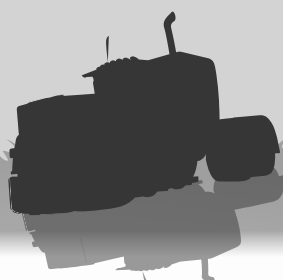
Chair: José Barbosa Neto (Brazil)

Keynote: Rubens Onofre Nodari (Brazil) - Genetic resources and plant breeding

Speaker 1: L.C.Federizzi (Brazil) - Genetics and Breeding of cereals for subtropical environments

Speaker 2: José Barbosa Neto (Brazil) - Genealogy of plant breeders in Southern Brazil

Speaker 3: Fernando Carvalho (Brazil) - 50 years of Plant Breeding





Program

09th

August, 2012 - Thursday

ORAL PRESENTATION

1:30 pm - 2:30 pm - RED AUDITORIUM

TITLE	PRESENTER
AGRICULTURAL PROJECT MANAGEMENT: SUGARCANE FARMING OPERATIONS CASE STUDY	Marcelo Sans Dodson
MAPPING RR TRAIT IN SOYBEAN GENOME BY GENOTYPING BY SEQUENCING METHODOLOGY	André Luiz de Lima Passianotto
RESPONSES AND CONTRIBUTIONS OF RICE CROPPING SYSTEM TO CLIMATE CHANGE: EVIDENCES FROM FIELD EXPERIMENTS IN CHINA	Weijian Zhang
THE RELATIONSHIP OF THE OSCPL1 GENE WITH THE SEED SHATTERING	Anderson Luis Nunes

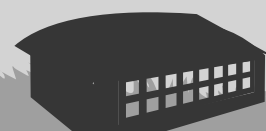
YELLOW AUDITORIUM

6:30 pm - 6:50 pm

Plenary Talk 07 - Agriculture Biotechnology in India - Usha B. Zehr (India)

Chair: Antonio Figueira (Brazil)

8:00 pm - Gaúcho's Typical Dinner





Program

10th

August, 2012 - Friday

YELLOW AUDITORIUM

8:30 am - 9:20 am

Plenary Talk 08 - Global Overview of the Adoption, Impact, and Future Prospects of Biotech/GM Crops
Clive James (USA)
Chair: Aluisio Borem (Brazil)

9:30 am - 10:20 am

Plenary Talk 9 - Plant Breeding in the Millennium: Priorities and Prospects" - Chittaranjan Kole (USA)
Chair: José Baldin Pinheiro (Brazil)

10:30 am - 11:00 am - Coffee Break

11:00 am - 12:30 am

YELLOW AUDITORIUM

Workshop 31 - Plant Abiotic Stress Responses

Chair: Marcelo Menossi & Marcia Margis (Brazil)

Keynote: Manuela Chaves (Portugal) - Crop resistance to abiotic stresses – mechanisms, traits and mitigation strategies

Speaker 1: Prakash Lakshmanan (Australia) - An integrated research framework to develop sugarcane for water-limited environments

Speaker 2: Marcelo Menossi (Brazil) - Sugarcane genes associated with drought tolerance

Speaker 3: Marcia Margis (Brazil) - ASR genes and aluminum responses in Rice

GREEN AUDITORIUM

Workshop 32 - Legume Genomics

Chair: Rajeev Kumar Varshney (India)

Keynote: Scott A Jackson (USA) - Genomes for crop legumes

Speaker 1: David J. Bertioli (Brazil) - The genomics of peanut and its wild relatives

Speaker 2: TBA

Speaker 3: Rajeev Varshney (India) - Genome and genomics of pigeonpea

BLUE AUDITORIUM

Workshop 33 - Fruit Crops

Chair: Marcos A. Machado (Brazil)

Keynote: Schuyler S. Korban (USA) - Genomic analysis for genetic improvement of economic traits in apple

Speaker 1: Patricia Ritschel (Brazil) - Genetic and breeding of grape in Brazil

Speaker 2: Humberto Prieto (Chile) - Genetic transformation in fruit crops

Speaker 3: Marcos A. Machado (Brazil) - From citrus genome to breeding: the challenge of integration

YELLOW AUDITORIUM

12:30 am

Closing session

- Invitation for 7th ICSC China - Prof. Wan Jianmin

- Closing remarks - Prof. Antonio Costa de Oliveira





Poster Session Program



Poster Session

07th

Tuesday

	Title and Authors	Area
001	DOES CROP INSURANCE POLICY PERFORM EFFICIENTLY?—AN ASSESSMENT WITH THE CASE OF WHEAT CROP IN HENAN PROVINCE IN CHINA'S MAJOR GRAIN-PRODUCING AREA Yang,RUIHUA; Liu,SHENG; Ju,RONGHUA; Xian,ZUDE; Liang,WEILI;	Agricultural Extension and Economics
002	PRODUCTION AND DRY MATTER PARTITIONING IN SOYBEAN CULTIVARS DUE TO PLANT POPULATIONS AND SOWING DATES Chaves,A; Rizzardi,MA; Pires,JLF; Boller,W;	Agronomy
003	VERTICAL DISTRIBUTION OF YIELD COMPONENTS IN SOYBEAN CULTIVARS OF INDETERMINED GROWTH HABIT UNDER PLANTS ARRANGEMENTS AND SOWING DATES Chaves,A; Rizzardi,MA; Ramos,HS; Ulrich,VR;	Agronomy
004	A FUNCTIONAL AND QUANTITATIVE APPROACH FOR ESTIMATING YIELD LOSSES DUE TO LATE DEFOLIATION IN SOYBEAN Enrico,JM; Kantolic,AG; Bodrero,M;	Agronomy
005	DOUBLE HAPLOID LINES COMBINING HIGH GRAIN NUMBER AND WEIGHT ARE PROMISSORY TO INCREASE YIELD POTENTIAL OF WHEAT Calderini,DF; Hasan,AK; Bustos,DV; Moure,S;	Agronomy
006	Eradication of blackleg disease of canola in Brazil – a success story Tomm,GO; Kutcher,HR; Easton,A;	Agronomy
007	EMERGENCY OF THE LOLIUM MULTIFLORUM BY SOWING DEPTH, STRAW COVER AND SOIL COMPACTION Galvan,JÔNATAS; Rizzardi,MAUROANTÔNIO; Galvan,MÁRCIO;	Agronomy
008	EFFICIENCY OF FOLIAR APPLICATION OF A NATURAL BIOSTIMULANT IN MAIZE CROP Messias,RS; Galli,V; Silveira,CAP; Silva,SDA; Rickes,E; Rombaldi,CV;	Agronomy
009	WHEAT EVOLUTION UNDER CLIMATE CHANGE WARMING Zhang, ZHENGBIN;	Agronomy
010	IMPACT OF NATURAL PLANT GROWTH REGULATORS ON THE GROWTH, YIELD AND QUALITY OF SUNFLOWER(HELIANTHUS ANNUUS L.) Rasul,F; Bilal,A; Khan,HZ; Cheema,SA; Ahmed,A; Khaliq,T; Saleem,MF; Rehman,H;	Agronomy
011	YIELD COMPONENTS IN THE STEM AND BRANCHES OF SOYBEAN CULTIVARS AFFECTED BY PLANT POPULATIONS AND SOWING DATES Chaves,A; Rizzardi,MA; Ramos,HS; Ulrich,VR;	Agronomy
012	WHEAT GRAIN YIELD VARIABILITY IN CROP SYSTEMS IN A LONG-TERM EXPERIMENT Santi,A; Dalmago,GA; Wuttke,D; Pires,JLF; Santos,HP; Cunha,GR; Fochesatto,E;	Agronomy
013	INFLUENCE OF SUBSTRATE DRAINED OF AGARICUS SP MEAL CINNAMON SEEDS AND FRUIT ON MELOIDOGYNE JAVANICA Faria,CMDR; Pereira,SGM; Dallemole-Giaretta,R; Botelho,RV; Mateus,MAF;	Agronomy



Poster Session

07th

Tuesday

	Title and Authors	Area
014	ESTIMATING WHEAT GRAIN YIELD POTENTIAL AT DIFFERENT GROWTH STAGES USING AN ACTIVE REFLECTANCE SENSOR Bredemeier,C; Variani,C; Almeida,D; Perin,J; Schmitz,JF; Rosa,AT;	Agronomy
015	MAIZE AND BRACHIARIA INTERCROPPING FOR IMPROVING NO-TILL SYSTEMS IN BRAZILIAN SUBTROPICAL REGION De-Bona,FD; Denatdin,JE; Faganello,A; Silva-Júnior,JP; Santi,A; Dalmago,GA;	Agronomy
016	DESCRIPTION OF THE DIFFERENT STRUCTURES USED IN THE CULTIVATION OF VEGETABLES IN PROTECTED ENVIRONMENT Padilha,FA; Magalhães,KS; Pedrosa,JA;	Agronomy
017	PRODUCTION OF TOMATO SEEDLINGS IN DIFFERENT SUBSTRATES Padilha,FA; Pedrosa,JA; Magalhães,KS;	Agronomy
018	EFFECT OF RAPID CANOPY DEVELOPMENT ON SEED YIELD OF SAFFLOWER IN THE NORTH OF IRAN Soleimanzadeh,H;	Agronomy
019	EFFECTS OF AZOTOBACTER AND NITROGEN CHEMICAL FERTILIZER ON YIELD AND YIELD COMPONENTS OF WHEAT (TRITICUM AESTIVUM L.) Soleimanzadeh,H;	Agronomy
020	VIABILITY OF RYEGRASS SEEDS GLYPHOSATE SENSITIVE AND RESISTANT Galvan,J; Rizzardi,MA;	Agronomy
021	VARIATIONS ON PHOSPHORUS ADSORPTION CAPACITY AS A FUNCTION OF WATERLOGGING Vale,MLC; Sousa,RO; Silva,JB; Sehn,CF;	Agronomy
022	NUTRIENT CONTENT IN LEAVES OF STRAWBERRY PLANTS TREATED WITH UV-C RADIATION DURING STRAWBERRY CROP Moreno,MB; Crizel,GR; Leite,TB; Cantillano,RFF; Rombaldi,CV;	Agronomy
023	TOTAL CHLOROPHYLLS CONTENT IN LEAVES OF STRAWBERRY PLANTS TREATED WITH UV-C RADIATION Moreno,MB; Crizel,GR; Leite,TB; Cantillano,RFF; Rombaldi,CV;	Agronomy
024	INFLUENCE OF SEPTORIA LEAF BLOTCH ON WHEAT YIELD AND PROTEIN ACCUMULATION UNDER N APPLICATIONS ON GRAINS IN DIFFERENT POSITIONS IN THE SPIKE Simón,MR; Liaudat,JP; Fleitas,AC; Castro,AC; Schalamuk,SJ;	Agronomy
025	EFFECT OF CANOLA SPATIAL PLANT ARRANGEMENTS ON THE LEAF AREA INDEX AND PRODUCTIVITY Bandeira,TP; Chavarria,G;	Agronomy
026	AGRONOMIC TRAITS OF THE HYBRID CANOLA HYOLA 61 UNDER DIFFERENT PLANT ARRANGEMENTS Bandeira,TP; Chavarria,G;	Agronomy



Poster Session

07th

Tuesday

	Title and Authors	Area
027	EXPANSINS EXPRESSION IN WHEAT GRAINS AFFECTED BY HIGH TEMPERATURE Lizana,XC; Calderini,DF;	Agronomy
028	CD AND ZN CONCENTRATION IN FLAX AND DURUM WHEAT ARE AFFECTED BY LONG-TERM PHOSPHORUS FERTILIZATION AND SOIL CHARACTERISTICS Grant,CA; Gao,X; Flaten,DN; Tenuta,M; Akinremi,W; Malhi,SS;	Agronomy
029	CANOLA RESPONSE TO N FERTILIZATION AS AFFECTED BY PRECEDING CROP AND LOCATION Grant,CA; Gao,X; Odonovan,JT; Zebarth,B; Blackshaw,RE; Lafond,GP; Harker,KN;Johnson,EN; Gan,Y;	Agronomy
030	BUILDING ALBERTA'S BIOECONOMY: USING BIOMASS IN INNOVATIVE WAYS Blade,SF;	Agronomy
031	RADIATION INTERCEPTION BY A CASSAVA (<i>Manihot esculenta</i>) CROP IN A DRY ENVIRONMENT Ogola,JBO; Mathews,C;	Agronomy
032	EFFECT OF GREEN MANURE LEGUME ROTATION WITH MAIZE ON SELECTED SOIL CHEMICAL PROPERTIES Odhiambo,JJO;	Agronomy
033	CAN AFRICAN SOILS SUPPLY A CRITICAL NEED OF SILICA FOR SUSTAINABLY INCREASING RICE YIELDS? Tsujiimoto,YT; Muranaka,SM; Saito,KS; Asai,HS;	Agronomy
034	COMBINED EFFECT OF MEPIQUAT CHLORIDE AND TRINEXAPAC-ETYL ON OIL COMPOSITION, SEED YIELD AND ENDOGENOUS GIBBERELLIN IN FLAX Kim,SANGKUK; Choi,HONGJIB;	Agronomy
035	HIDRIC STATUS IN MAIZE PLANTS AS A FUNCTION OF NO TILLAGE SOIL MANAGEMENT Dalmago,GA; Faganello,A; Denardin,JE; Fochesatto,E; Santi,A;	Agronomy
036	SUGRACANE PRODUCTION IN LOWLANDS PLANTED OVER RIDGES MADE WITH A RICE'S LEVEE-PLOW Theisen,G; Fipke,MV; Reis,A; Bonow,JFL; Silva,SDA;	Agronomy
037	KNIFE-ROLLER: A METHOD FOR LESS SOIL-DISTURBANCE IN GROUND LEVELING AT LOWLANDS PADDIES Theisen,G; Bonow,JFL; Fipke,MV; Silva,JJC; Vernetti-Junior,FJ;	Agronomy
038	SPACE ARRANGEMENTS AND CONSORTIUM IN THE INITIAL DEVELOPMENT OF JATROPHA CULTURE Heiffig-Aguila,LS; Gallo,PB; Saavedra-Aguila,J;	Agronomy
039	MORPHO-PHYSIOLOGICAL TRAITS OF SOYBEAN CULTIVAR NS4823-RR UNDER WATER DEFICIT IN GREENHOUSE ENVIRONMENT Zilio,M; Souza,CA; Correa,C; Stefen,DLV; Ataide,RCN; Sponchiado,JC; Coelho,CMM;	Agronomy



Poster Session

07th

Tuesday

	Title and Authors	Area
040	YIELD COMPONENTS OF SOYBEAN CULTIVAR NS4823-RR UNDER WATER STRESS IN GREENHOUSE ENVIRONMENT Zilio,M; Souza,CA; Werner,F; Sponchiado,JC; Tormem,ME; Zanesco,PR;	Agronomy
041	PRODUCTIVITY AND SANITY OF CACAO (<i>Theobroma cacao</i> L.) GENOTYPES IN THE CENTRAL ECUADORIAN COAST Sánchez-Mora,SMFD; Garces-Fiallos,Garcés, F.R.; Vera-Chang,Vera, Ch.J.;Ramos-Remache,Ramos, R.R.; Medina-Jara,Medina, S.M.;	Agronomy
042	CURCUMIN AND MINERAL CONTENTS OF TURMERIC (<i>CURCUMA LONGA</i> L.) AT DIFFERENT GROWTH STAGES IN OKINAWA, JAPAN Hossain,MA; Akamine,H; Ichiro,N; Tamaki,M;	Agronomy
043	Maize (<i>Zea mays</i> L.) performance under competition with C4 weed species Soufizadeh,Saeid; AghaAlikhani,Majid; Bannayan,Mohammad; Zand,Eskandar;Hoogenboom,Gerrit; M. Manschadi,Ahmad;	Agronomy
044	EVALUATION OF DROUGHT TOLERANCE INDICES AND THEIR RELATIONSHIP WITH GRAIN YIELD OF WHEAT GENOTYPES Ehteshami,SEYEDMOHAMMADREZA; Ebrahimzadeh,MOHAMMADREZA;	Agronomy
045	DEPARTMENT OF AGROECOLOGY, ENVIRONMENTAL SCIENCES RESEARCH INSTITUTE, SHAHID BEHESHTI UNIVERSITY Deihimfard,REZA; Nassiri,MEHDI; Koocheki,ALIREZA;	Agronomy
046	EFFECT OF NITROGEN TOPDRESSING ASSOCIATED WITH THE PLANT GROWTH RETARDANT ON YIELD OF WHEAT CV MIRANTE Stefen,DLV; Souza,CA; Cechinel,MH; Ataide,RCN; Tormem,ME; Werner,F;	Agronomy
047	ALTERATION IN THE CRUDE PROTEIN OF WHEAT GRAINS DUE TOPDESSING NITROGEN ASSOCIATED WITH PLANT GROWTH RETARDANT Stefen,DLV; Souza,CA; Cechinel,MH; Ataide,RCN; Tormem,ME; Zanesco,PR;	Agronomy
048	EVALUATION OF FUNGICIDE TREATMENT FOR FUSARIUM HEAD BLIGHT SUPPRESSION IN SPRING WHEAT Santana,FMS; Cargnin,AD;	Agronomy
049	SURVEY OF FUNGI IN CROP RESIDUES ON SOILS UNDER DIFFERENT MANAGERMENTS. Santana,FMS; Cargnin,AD; Dalmago,GAD; Clebsch,CCC; Kovaleski,MK;	Agronomy
050	INHERITANCE OF RESISTANCE TO NET BLOTCH (<i>DRECHSLERA TERES</i>) IN A BARLEY RANDOM INBRED POPULATION Santana,FMS; Minella,EM; Cargnin,AC; Clebsch,CCC; Kovaleski,MK;	Agronomy
051	AGRONOMY ENGINEER Leão,PCS; Lima,MAC; Silva,SF; Trindade,DCG;	Agronomy
052	GROWTH RESPONSE OF WINTER WHEAT (<i>TRITICUM AESTIVUM</i> L.) TO WARMING WITH DIFFERENT DIURNAL TEMPERATURE RANGES UNDER FIELD CONDITIONS IN EAST CHINA Zhang,WJ;	Agronomy



Poster Session

07th

Tuesday

	Title and Authors	Area
053	CANOLA YIELD, PROTEIN AND OIL CONTENT UNDER DIFFERENTS DENSITIES AND ROW SPACING Pedersen,AC; Santos,FL; Rodrigues,VM; Astolfi,E; Tomm,GO; Chavarria,G;	Agronomy
054	DETECTION OF RALSTONIA SOLANACEARUM IN POTATO TUBERS Figueiró,AA; Duarte,V;	Agronomy
055	CUTTING THE ABOVEGROUND PARTS OF HAIRY VETCH ENHANCES N UPTAKE OF THE MIXED-CROPPED OAT GROWN AS GREEN MANURES Arata-Tarui,AT; Atsushi-Matsumura,AM; Hiroyuki-Daimon,HD;	Agronomy
056	CYTOTOXICITY OF AQUEOUS EXTRACT OF TROMBETEIRA ANTHERS ON LETTUCE SEEDS Silva-Fernandes,B; Auler,PA; Soares-Lopes,MR; Saleh-Ribeiro,M; Gomes-Rocha,BH;	Agronomy
057	TREATMENT OF SEEDS OF ZEA MAYS WITH VEGETAL REGULATORS AND MINERAL NUTRIENTS Cossa,CA; Sorace,MAF; Osipe,R; Campos,FG; Camolese,AC; Villela,TT; Castro,IR;Troost,ME;	Agronomy
058	EFFECT OF THE INOCULATION IN THE INITIAL DEVELOPMENT OF SOYBEAN (GLYCINE MAX) Cossa,CA; Sorace,MAF; Osipe,R; Campos,FG; Camolese,AC; Villela,TT; Castro,IR;UENP-CLM;	Agronomy
059	BIOSTIMULANT AND COMMERCIAL INOCULANT IN THE GLYCINE MAX PRODUCTION Cossa,CA; Sorace,MAF; Osipe,R; Campos,FG; Camolese,AC; Villela,TT; Castro,IR;Troost,ME; Tashima,H;	Agronomy
060	GENETIC UNIFORMITY OF MORPHOLOGICAL CHARACTERISTICS AND CYTOGENETIC ANALYSIS OF BRAZILIAN WHEAT CULTIVARS Scariot,G; Brammer,SP; Scheeren,PL; Castro,RL;	Agronomy
061	DESICCATION TIMING OF VETCH AND ITS EFFECTS ON MAIZE CROP. Borba-Menezes,G; Régis-Ferreira,P+A1:C166; Correia,S; Menagati,G; Barreto-Maass,M;Soares-Guterres,B;	Agronomy
062	SEEDLINGS PRODUCTION OF YELLOW MOMBIN (SPONDIAS MOMBIN L.) GROWN ON SUBSTRATES OF AGROFORESTRY RESIDUES Lima,MLB; Lima,AA; Carvalho,CAC; Lima,LA; Beber,PM; Paiva,AV;	Agronomy
063	INFLUENCE OF EXHAUSTED SUBSTRATE OF PLEUROTUS SP. ON MELOIDOGYNE JAVANICA Faria,MV; Ferreira,SGM; Dallemole-Giaretta,R; Faria,CMDR; Botelho,RV;	Agronomy
064	INFLUENCE OF THE NITROGEN ON THE YIELD AND QUALITY OF THE WHEAT GRAIN Pereira,T; MANTOVANI,A; DRUM,G; DURLI,MM; MATHIAS,V;	Agronomy
065	PRODUCTIVITY AND QUALITY OF BEAN GRAINS (PHASEOLUS VULGARIS L.) IN FUNCTION OF DOSE AND TIME OF NITROGEN APPLICATION Bones,LF; Coelho,CMM; Pereira,T; Durli,MM; Mantovani,A;	Agronomy
066	COMPARATIVE OF FUNGICIDES FOR SEED TREATMENT OF WHEAT Carvalho-Nathalia,NLC; Camera-Juliane,JNC; Ranzi-Camila,CR; Bonini-Cleiton,CLB;Guths-Guilherme,GG;	Agronomy



Poster Session

07th

Tuesday

	Title and Authors	Area
067	VIRULENCE OF CERCOSPORA SOJINA ISOLATES IN SOY Camera-Juliane,JNL; Carvalho-Nathália,NLC; Deuner-Carolina,CCD;	Agronomy
068	PATHOGENICITY OF THREE RACES OF CERCOSPORA SOJINA IN SOY Camera-Juliane,JNC; Carvalho-Nathalia,NLC; Deuner-Carolina,CCD;	Agronomy
069	MORPHOLOGICAL CHANGES IN ROOTS OF PISUM SATIVUM L. INOCULATED WITH PREINCUBATED RHIZOBIA WITH NARINGENIN Satori-Nakamura,SN; Atsushi-Matsumura,AM; Hiroyuki-Daimon,HD;	Agronomy
070	MORPHI-AGRONOMIC CHARACTERIZATION OF SYNTHETIC WHEATS ACCESSIONS (TRITICUM DURUM X AEGILOPS TAUSCHII) Teixeira,T; Toniazco,C; Brammer,SP; Cargnin,A;	Agronomy
071	EVALUATION OF THE EFFECTS OF CULTIVARS AND NUTRITIONAL ENVIRONMENTS ON DYNAMICS OF LEAF AREA INDEX OF RICE BY USING PLANT CANOPY ANALYZER Hirooka,Y; Homma,K; Shiraiwa,T; Kuwada,M;	Agronomy
072	INITIAL GROWTH OF JATROPHA CURCAS L. AS A FUNCTION OF SOURCES AND DOSES OF ORGANIC FERTILIZERS Lima,MLB; Ruppenthal,V; Schulz,DG; Fradoloso,JF; Fey,R; Zoz,T; Lana,MC;	Agronomy
073	EFFECTS OF STONE MULCH ON WATER USE AND GRAIN YIELD IN WHEAT GROWN UNDER SOIL WATER DEFICIT STRESS Inagaki,MN;	Agronomy
074	EFFECTS OF LEAF REMOVAL AND TOPPING ON YIELD AND QUALITY OF GRAPE 'SYRAH' IN THE SÃO FRANCISCO VALLEY, NORTHEAST BRAZIL. Leão,PCS; Lima,MAC; Silva,SF; Trindade,DCG;	Agronomy
075	IMPROVEMENT OF COLOR OF CRIMSON SEEDLESS GRAPE BY PLANT REGULATORS IN THE SÃO FRANCISCO VALLEY, NORTHEAST BRAZIL. Leão,PCS; Lima,MAC; Santos,FC; Trindade,DCG;	Agronomy
076	GROWING QUINOA UNDER HARSH CONDITIONS IN WADI EL-NATROON REGION, EGYPT. Shams,AS;	Agronomy
077	AGRONOMIC EFFECTS ON IRRIGATED SPRING WHEAT UNDER CONSERVATION AGRICULTURE USING PERMANENT RAISED BED IN NORTHWEST CHINA Ma,ZHM;	Agronomy
078	GROWTH AND YIELD OF NERICA4 UNDER FIELD CONDITIONS IN SUDAN Samejima,H; Babiker,AGT; Yagoub,SO; Sugimoto,Y;	Agronomy
079	INVESTIGATION OF SUPERIOR PARENTS AND HYBRID COMBINATIONS IN RESPECT TO KAPAS YIELD AND YIELD ATTRIBUTING CHARACTERS AND FORMING HETEROTIC BOXES FOR EXPLOITATION IN COTTON (GOSSYPIMUM HIRSUTUM L.) Alkuddsi,YANAL;	Crop Breeding & Genetics
080	MAPPING AND VALIDATION OF QSPP7, A QTL CONTROLLING SPIKELETS PER PANICLE USING NIL FROM AN INTERSPECIFIC CROSS IN RICE Balkunde,SG; Le,Hung Linh; Lee,Hyun-Sook;	Crop Breeding & Genetics



Poster Session

07th

Tuesday

	Title and Authors	Area
081	BRS SATURNO – TRITICALE CULTIVAR Nascimento-Jr,ANJ; Sôe-Silva,MSS; Caierão,EC; Luiz-Scheeren,PLS;	Crop Breeding & Genetics
082	EXPANDING PHOTOSYNTHETIC RSEM_CROP MODELS WITH NDVI COMPARISON BETWEEN MODIS AND SPOT FOR YIELDS IN CONTINENTAL REGIONS Kaneko,D; Kumakura,T;	Crop Breeding & Genetics
083	LARGE-SCALE CHARACTERIZATION OF DROUGHT PATTERN: CURRENT AND FUTURE TRENDS IN THE AUSTRALIAN WHEATBELT Chenu,K; Chapman,SC;	Crop Breeding & Genetics
084	ENHANCING CROP PRODUCTIVITY IN SEVERELY WATER-LIMITED ENVIRONMENTS – AN EXAMPLE OF PEARL MILLET IMPROVEMENT IN INDIA Yadav,OP;	Crop Breeding & Genetics
085	CONTRIBUTION OF MORPHO-PHYSIOLOGICAL DESCRIPTORS ON DETERMINATION OF GENETIC DISSIMILARITY IN RICE GENOTYPES Streck,EA; Magalhães-Jr,AM; Fagundes,PRR; Franco,DF; Severo,ACM; Fonseca,GM; Aguiar,GA; Lopes,JL; Oliveira,FA;	Crop Breeding & Genetics
086	FOURTY YEARS OF WHEAT BREEDING ACTIVITIES AT IAPAR, BRAZIL Riede,CR; Campos,LAC; Scholz,MBS; Okuyama,LA; Garbuglio,DD;	Crop Breeding & Genetics
087	A MIXED-MODEL APPROACH FOR SELECTION OF SUPERIOR SUGARCANE VARIETIES USING PEDIGREE INFORMATION Freitas,EG; Pastina,MM; Garcia,AAF;	Crop Breeding & Genetics
088	GENETIC VARIABILITY IN A F2 SOYBEAN POPULATION FOR TRAITS ASSOCIATED WITH RESISTANCE TO STINK BUG COMPLEX Bermudez,FP; Moller,M; Santos,MF; Rocha,F; Ferreira,M; Baldin,JP;	Crop Breeding & Genetics
089	PARTICIPATORY SELECTION OF BLACKBERRY RUBUS GLAUCUS BENTH IN THE NORTH EASTERN REGION OF COLOMBIA, SOUTH AMERICA Cancino-Escalante,GO; Quevedo-Garcia,E; Villamizar,CE; Díaz-Carvajal,C;	Crop Breeding & Genetics
090	ESTIMATION OF GENETIC AND PHENOTYPIC PARAMETERS FOR FRUIT TRAITS IN A FULL-SIB FAMILY OF SWEET PASSION FRUIT USING MIXED MODELS Pereira,GS; Gazaffi,R; Nunes,ES; Laperuta,LC; Geraldi,IO; Vieira,MLC; Garcia,AAF;	Crop Breeding & Genetics
091	OVERCOMING SELF-INCOMPATIBILITY IN PASSIFLORA EDULIS SIMS BY CHEMICAL TREATMENT OF STIGMAS Madureira,HCM; Pereira,TNSP; Cunha,MC;	Crop Breeding & Genetics
092	GENETIC VARIATION IN A MAIZE POPULATION OF RILS: II- HERITABILITY STUDY OF THE ECO-PHYSIOLOGICAL DETERMINANTS OF KERNEL WEIGHT. Piedra,C; Bender,R; Dandrea,K; Cerri,A; Cirilo,A; Otegui,M;	Crop Breeding & Genetics
093	AGRONOMIC TRAITS AND PHOTOSYNTHETIC CHARACTERISTICS OF THE CHLOROPHYLL-DEFICIENT WHEAT MUTANT MT6172 DERIVED FROM SPACEFLIGHT MUTAGENESIS Guo,HJ; Zhao,HB; Zhao,LS; Gu,JY; Zhao,SR; Li,JH; Liu,LX;	Crop Breeding & Genetics
094	GENOTYPIC VARIATION FOR BRITTLE-SNAP SUSCEPTIBILITY IN MAIZE (ZEA MAYS L.): PHENOTYPING OF STALK BREAKAGE AND RELATED TRAITS IN A RILS POPULATION Rodriguez,JG; Kussrow,N; Pirchi,IL; Cirilo,AG; Cerri,AM; Otegui,ME;	Crop Breeding & Genetics



Poster Session

07th**Tuesday**

	Title and Authors	Area
095	NOVEL GRAPE CULTIVARS ADAPTED TO BRAZILIAN GROWTH CONDITIONS SUITABLE FOR QUALITY-WINE PRODUCTION Ritschel,P; Almeida-Camargo,UAC; Garcia-Maia,JD; Zanus,MC; Guerra,CC;	Crop Breeding & Genetics
096	NOVEL BRAZILIAN GRAPE CULTIVARS FOR JUICE PROCESSING Ritschel,P; Camargo,UA; Maia,JGG; Zanus,MC;	Crop Breeding & Genetics
097	IDENTIFICATION OF QTL ASSOCIATED WITH TASSEL AND FLOWERING TRAITS IN CORN Wietholter,P; Terra,TF; Fuller,TN; Rodrigues,JA; Tessele,C; Sereno,MJCM; Barbosa-Neto,JA;	Crop Breeding & Genetics
098	REACTION OF IRRIGATED RICE GENOTYPES TO BIOLOGICAL NITROGEN FIXATION Fagundes,PRR; Mattos,MLT; Magalhães-Júnior,AM; Severo,ACM; Azambuja,VV;Krunst-Júnior,E;	Crop Breeding & Genetics
099	RICE BIOTECHNOLOGY: HOW CAN WE FEED THE BILLIONS? Zhang,Q;	Crop Breeding & Genetics
100	ARTIFICIAL HYBRIDIZATION IN GÉRBERA: SEED FORMATION AND SEGREGATION OF THE OBTAINED PROGENY Cardoso,RDL; Milach,SCK; Grando,MF; Augustin,L; Susin,M; Scorteganha,A; Machado,C;	Crop Breeding & Genetics
101	PERFORMANCE SCORE AS A TOOL FOR CHOICE AND SELECTION OF WHEAT CULTIVARS Castro,RL; Caierão,E; Silva,MS; Scheeren,PL; Cargnin,A; Moresco,ER; Guarienti,EM;Miranda,MZ;	Crop Breeding & Genetics
102	RESISTANCE OF SEEDLESS TABLE GRAPES CULTIVARS AND SELECTIONS TO DOWNY MILDEW Naves,RL; Ritschel,P; Santana,APS; Camargo,UA; Maia,JDG;	Crop Breeding & Genetics
103	POLYMERIC PROTEINS AND THEIR ASSOCIATION WITH GRAIN YIELD IN HARD RED SPRING WHEAT LINES Tsilo,TJ; Hareland,GA; Ohm,JB; Anderson,JA;	Crop Breeding & Genetics
104	EVALUATION OF SOME EXOTIC DURUM WHEAT (TRITICUM DURUM DESF.) GENOTYPES IN EGYPT 2. CORRELATION AND PATH COEFFICIENT ANALYSIS OF GRAIN YIELD RELATED TO YIELD COMPONENTS Abd El-Ghany,HM; Ibrahim,MM; El-Gharbawy,MM;	Crop Breeding & Genetics
105	SOLATION AND EXPRESSION PATTERN CHARACTERIZATION OF TWO COTTON (GOSSYPIUM HIRSUTUM) FLOWER-SPECIFIC PROMOTERS Lambret-Frotté,JS; Artico,S; Nardeli,SM; Grossi-Sa,F; Alves-Ferreira,M;	Crop Breeding & Genetics
106	INVESTIGATING DIFFERENCES IN RESPONSE TO RHIZOCTONIA SOLANI AG 8 IN THE DIVERSE WILD BRACHYPODIUM DISTACHYON POPULATION TO DISCOVER MECHANISMS FOR RESISTANCE TO RHIZOCTONIA ROOT ROT IN WHEAT. Schneebeli,K; Chochois,V; Mathesius,U; Watt,M;	Crop Breeding & Genetics
107	RELATIONSHIP BETWEEN NORMALIZED DIFFERENCE VEGETATION INDEX (NDVI) AND GRAIN YIELD IN WINTER WHEAT UNDER TERMINAL HEAT STRESS Sharma,R; Hazratkulova,S; Alikulov,S; Yuldashev,T; Khalikulov,Z; Ziyadullaev,Z; Turok,J;	Crop Breeding & Genetics



Poster Session

07th**Tuesday**

	Title and Authors	Area
108	INDIRECT SELECTION OF OAT GENOTYPES (AVENA SATIVA L.) IN RESPONSE TO IRON STRESS Danielowski,R; Peters,JA; Kavalko,SAF; Nornberg,R; Costa-Oliveira,A; Maia,LC;	Crop Breeding & Genetics
109	PHENOTYPIC AND MOLECULAR ANALYSIS IN SEGREGATING POPULATION (F2) WHITE OATS FOR THE CONTENT OF B-GLUCAN IN GRAIN Silveira,SFS; Oliveira,DCS; Crestani,M; Luz,VK; Viana,T; Wolter,DD; Zimmer,CM;Feguedo,R; Gutkoski,LC; Maia,LC; Oliveira,AC;	Crop Breeding & Genetics
110	MOLECULAR CHARACTERIZATION OF JATROPHA CURCAS ACCESSIONS Galli,V; Kneib,RB; Borowsky,JM; Silva,SDA;	Crop Breeding & Genetics
111	GENETIC VARIABILITY OF SACCHARUM SPP. USING SSR MARKERS Galli,V; Kneib,RB; Silva,SDA;	Crop Breeding & Genetics
112	MAIZE LANDRACES WITH POTENTIAL TO ZEAXANTHIN BIOFORTIFICATION Galli,V; Labonde,J; Borowsky,J; Silva,SDA; Messias,RS;	Crop Breeding & Genetics
113	GENERAL ABILITY COMBINING FOR YIELD COMPONENTS OF F1 AND F2 HYBRIDS WHEAT EVALUATED IN TWO ENVIRONMENTAL CONDITIONS Hagemann,TR; Grol,EL; Barretta,D; Lemes-Silva,C; Capelin,MA; Benin,G; Costa-Oliveira,A;	Crop Breeding & Genetics
114	ESTIMATES GENETIC AND GENERAL COMBINING ABILITY OF YIELD IN SEGREGATING POPULATIONS OF SPRING WHEAT Capelin,MA; Hagemann,TR; Munaro,LB; Sassi,LHS; Dalló,SC; Oliveira,L; Benin,G;Costa-Oliveira,A;	Crop Breeding & Genetics
115	CORRELATION AND PATH COEFFICIENT ANALYSIS OF YIELD COMPONENTS IN COTTON (GOSSYPIMUM HIRSUTUM L.) Alkuddsi,YANAL;	Crop Breeding & Genetics
116	DEVELOPMENT OF HIGH GRAIN PROTEIN AND LYSINE RICH GENOTYPES IN RICE Bangalorechannappa,Dr Keshava Murthy;	Crop Breeding & Genetics
117	HYBRID BREEDING IN BRAZILIAN SPRING WHEAT: HETEROSIS FOR YIELD AND ITS COMPONENTS Beche,E; Capelin,MA; Munaro,LB; Silva,CL; Pagliosa,ES; Benin,G;	Crop Breeding & Genetics
118	MORPHOLOGICAL AND AGRONOMIC TRAITS OF THREE ARROWLEAF CLOVER POPULATIONS Bortolini,F; Duarte,JG; Mittelman,A; Rosa,TC; Pires,ES;	Crop Breeding & Genetics
119	HETEROSIS STUDIES INVOLVING COMPACT AND ROBUST PLANT TYPES FOR YIELD AND YIELD COMPONENTS IN COTTON (Gossypium hirsutum L.) Alkuddsi,YANAL;	Crop Breeding & Genetics
120	GENETIC DIVERSITY EVALUATION OF TRITICUM TAUSCHII ACCESSES USING MICROSATELLITES MARKERS Bonato,ALV; Brammer,SP; Almeida,AB; Cordeiro,MCR;	Crop Breeding & Genetics
121	GRAIN YIELD PATH ANALYSIS IN WHEAT CULTIVARS GROWN IN PELOTAS Kavalko,SAF; Figueiredo,RG; Zimmer,CM; Santos,RL; Danielowski,R; Luche,H; Maia,LC;Oliveira,AC;	Crop Breeding & Genetics



Poster Session

07th

Tuesday

	Title and Authors	Area
122	DIALLEL ANALYSIS IN WHEAT GENOTYPES SUBJECTED TO FLOODING STRESS Kavalco,SAF; Tessmann,EW; Figueiredo,RG; Groli,EL; Zimmer,CM; Santos,RL; Nornberg,R;Maia,LC; Oliveira,AC;	Crop Breeding & Genetics
123	JAPANESE UPLAND RICE BREEDING AND YIELD FORMATION FRAMEWORK FOR IMPROVEMENT OF DROUGHT RESISTANCE IN RICE Kamoshita,A;	Crop Breeding & Genetics
124	GENETIC DIVERGENCE AMONG GLOBE ARTICHOKE CLONES Reolon-Costa,A; Grando,MF; Cravero,VP; Morlin,B;	Crop Breeding & Genetics
125	MAPPING QTLs FOR MESOCOTYL ELONGATION IN WEEDY RICE Lee,HYUNSOOK; Kang,JUWON;	Crop Breeding & Genetics
126	CHARACTERISTICS OF EARLY HEADING RICE (ORYZA SATIVA L.) LINES DERIVED FROM GAMMA-RAY IRRADIATION Ryu,JAIHYUNK; So,HYUNSU; Lyu,JAEL; Bae,CHANGHYU;	Crop Breeding & Genetics
127	LARGE-SCALE EXPRESSION OF GENES INVOLVED IN JASMONATES BIOSYNTHESIS IN COFFEE PLANTS INFESTED WITH LEAF MINER Cardoso,DC; Martinati,JC; Giachetto,PF; Guerreiro-Filho,O; Vidal,RO; Carazzolle,MF;Maluf,MP;	Crop Breeding & Genetics
128	GENETIC STABILITY IN BRAZILIAN WHEAT CULTIVARS DETERMINED BY POLLEN VIABILITY Urio,EA; Brammer,SP; Cargnin,A;	Crop Breeding & Genetics
129	VIABILITY OF TOTAL POLLEN IN POTATO DIPLOID CLONES AND FREQUENCY OF 2N POLLEN AFTER COLD STORE Savoldi,M; Bock,JL; Almeida,N; Suzin,M; Augustin,L;	Crop Breeding & Genetics
130	ESTIMATE OF HETEROSIS AND INBREEDING DEPRESSION FOR CHARACTER FALLING NUMBER WET IN WHEAT Nornberg,R; Luche,HS; Tessmann,EW; Olivo,M; Zimmer,CM; Figueiredo,R; Maia,LC; Costadeoliveira,A;	Crop Breeding & Genetics
131	QTL DETECTION FOR LIPID CONTENT IN BROWN RICE OF A HIGH-LIPID RICE Kim,NH; Kim,TH; Sohn,JK;	Crop Breeding & Genetics
132	DETECTION OF QUANTITATIVE TRAIT LOCI (QTL) ASSOCIATED WITH RESISTANCE TO WHITE BACKED PLANTHOPPER USING DOUBLED HAPLOID POPULATION IN RICE Kim,THK; Sohn,JKS;	Crop Breeding & Genetics
133	BREEDING BIOFORTIFIED COMMON BEAN CULTIVARS AT IAPAR Moda-Cirino,V; Pavan,MA; Sousa,RA;	Crop Breeding & Genetics
134	SELECTING PARENTAL WHEAT LINES BY DNA MARKERS AIMING TO INCREASE THE GENETIC DIVERSITY AND THE LEVEL OF RESISTANCE TO LEAF RUST IN BRAZILIAN GERmplasm Casassola,AC; Brammer,SP; Chaves,MS; Caierão,E; Wietholer,P;	Crop Breeding & Genetics
135	GENETIC DISTANCE AMONG WHITE OAT CULTIVARS (AVENA SATIVA L.) IN RESPONSE TO MANGANESE STRESS Tessmann,EW; Nornberg,R; Luche,HS; Kavalco,SAF; Zimmer,CM; Groli,EL; Maia,LC;Costa-Oliveira,A;	Crop Breeding & Genetics



Poster Session

07th

Tuesday

	Title and Authors	Area
136	ADAPTIVE TRAITS IN OAT BREEDING IN BRAZIL Luche,HS; Olivo,M; Nornberg,R; Kavalco,SAF; Tessmann,EW; Santos,RL; Silva,JAG;Maia,LC; Oliveira,CA;	Crop Breeding & Genetics
137	VARIABILITY FOR AGRONOMICALLY IMPORTANT TRAITS IN RICE MUTANT FAMILIES Luz,VK; Fonseca,GM; Groli,EL; Neves,CG; Figueiredo,R; Baretta,D; Silveira,SFS; Kopp,MM;Magalhães-Júnior,AM; Maia,LC; Oliveira,AC;	Crop Breeding & Genetics
138	PRODUCTION OF DOUBLED HAPLOID LINES FOR THE EMBRAPA BARLEY BREEDING PROGRAM IN BRAZIL – A SHORTCUT FOR THE DEVELOPMENT OF NEW VARIETIES Scagliusi,SM; Minella,E;	Crop Breeding & Genetics
139	BREEDING COTTON GENOTYPES FOR THE NEEDS OF ORGANIC SITUATION IN DEVELOPING COUNTRIES Patil,SS; Roner,TINA; Baruah,RAJEEV; Ambatipudi,ARUN; Messmer, MONICA;Forster,DIONYS;	Crop Breeding & Genetics
140	DEVELOPMENT OF HETEROTIC GROUPS BASED ON THE PERFORMANCE OF CROSSES Rajeev,S; Patil,SS; Ranganath,HM; Swathi,P; Pranesh,KJ; Pooja,VGOANKAR;	Crop Breeding & Genetics
141	GERMINATION POTENTIAL OF HALF-SIB PROGENIES OF GLOBE ARTICHOKE Reolon-Costa,A; Grando,MF; Cravero,VP; Didoné,S; Satori,G; Barbosa,D;	Crop Breeding & Genetics
142	TARGET GENOTYPE BASED CHOICE OF BREEDING METHODS IN VARIETAL DEVELOPMENT OF SELF POLLINATED CROPS Patil,SS; Manjula,MS; Rajeev,SUNDAR; Kenchareddi,HG;	Crop Breeding & Genetics
143	GENETIC CORRELATION” A REFINED LEVEL OF DETERMINING ASSOCIATION OF QUANTITATIVE CHARACTERS IN COTTON Ranganath,HM; Patil,SS; Rajeev,S; Manjula,SM;	Crop Breeding & Genetics
144	DEVELOPMENT AND EXPLOITATION OF HETEROTIC GROUPS IN COTTON Patil,SS; Manjula,SM; Rajeev,S; Pranesh,KJ; Ranganath,HM; Swathi,P; Pooja,VGOANKAR;	Crop Breeding & Genetics
145	EVALUATION OF STRAINS OF IRRIGATED RICE AS TO THE TOXICITY OF IRON. Almeida-Aguiar,G;	Crop Breeding & Genetics
146	RECOVERY OF PHENOLIC COMPOUNDS OF RICE BRAN. Christ-Ribeiro,A; Costa-Bretanha,C; Giacobbo-Luz,G; Moraes-Souza,M; Badiale-Furlong,E;	Crop Ecology, Management & Quality
147	QUANTIFICATION OF DEOXYNIVALENOL IN WHEAT USING NEAR INFRARED REFLECTANCE SPECTROSCOPY Tibola,CS; Fernandes,JMC; Bernardi,CMG;	Crop Ecology, Management & Quality
148	DETECTION OF DEOXYNIVALENOL IN WHEAT SAMPLES USING CHROMATOGRAPHIC AND SCREENING METHODS Tibola,CS; Lukow,OM; Adams,K; Tittlemier,SA; Fernandes,JMC;	Crop Ecology, Management & Quality
149	WINTER COVER CROPS TO PADDY RICE SUSTENTABILITY Luz-Correia,S; Boeni,M; Silva,PRF; Anghinoni,I; Carmona,GI; Maass,MB;	Crop Ecology, Management & Quality



Poster Session

07th

Tuesday

	Title and Authors	Area
150	DRIS NORMS RELATED TO SOYBEAN GRAIN OIL CONTENT Castamann,A; Escosteguy,PAV; Berres,D; Zanella,S;	Crop Ecology, Management & Quality
151	HOW MUCH IS TOO MUCH: A SYSTEM ANALYSIS ON PRODUCTIVITY AND NITROGEN INTENSITY OF THE WHEAT-MAIZE SYSTEM IN NORTH CHINA PLAIN Liang,WL; Carberry,P; Chen,F; Whish,J; Wang,GY; Li,RX; Xia,AP;	Crop Ecology, Management & Quality
152	RELATIONSHIP BETWEEN WHEAT GLUTEN COLOR AND WHEAT QUALITY: PRELIMINARILY RESULTS Miranda,MZ; Caetano,VR; Scheeren,PL; Tiggemann,L; Tatsch,P; Oro,T;	Crop Ecology, Management & Quality
153	SOLVENT RETENTION CAPACITY TEST DETERMINED BY NEAR INFRARED LIGHT TECHNOLOGY TO INVESTIGATE WHEAT QUALITY PERFORMANCE Miranda,MZ; Tibola,CS; Bordignon,JR; Delanora,R; Elkhouri,M; Pieri,FLZ; Tatsch,PO;Guarienti,EM; Caierão,E;	Crop Ecology, Management & Quality
154	EFFECTS OF PLASTIC FILM MULCHES ON SOIL TEMPERATURE AND MOISTURE AND WATERMELON PRODUCTION IN GRAVEL-MULCHED LAND IN SEMIARID AREA Zhongming,ZHM;	Crop Ecology, Management & Quality
155	THE EFFECTS OF LATITUDE CHANGE TO GROWTH DURATION AND HEADING DATE OF RICE ACCORDING TO RIPENING ECOTYPE AND TRANSPLANTING TIME IN KOREA Ku,BONIL; Choi,MINKYU; Kang,SHINGU; Sang,WANKYU; Park,HONGKYU; Kim,YOUNGDOO;Kim,BOKYEONG;	Crop Ecology, Management & Quality
156	PECTINASE AND AMYLASE PRODUCTION BY RHIZOPUS ORYZAE E TRICHODERMA REESEI FERMENTATION UTILIZATING RICE HUSK AND BRAN Mendes,GL; Kupski,L; Silvello,MAC; Lima,TS; Fontes,MRV; Garda-Bufferon,J;Badiale-Furlong,E;	Crop Ecology, Management & Quality
157	PROMISING ANTIFUNGAL EFFECT OF PHENOLICS EXTRACTED FROM SPIRULINA ON FUSARIUM GRAMINEARUM GROWTH Mendes,GL; Pagnussatt,FA; Filoda,PF; Darley,F; Delponte,EM; Garda-Bufferon,J;Badiale-Furlong,E;	Crop Ecology, Management & Quality
158	ENZYMATIC PROFILE AND INHIBITOR FRACTION FROM SEVERAL WHEAT VARIETIES (TRITICUM AESTIVUM L.) Mendes,GL; Pagnussatt,FA; Leal,CA; Badiale-Furlong,E;	Crop Ecology, Management & Quality
159	PHOTO-MORFOGENIC PROCESS REGULATED BY B-PHYTOCHROMES AND THEIR EFFECTS ON PLANT-TO-PLANT VARIABILITY OF MAIZE (ZEA MAYS.L) CROPS Wies,G; Maddonni,GA;	Crop Ecology, Management & Quality
160	DETECTION OF FUSARIUM MYCOTOXIN IN WHEAT GRAIN USING FLUORESCENCE FINGERPRINT Fujita,K; Tsuta,M; Sugiyama,J; Nakagawa,H; Yoshimura,M; Kokawa,M; Shibata,M;	Crop Ecology, Management & Quality
161	EFFECT OF RESIDUAL ROOT N OF FABA BEAN ON THE GROWTH, YIELD AND N UPTAKE OF THE SUCCEEDING TURMERIC (CURCUMA LONGA L.) CROP Yamawaki,K; Hattori,R; Matsumura,A; Hossain,MA; Daimon,H;	Crop Ecology, Management & Quality
162	DIAGNOSIS OF RICE GROWTH AND NITROGEN NUTRITION STATUS USING DIGITAL CAMERA IMAGE ANALYSIS Lee,KJ; Choi,DW; Park,SJ; Lee,BW;	Crop Ecology, Management & Quality



Poster Session

07th

Tuesday

	Title and Authors	Area
163	ANALYSIS OF SOIL ORGANIC CARBON AND RICE YIELD, QUALITIES IN 21 YEARS NO-TILL AND TILLAGE PADDY FIELD Youngmin-Jin,JYM;	Crop Ecology, Management & Quality
164	DETERMINATION OF MYCOTOXINS PRODUCED BY FUSARIUM GRAMINEARUM IN PRESENCE AND ABSENCE OF ESTROBIRULINS FUNGICIDES Heidtmann-Bemvenuti,R; Nora,NS; Kraide,LE; Manetti,KO; Badiale-Furlong,E;	Crop Ecology, Management & Quality
165	MEASURE OF GLUCOSAMINE AND ERGOSTEROL AS AN INDICATOR OF INHIBITION OF FUSARIUM GRAMINEARUM BY ESTROBIRULIN FUNGICIDES Heidtmann-Bemvenuti,R; Nora,NS; Kraide,LE; Manetti,KO; Badiale-Furlong,E;	Crop Ecology, Management & Quality
166	COUPLING REMOTE SENSING DATA WITH CROPGRO-SOYBEAN MODEL TO IMPROVE YIELD MONITORING Park,SJ; Ban,HY; Ahn,SJ; Choi,DH; Lee,BW;	Crop Ecology, Management & Quality



Poster Session

09th

Friday

	Title and Authors	Area
001	DIFFERENCES IN GRAIN YIELD GENERATION BETWEEN WHEAT AND BARLEY Abeledo,LG; Alzueta,I; Miralles,DJ;	Crop Physiology and metabolism
002	Effect of Selenium Levels on Antioxidant Enzymes under Drought Stress in Sunflower Soleimanzadeh,H;	Crop Physiology and metabolism
003	EFFECTS OF DROUGHT STRESS ON RADIATION USE EFFICIENCY AND YIELD OF WINTER CANOLA (BRASSICA NAPUS L.) Vafabakhsh,J; Nassiri-Mahallati,M; Koocheki,A;	Crop Physiology and metabolism
004	HOW HIGH TEMPERATURE AFFECTS WHEAT GROWTH AND DEVELOPMENT Chenu,K; Oudin,F; Chapman,SC; Dreccer,MF; Hammer,GL;	Crop Physiology and metabolism
005	EFFECT OF STROBILURIN PYRACLOSTROBIN IN THE RATE OF CARBON ASSIMILATION, NITRATE REDUCTASE ACTIVITY AND YIELD OF SOYBEAN Schwantes,AP; Dourado-Neto,D; Fagan,EB; Rodrigues,MAT; Martins,KV; Galdi,G;	Crop Physiology and metabolism
006	PHYSIOLOGICAL CHARACTERIZATION OF STROBILURIN PYRACLOSTROBIN ACTION ON GAS EXCHANGE IN CORN AND SOYBEAN Schwantes,AP; Dourado-Neto,D; Fagan,EB; Rodrigues,MAT; Martins,KV; Lacerda,MP;	Crop Physiology and metabolism
007	GENE EXPRESSION CHANGES ASSOCIATED WITH WOOLLINESS PREVENTION IN PEACH, FOLLOWING PRE-HARVEST APPLICATION OF GIBBERELIC ACID Pegoraro,C; Tadiello,A; Chaves,FC; Trainotti,L; Oliveira,AC; Rombaldi,CV;	Crop Physiology and metabolism
008	MOLECULAR MECHANISMS INVOLVED IN PARTIAL CROWN RUST RESISTANCE IN OAT Figueiró,AA; Reese,N; Gonzalez,J; Pacheco,MT; Delatorre,CA;	Crop Physiology and metabolism
009	SEARCHING FOR ALUMINUM-TOLERANCE MECHANISMS IN AVENA SATIVA Delatorre,CA; Schneider,AB; Hervé,CB; Islamovic,E; Jackson,EW;	Crop Physiology and metabolism
010	ROOT DIVERSITY ANALYSIS OF MAIZE INBRED LINES AND HYBRIDS UNDER LOW AND HIGH PHOSPHORUS Matos,FM; Meirelles,WF; Negri,BF; Mendes,FF; Moreira-Guimarães,LJ; Parentoni,SN;Vidigal-Filho,PS; Sousa,SM;	Crop Physiology and metabolism
011	PHYSIOLOGICAL RESPONSE OF SOYBEAN PLANTS IN VEGETATIVE AND REPRODUCTIVE PHASES TO STROBILURIN PYRACLOSTROBIN APPLICATION Brendler,FB; Dourado-Neto,D; Fagan,EB; Rodrigues,MAT; Martins,KV; Lacerda,MP;	Crop Physiology and metabolism
012	PHYSIOLOGICAL CHARACTERIZATION OF STROBILURIN PYRACLOSTROBIN ACTION ON GAS EXCHANGE IN COTTON Oliveira,FB; Dourado-Neto,D; Fagan,EB; Rodrigues,MAT; Martins,KV; Soares,LH; Lacerda,MP;	Crop Physiology and metabolism
013	SPIKE FERTILITY INDEX IN WHEAT: TRAIT PERFORMANCE UNDER DIFFERENT CROP GROWTH CONDITIONS Gonzalez,FG; Terrile,II;	Crop Physiology and metabolism
014	WATERLOGGING IN WHEAT AND BARLEY AND ITS EFFECT ON GRAIN YIELD GENERATION De-Sanceledonio,R; Abeledo,LG; Miralles,DJ;	Crop Physiology and metabolism



Poster Session

09th

Friday

	Title and Authors	Area
015	ROOT MORPHOLOGICAL ANALYSIS OF A MAIZE DIVERSITY PANEL Magalhães,KS; Negri,BF; Desousa,SM;	Crop Physiology and metabolism
016	INFLUENCE OF DEFOLIATION LEVELS IN THE YIELD COMPONENTS OF SOYBEAN Martins,KV; Dourado-Neto,D; Fagan,EB; Rodrigues,MAT; Soares,LH; Schwantes,AP;	Crop Physiology and metabolism
017	PHYSIOLOGICAL EFFECTS OF PYRACLOSTROBIN (STROBILURIN) APPLICATION IN SOYBEAN FACTORS PRODUCTION Martins,KV; Dourado-Neto,D; Fagan,EB; Rocrigues,MAT; Soares,LH; Oliveira,FB; Galdi,G;	Crop Physiology and metabolism
018	MORPHOLOGICAL CHARACTERISTICS AND FUNCTIONAL DIFFERENTIATION OF AMYLOPLASTS IN TUBERS OF YAMS Kawasaki,MICHIO; Yoshida,HAYURU; Takahashi,KYOKO;	Crop Physiology and metabolism
019	NUTRIENT UPTAKE AND UPTAKE EFFICIENCY OF WHEAT AT DIFFERENT DEVELOPMENT STAGES UNDER SOIL ALUMINUM TOXICITY AT FIELD CONDITIONS Valle,SR; Pinochet,D; Calderini,DF;	Crop Physiology and metabolism
020	PHYSIOLOGICAL RESPONSES OF SOYBEAN PLANTS AT DIFFERENT GROWTH STAGES UNDER DROUGHT STRESS Xu,C; Yuan,Y; Xu,KZ; Zhang,P; Ji,P; Zhao,LP;	Crop Physiology and metabolism
021	CHANGES OF ROOT ACTIVITY AND ITS CORRELATION WITH BIOMASS OF ABOVE-GROUND ORGANS OF SOYBEAN CULTIVARS RELEASED IN DIFFERENT YEARS Ji,JP; Xu,XKZ; Yang,YCW; Xu,XC; Feng,FYD; Zhang,ZP;	Crop Physiology and metabolism
022	STUDY ON THE CHANGES OF SOYBEAN DIFFERENT NODE SOURCE-SINK RELATIONSHIP IN DIFFERENT YEAR Feng,FYD; Xu,XKZ; Yang,YCW; Xu,XC; Ji,JP; Zhang,ZP;	Crop Physiology and metabolism
023	POST FLOWERING TEMPERATURE AFFECTS YIELD AND OIL CONTENT IN CANOLA (<i>Brassica napus</i> L.). Vilarinho,MP; Rondanini,DP; Miralles,DJ;	Crop Physiology and metabolism
024	EFFECT OF FOLIAR APPLICATION OF A NATURAL BIOSTIMULANT IN MAIZE AMINO ACID COMPOSITION Leão,PCS; Lima,MAC; Santos,FC; Trindade,DCG;	Crop Physiology and metabolism
025	INFLUENCES OF PROTON BEAM IRRADIATION ON EARLY GROWTH AND PASTING PROPERTIES OF STARCH IN RICE Kim,SK; Kim,KR; Kim,HY;	Crop Physiology and metabolism
026	CHARACTERIZATION OF SOME BAF/UDESC COMMON BEAN LANDRACES TO ALUMINUM AND LOW PH IN SAND CULTURE WITH NUTRIENT SOLUTION Souza,CA; Tormem,ME; Zanesco,PR; Zilio,M; Faccin,TR; Stefen,DLV; Coelho,CMM;	Crop Physiology and metabolism
027	EFFECT OF GROWTH RETARDANT ON WHEAT CV. ONIX PLANT MORPHOLOGIC ATTRIBUTES AND ITS YIELD COMPONENTS Souza,CA; Zanesco,PR; Tormem,ME; Zilio,M; Stefen,DLV; Faccin,TR; Coelho,CMM;	Crop Physiology and metabolism
028	PRODUCTION AND CHEMICAL COMPOSITION OF THE ESSENTIAL OIL OF <i>Artemisia annua</i> L. VARIETY ARTEMIS SUBMITTED A NPK FERTILIZATION LEVELS Paladini,MV; Capelin,D; Marchese,JA; Marques,MOM;	Crop Physiology and metabolism



Poster Session

09th

Friday

	Title and Authors	Area
029	PRODUCTION AND CHEMICAL COMPOSITION OF THE ESSENTIAL OIL OF ARTEMISIA ANNUA L. VARIETY ARTEMIS ELICITED WITH ACIBENZOLAR-S-METHYL AND HARPIN PROTEIN Paladini,MV; Capelin,D; Marchese,JA; Marques,MOM;	Crop Physiology and metabolism
030	EVALUATION OF YIELD POTENTIALITY AND STABILITY IN G.HIRSUTUM COTTON VARIETIES IN INDIA Patil,BC; Pawar,KN; Babu,AG; Shaheen,AB;	Crop Physiology and metabolism
031	RELATIONSHIP BETWEEN GRAIN WEIGHT AND SPIKE FERTILITY INDEX IN WHEAT Gonzalez,FG; Gazaba,LN; Terrile,II;	Crop Physiology and metabolism
032	DAILY VARIABLE MICRO-CLIMATE AFFECTED ON RUBBER PRODUCTION Chantuma,PISAMAI;	Crop Physiology and metabolism
033	PLANT GROWTH REGULATOR AND DENSITY: EFFECTS ON THE LEAF AREA INDEX OF CORN Pedersen,AC; Mello,N; Giacomini,R; Chavarria,G;	Crop Physiology and metabolism
034	BIOCHEMICAL MECHANISMS INVOLVED IN PARTIAL CROWN RUST RESISTANCE IN OAT Figueiró,AA; Reese,N; Gonzalez,J; Pacheco,MT; Delatorre,CA;	Crop Physiology and metabolism
035	PROTEOMIC ANALYSIS OF ZEA MAYS VARIETY DKB240 INOCULATED WITH AZOSPIRILLUM BRASILENSE Fp2 Faleiro,AC; Espíndula,E; Pereira,TP; Arisi,ACM;	Crop Physiology and metabolism
036	GROWTH RESPONSE AND NITROGEN USE EFFICIENCY OF HIGH YIELD JAPONICA RICE TO VARIABLE NITROGEN FERTILIZATION Kang,SG; Hassan,MS; Park,HG; Choi,MK; Ku,BI; Kim,YD; Park,TS; Kim,BK;	Crop Physiology and metabolism
037	PARTIAL ROOTZONE DRYING IN SUGARCANE: EFFECTS ON GROWTH AND PHOTOSYNTHETIC CAPACITY Ribeiro,MS; Campostrini,E; Couto,TR; Netto,AT; Nogueira,RJMC;	Crop Physiology and metabolism
038	KERNEL GROWTH AND QUALITY TRAITS OF MAIZE HYBRIDS WITH DIFFERENT END-USE AT CONTRASTING POST-FLOWERING THERMAL ENVIRONMENTS Mayer,LI; Ordóñez,RA; Savin,R; Cirilo,AG; Maddonni,GA;	Crop Physiology and metabolism
039	INTER-PLANT VARIABILITY OF PLANT GROWTH AND DEVELOPMENT OF CONVENTIONAL AND TRANSGENIC MAIZE HYBRIDS Laserna,MP; López,CG; Maddonni,GA;	Crop Physiology and metabolism
040	PHYSIOLOGICAL TRAITS LINKED BY TOLERANCE TO FOLIAR DISEASES IN BREAD WHEAT (TRITICUM AESTIVUM L.) Serrago,RA; Lo-Valvo,PJ; Miralles,DJ;	Crop Physiology and metabolism
041	GRAIN WEIGHT RESPONSE TO FOLIAR DISEASES CONTROL IN WHEAT CROPS WITH DIFFERENT SOURCE-SINK RATIO Lo-Valvo,PJ; Serrago,RA; Miralles,DJ;	Crop Physiology and metabolism
028	ANALYSIS OF THE PHYSIOLOGICAL QUALITY AND EVALUATION OF ENZYMATIC ACTIVITY OF CATALASE AND SUPEROXIDE DISMUTASE IN CASTOR BEAN SEEDS (RICINUS COMMUNIS L.) CV BRS ENERGY IRRADIATED WITH CO-60 Ebeling-Viana,V; Moreira-Lopes,A; Anjos-Silva,SD; Bobrowski,VL; Deuner,S;	Crop Physiology and metabolism



Poster Session

09th

Friday

	Title and Authors	Area
043	COTTON LEAF GAS EXCHANGE AS AFFECTED BY LEAF AGE AND PHOTOSYNTHETIC PHOTON FLUX DENSITY Rosolem,CA; Echer,FR; Werle,R; Sirtoli,L; Rodrigues,JD;	Crop Physiology and metabolism
044	LOCALIZATION OF REACTIVE OXYGEN SPECIES AND CHANGE OF ANTIOXIDANTS IN MESOPHYLL AND BUNDLE SHEATH CHLOROPLASTS OF MAIZE UNDER SALINITY Omoto,E; Nagao,H; Taniguchi,M; Miyake,H;	Crop Physiology and metabolism
045	HEAT STRESS IN TEMPERATE AND TROPICAL MAIZE HYBRIDS: KERNEL WEIGHT DETERMINATION Rattalino-Edreira,JI; Otegui,ME;	Crop Physiology and metabolism
046	PHENOTYPES AND GENES ASSOCIATED WITH ROOT TRAITS UNDERLYING PHOSPHORUS ACQUISITION EFFICIENCY IN MAIZE Desousa,SM; Clark,RT; Mendes,FF; Oliveira,AC; Kochian,LV; Vasconcelos,MJV;Parentoni,SN; Guimarães,CT; Magalhães,JV;	Crop Physiology and metabolism
047	EFFECTS OF STROBILURIN PYRACLOSTROBIN ON ANTIOXIDANTS ENZYMES IN SOYBEAN Lacerda,MP; Dourado-Neto,D; Fagan,EV; Rodrigues,MAT; Martins,KV; Soares,LH;	Crop Physiology and metabolism
048	INFLUENCE OF STROBILURIN PYRACLOSTROBIN ON HORMONE LEVELS IN SOYBEAN Lacerda,MP; Dourado-Neto,D; Fagan,EB; Rodrigues,MAT; Martins,KV; Soares,LH;	Crop Physiology and metabolism
049	PLANT PHENOLOGY OF SOYBEAN GENOTYPES CULTIVATED FROM SEPTEMBER TO FEBRUARY IN SOUTH BRAZIL Strieder,ML; Bertagnolli,PF; Pires,JLF; Cunha,GR;	Crop Physiology and metabolism
050	FENUGREEK: A POTENTIAL LEGUME FOR MULTIPURPOSE USE Islam,MA; Krall,JM; Cecil,WK; Nachtman,JJ; Baumgartner,RE; Bandara,M; Acharya,S;	Forage & Grazing Lands
051	STEM ELONGATION OF ELEPHANT GRASS SUBJECTED TO STRATEGIES OF ROTATIONAL STOCKING MANAGEMENT Pereira,LET; Silva,SC; Paiva,AJ; Santos,TM; Geremia,EV; Vicente,SF; Oliveira,LP;	Forage & Grazing Lands
052	GROWTH AND ROOT:SHOOT DRY MATTER PARTITIONING IN SEEDLING LUCERNE (MEDICAGO SATIVA L.) DIFFER WITH SOWING DATE AND WATER AVAILABILITY Sim,RE; Moot,DJ; Brown,HE; Teixeira,El;	Forage & Grazing Lands
053	DRYING METHODS AND THE CHEMICAL COMPOSITION OF CATTLE EXTRUSA SAMPLES Vicente,SF; Da-Silva,SC; Paiva,AJ; Geremia,EV; Santos,TM; Pereira,LET; Oliveira,LP;	Forage & Grazing Lands
054	INFLUENCE OF CATTLE EXCRETA PATCHES ON SOIL ACIDITY IN RANGELAND OF SOUTHERN BRAZIL Soares,ABS; Viccini,RV; Assmann,TSA;	Forage & Grazing Lands
055	BEEF HEIFERS PERFORMANCE GRAZING WARM-SEASON GRASS PASTURES IN SOUTHERN BRAZIL Glienke,CLG; Rocha,MGR; Potter,LP;	Forage & Grazing Lands
056	INFLUENCE OF GRAZING AND NITROGEN LEVELS OVER BLACK OAT NITROGEN RELEASE ON CROP-LIVESTOCK SYSTEM Assmann,TS; Caldas,TS; Assmann,AL; Adami,PF;	Forage & Grazing Lands



Poster Session

09th

Friday

	Title and Authors	Area
057	CONTENT OF NUCLEAR DNA IN BRACHIARIA SPECIES ASSESSED BY FLOW CYTOMETRY Chiari,L; Carvalho,CR; Valle,CB; Simeão,RM; Jank,L; Barrios,SCL; Alves,GF;	Forage & Grazing Lands
058	AVALIAÇÃO BROMATOLÓGICA DE GENÓTIPOS DE MILHO UTILIZADOS PARA SILAGEM Sonia-Santos,SS; Newton-Martin,TN; Patricia-Bertoncelli,PB; Piran-Filho,FA;Luiz-Habitzreiter,TL; Grolli-Carvalho,AF;	Forage & Grazing Lands
059	CARACTERIZAÇÃO MORFOLÓGICA E PARTIÇÃO DE MATÉRIA SECA DE GENÓTIPOS DE MILHO UTILIZADOS PARA SILAGEM Sonia-Santos,SS; Newton-Martin,TN; Patricia-Bertoncelli,PB; Piran-Filho,FA; Luiz-Habitzreiter,TL; Grolli-Carvalho,AF;	Forage & Grazing Lands
060	AVALIAÇÃO MORFOLÓGICA, PRODUTIVA E PARTIÇÃO DE MATÉRIA SECA DE GENÓTIPOS DE MILHO UTILIZADOS PARA SILAGEM Sonia-Santos,SS; Newton-Martin,TN; Patricia-Bertoncelli,PB; Piran-Filho,FA;Luiz-Habitzreiter,TL; Grolli-Carvalho,AF;	Forage & Grazing Lands
061	WHITE CLOVER ROOTS PRODUCTION AND NODULATION SUBMITTED TO BORON LEVELS Assmann,AL; Rodrigues-Silva,M; Assmann,TS; Soares,AB;	Forage & Grazing Lands
062	IN SILICO SEARCH FOR CIS REGULATORY ELEMENTS IN THE PROMOTER REGION OF AGAMOUS GENE IN ORYZA SATIVA Guerra,G; Silva,GJ; Maia,LC; Oliveira,AC;	Genomics, Molecular Genetics and Biotechnology
063	STRATEGY FOR IDENTIFICATION OF CIS REGULATORY ELEMENTS RESPONSIBLE FOR EXPRESSION PATTERNS IN RICE Silva,GJ; Guerra,G; Maia,LC; Costadeoliveira,A;	Genomics, Molecular Genetics and Biotechnology
064	STRATEGY FOR IDENTIFICATION OF CIS REGULATORY ELEMENTS RESPONSIBLE FOR EXPRESSION PATTERN IN DEVELOPMENT OF RICE WITH ESTRESS CONDITION Silva,GJ; Pegoraro,C; Maia,LC; Costa-Oliveira,A;	Genomics, Molecular Genetics and Biotechnology
065	OSPDI IS A CRITICAL FACTOR IN ENDOSPERM AND ALEURONE LAYER DEVELOPMENT Kim,YJ; Choi,SH; Kim,SI; Koh,HJ; Seo,HK;	Genomics, Molecular Genetics and Biotechnology
066	CBL-INTERACTING PROTEIN KINASE 1 FROM BRASSICA RAPA ENHANCED MULTIPLE ABIOTIC STRESS TOLERANCE IN RICE Abdula,SE; Lee,HJ; Jee,MG; Jang,DW; Kang,KK; Cho,YG;	Genomics, Molecular Genetics and Biotechnology
067	SELECTION OF SOYBEAN PROMOTERS RELATED TO DROUGHT RESPONSE IN ROOT Jordano-Conforte,AJ; Guimarães-Dias,FG; Giovanella-Kampmann,LG; Neves-Borges,AC; Bencke,MB; Alves-Ferreira,MA;	Genomics, Molecular Genetics and Biotechnology
068	IDENTIFICATION OF CONSERVED AND NOVEL MIRNAS IN DEVELOPING BRASSICA NAPUS SEEDS BY DEEP SEQUENCING Korbes,AP; Machado,RD; Guzman,F; Almerão,MP; De-Oliveira,LFV; Loss,G;Turchetto-Zolet,AC; Cagliari,A; Maraschin,FS; Margis-Pinheiro,M; Margis,R;	Genomics, Molecular Genetics and Biotechnology
069	COMPREHENSIVE PREDICTION OF MIRNA TARGETS INVOLVED IN LIPID METABOLISM OF BRASSICA NAPUS Machado,RD; Korbes,AP; Loss,G; Turchetto-Zolet,AC; Cagliari,A; Maraschin,FS; Margis-Pinheiro,M; Margis,R;	Genomics, Molecular Genetics and Biotechnology
070	CHARACTERIZATION OF A NOVEL MEMBER OF THE SOYBEAN UREASE GENE FAMILY Wiebke-Strohm,B; Ligabue-Braun,R; Homrich,MS; Pasquali,G; Bodanese-Zanettini,MH;	Genomics, Molecular Genetics and Biotechnology



Poster Session

09th

Friday

	Title and Authors	Area
071	GERMINATION AND DEVELOPMENT OF SOYBEAN IS AFFECTED BY UREASE ABSENCE Rechenmacher,C; Wiebke-Strohm,B; Bodanese-Zanettini,MH;	Genomics, Molecular Genetics and Biotechnology
072	DATA MINING OF GENES RESPONSIVE TO DROUGHT IN COFFEA ARABICA USING EST LIBRARIES Silva,FSP; Azevedo,F; Nobres,P; Loh,R; Alves-Ferreira,M; Patreze,CM;	Genomics, Molecular Genetics and Biotechnology
073	CONSTRUCTION OF PLASMID FOR GENETIC TRANSFORMATION IN RICE AND TOMATO AIMING AT TOLERANCE TO DIFFERENT ABIOTIC STRESSES Pegoraro,C; Kruger,MM; Santos,RS; Margis,MMANP; Maia,LC; Rombaldi,CV; Oliveira,AC;	Genomics, Molecular Genetics and Biotechnology
074	SEARCHING FOR ALUMINUM-TOLERANCE MECHANISMS IN <i>Avena sativa</i> Delatorre,CA; Schneider,AB; Hervé,CB; Islamovic,E; Jackson,EW;	Genomics, Molecular Genetics and Biotechnology
075	THE SEQUENCING OF ORYZA GLUMAEPATULA STEUD. Farias,DR; Chaparro,C; Maia,LC; Barbosa-Neto,JF; Panaud,O; Oliveira,AC;	Genomics, Molecular Genetics and Biotechnology
076	TEMPERATURE STRESS EFFECT DURING INFECTION OF MAIZE IMMATURE EMBRYO BY AGROBACTERIUM TUMEFACIENS EHA101:PTF102 Silva,MR; Didoné,DA; Almeida,VO; Torres,B; Ceccon,CC; Suzin,M; Grando,MF;	Genomics, Molecular Genetics and Biotechnology
077	GENETIC TRANSFORMATION OF COWPEA WITH THE GENE OF METHIONINE-RICH DELTA-ZEIN FROM MAIZE Citadin,CT; Andrade,ER; Aragão,FJL;	Genomics, Molecular Genetics and Biotechnology
078	EPIGENETIC REGULATION IN DIFFERENT GENOTYPES OF SUGARCANE SUBMITTED TO DROUGHT STRESS Thiebaut,F; Tanurdzic,M; Grativol,C; Vieira,T; Vincentini,R; Hemerly,AS; Martienssen,RA;Ferreira,PCG;	Genomics, Molecular Genetics and Biotechnology
079	ALLELIC VARIATION IN THE TAALMT1 PROMOTER REGION AND ALUMINIUM RESISTANCE IN A BRAZILIAN WHEAT COLLECTION Pereira,JF; Barichello,D; Aguilera,JG; Consoli,L; Silva-Júnior,JP;	Genomics, Molecular Genetics and Biotechnology
080	IDENTIFICATION AND PRELIMINARY PROMOTER ANALYSIS OF SOYBEAN GENES INDUCED UNDER DROUGHT STRESS IN LEAVES Giovannella-Kampmann,L; Jordano-Conforte,A; Guimarães-Dias,F; Neves-Borges,A;Bencke,M; Alves-Ferreira,M;	Genomics, Molecular Genetics and Biotechnology
081	THE EFFECT OF COLD AND 2-HNA (2 HYDROXY-NICOTINIC ACID) TREATMENTS ON ISOLATED MICROSPORE CULTURE AND ANDROGENIC RESPONSE OF DIFFERENT BRAZILIAN WHEAT GENOTYPES Poersch,LB; Scagliusi,SM; Lau,EY; Bodanese-Zanettini,MH;	Genomics, Molecular Genetics and Biotechnology
082	EXPRESSION PROFILE OF SUGARCANE ETHYLENE SIGNALING GENES DURING DROUGHT STRESS IN RESPONSE TO INOCULATION WITH BENEFICIAL DIAZOTROPHIC BACTERIA Vargas,L; Rojas,C; Ferreira,PCG; Hemerly,AS;	Genomics, Molecular Genetics and Biotechnology
083	SOYBEAN WRKY FAMILY ANNOTATION AND FUNCTIONAL CHARACTERIZATION OF GENES INVOLVED IN THE RESPONSE TO PHAKOPSORA PACHYRHIZI Bencke,M; Wiebke-Strohm,B; Bucker-Neto,L; Mancini,E; Osorio,MB; Homrich,MS;Carvalho,MCCG; Stolf,R; Margis-Pinheiro,M; Weber,RLM; Cabreira,C; Westergaard,G;Marcelino-Guimarães,FC; Abdelnoor,RV; Bodanese-Zanettini,MH;	Genomics, Molecular Genetics and Biotechnology
084	LOCATION OF THE RESISTANCE TO TAN SPOT IN WHEAT Simón,MR;	Genomics, Molecular Genetics and Biotechnology



Poster Session

09th

Friday

	Title and Authors	Area
085	GENETIC SIMILARITY AMONG RACES OF PUCCINIA TRITICINA, CAUSAL AGENT OF WHEAT LEAF RUST, OCCURRING IN SOUTHERN BRAZIL Wietholter,P; Brammer,SP; Moras,A; Chaves,MS;	Genomics, Molecular Genetics and Biotechnology
086	TRANSCRIPT EXPRESSION EVALUATE FROM EXPRESSED SEQUENCE TAG AND GENES ASSOCIATED TO FLORAL SENESCENCE IN GERBERA Cardoso,RDL; Jiang,CZ; Donnelly,L; Milach,SCK; Grando,MF;	Genomics, Molecular Genetics and Biotechnology
087	FUNCTIONAL CHARACTERIZATION OF MADS-BOX GENES OF GOSSYPIUM HIRSUTUM INVOLVED IN THE OVULE AND FRUIT DEVELOPMENT Moura,SM; Nardeli,SM; Artico,S; Lambret Frotte,JS; Brilhante,O; Grossi-de-Sá,MF;Alves-Ferreira,M;	Genomics, Molecular Genetics and Biotechnology
088	OVEREXPRESSION OF GLUTAMINE SYNTHETASE (GS) IN RICE ENHANCES TOLERANCE TO CADMIUM AND ABIOTIC STRESSES Lee,HJ; Abdula,SE; Jee,MK; Jang,DW; Park,SH; Yoon,UH; Kim,TH; Cho,YG;	Genomics, Molecular Genetics and Biotechnology
089	OVEREXPRESSION OF UDP-GLUCOSE-4-EPIMERASE 1 (UGE1) INCREASES YIELD AND ENHANCED DROUGHT TOLERANCE IN RICE Abdula,SE; Lee,HJ; Jee,MG; Jang,DW; Cho,YG;	Genomics, Molecular Genetics and Biotechnology
090	GENERATION AND ANALYSIS OF EXPRESSED SEQUENCE TAGS IN RYE Ogura,Y; Murata,M;	Genomics, Molecular Genetics and Biotechnology
091	DIACYLGLYCEROL ACETYLTRANSFERASE (DGAT) ENZYMES: A PHYLOGENETIC ANALYSIS AND COMPARATIVE GENE EXPRESSION IN SOYBEAN Turchetto-Zolet,AC; Christoff,AP; Loss,G; Korbes,AP; Cagliari,A; Maraschin,FS; Margis-Pinheiro,M; Margis,R;	Genomics, Molecular Genetics and Biotechnology
092	IDENTIFICATION OF CHROMOSOMAL 1BL.1RS TRANSLOCATION IN WHEAT GENOTYPES BY GENOMIC IN SITU HYBRIDIZATION Brammer,SP; Casassola,A; Volpato,V; Morás,A; Cargnin,A; Almeida,N; Chaves,MS;	Forage & Grazing Lands
093	GLOBAL EXPRESSION ANALYSIS OF A. THALIANA TRANSGENIC LINES OVEREXPRESSING THE COFFEE HOMEBOX GENE CAHB7 RELATED TO INCREASED DROUGHT STRESS TOLERANCE. Loh,R; Alves-Ferreira,M;	Genomics, Molecular Genetics and Biotechnology
094	VALIDATION OF MOLECULAR MARKERS TO STEM RUST RESISTANCE GENES IN BRAZILIAN WHEAT GENOTYPES Casassola,A; Brammer,SP; Chaves,MS; Fagundes,BS; Da-Silva,PR;	Genomics, Molecular Genetics and Biotechnology
095	A SEQUENCE DIVERSITY ANALYSIS OF ACCESSIONS OF COMMON BEAN (PHASEOLUS VULGARIS L.) BASED ON AN IRON REDUCTASE GENE (FRO1) Diniz,AL; Zucchi,MI; Vieira,MLC;	Genomics, Molecular Genetics and Biotechnology
096	IDENTIFICATION OF LESION MIMIC MUTANTS TYPE C2H2 IN SOYBEAN (GLYCINE MAX) Cabreira,C; Cagliari,A; Bucker-Neto,L; Pinheiro-Margis,M; Bodanese-Zanettini,MH;	Genomics, Molecular Genetics and Biotechnology
097	DIFFERENTIAL GENE EXPRESSION RELATED TO LIGNIN CONTENT AND THE TEGUMENT COLOR OF SOYBEAN SEEDS Ramirez-Monzon,DL; Bevilacqua-Borges,C; Maia,LC; Zimmer,PD;	Genomics, Molecular Genetics and Biotechnology
098	PROTOCOL ADJUSTMENT FOR GENETIC TRANSFORMATION OF WHEAT BY AGROBACTERIUM TUMEFACIENS Roesler,EA; Yamazaki-Lau,E;	Genomics, Molecular Genetics and Biotechnology



Poster Session

09th

Friday

	Title and Authors	Area
099	CHARACTERIZATION OF THE PPR_2 GENE IN RESPONSE TO THE PHAKOPSORA PACHYRHIZI INFECTION Castilhos,G; Bucker-Neto,L; Campos,LL; Fonini,LS; Rechenmacher,C; Cabreira,C;Wiebke-Strohm,B; Bodanese-Zanettini,MH; Margis-Pinheiro,M;	Genomics, Molecular Genetics and Biotechnology
100	IDENTIFICATION OF GENES AND MOLECULAR MECHANISM FOR BACTERIAL PUSTULE IN SOYBEAN. Choi,IS; Kim,SY; Kim,YC; Kim,ST;	Genomics, Molecular Genetics and Biotechnology
101	DISCOVERY OF MUNGBEAN SINGLE NUCLEOTIDE POLYMORPHISMS USING NEXT-GENERATION SEQUENCING TECHNOLOGY Van,K; Kang,Y; Han,KS; Jang,HJ; Lee,SH;	Genomics, Molecular Genetics and Biotechnology
102	DOMESTICATION OF SOYBEAN: INVESTIGATION OF GLYCINE MAX AND GLYCINE SOJA DIVERGENCE TIMES USING LOW COVERAGE NGS SEQUENCING Kim,SK; Kang,Y; Yoon,MY; Kim,MY; Van,K; Lee,SH;	Genomics, Molecular Genetics and Biotechnology
103	STUDY ON THE ROLE OF 15 ERFS SUBMITTED TO IRON TOXICITY STRESS Kruger,MM; Pegoraro,C; Santos,RS; Maia,LC; Oliveira,AC;	Genomics, Molecular Genetics and Biotechnology
104	ACCUMULATION OF TRANSCRIPTS OF GENES OF THE TIM/TOM AND TIC/TOC COMPLEXES IN RICE PLANTS UNDER STRESS BY ANOXIA Kruger,MM; Pegoraro,C; Santos,RS; Mertz,LM; Rombaldi,CV; Oliveira,AC;	Genomics, Molecular Genetics and Biotechnology
105	EFFECTS OF HYPOXIA STORAGE ON GENE TRANSCRIPT ACCUMULATION DURING TOMATO FRUIT RIPENING Kruger,MM; Pegoraro,C; Santos,RS; Mandabula,F; Tiecher,A; Maia,LC; Rombaldi,CV;Oliveira,AC;	Forage & Grazing Lands
106	HIGH-RESOLUTION TEMPORAL PROFILING OF TRANSCRIPTS DURING ARABIDOPSIS EXPOSITION TO TO HYDROCARBONS MIXTURE REVEALS A DISTINCT CHRONOLOGY OF PROCESSES AND REGULATION Saad,CF; Nardeli,SM; Wilwerth,MW; Caetano,VS; Alves,MR; Reinert,F; Oliveira,AC; Paes,JES;Peixoto,R; Ferreira,MA;	Genomics, Molecular Genetics and Biotechnology
107	DATA MINING OF CO2 RESPONSIVE GENES IN A. THALIANA AND COFFEE SPECIES Nobres,P; Azevedo,F; Loh,R; Patreze,CM; Alves-Ferreira,M;	Genomics, Molecular Genetics and Biotechnology
108	PROSPECTING EPIGENETIC MARKERS FOR STRESS ANALYSIS USING SIMPLE SEQUENCE REPEATS PRESENT IN RICE GENOME Santos,RS; Kruger,MM; Pegoraro,C; Groli,EL; Maia,LC; Rombaldi,CV; Oliveira,AC;	Genomics, Molecular Genetics and Biotechnology
109	TRANSCRIPTIONAL REGULATION OF 15 ETHYLENE RESPONSE FACTORS IN RICE SHOOTS SUBJECTED TO OXYGEN DEPLETION STRESS Santos,RS; Kruger,MM; Pegoraro,C; Figueiredo,R; Maia,LC; Rombaldi,CV; Oliveira,AC;	Genomics, Molecular Genetics and Biotechnology
110	ETHYLENE RESPONSE FACTORS A STUDY ABOUT SIMILARITIES OF TRANSCRIPTIONAL RESPONSE OF RICE UNDER OXYGEN DEPLETION AND IRON TOXICITY STRESS Santos,RS; Kruger,MM; Pegoraro,C; Figueiredo,R; Maia,LC; Rombaldi,CV; Oliveira,AC;	Genomics, Molecular Genetics and Biotechnology
111	FINE MAPPING OF THE LOW-AMYLOSE CHARACTERISTICS OF RICE CULTIVAR BAEGJINJU Lee,JHL; Shim,JHS; Lee,JYL; Cho,JHC; Song,YCS; Yeo,USY; Oh,MGO; Sohn,JKS; Nam,MHN;	Genomics, Molecular Genetics and Biotechnology



Poster Session

09th

Friday

	Title and Authors	Area
112	MOLECULAR MARKER FOR IRON TOXICITY BASED IN THE POLYMORPHISM OF PROMOTERS AND GENES OF METALLOTHIONEIN FAMILY IN RICE Souza,TM; Finatto,T; Silva,GJ; Guerra,G; Oliveira,AC;	Genomics, Molecular Genetics and Biotechnology
113	AUXIN SIGNALING IN SUGARCANE ROOT GROWTH PROMOTION BY DIAZOTROPHIC BACTERIA Carvalho,TLG; Bomfim,ACJS; Pragana,MLF; Vicentini,R; Baldani,JI; Hemerly,AS;	Genomics, Molecular Genetics and Biotechnology
114	INFLUENCE OF DIFFERENT GROWTH REGULATORS ON SHOOT REGENERATION OF JATROPHA CURCAS L. Lima,MLB; Lima,VSF; Carvalho,CPS; Campos,FAP;	Genomics, Molecular Genetics and Biotechnology
115	DEVELOPMENT OF ECO-FRIENDLY TRANSGENIC CROPS FOR SUSTAINABLE DEVELOPMENT ON MARGINAL LANDS Kim,YH; Kim,MD; Kim,SH; Jeong,JC; Lee,HS; Kwak,SS;	Genomics, Molecular Genetics and Biotechnology
116	TRANSCRIPTIONAL AND METABOLIC PROFILING OF TWO APPLE TREE CULTIVARS CONTRASTING IN CHILLING REQUIREMENT Falavigna,VS; Porto,DD; Anzanello,R; Buffon,V; Souza,DA; Margis-Pinheiro,M; Pasquali,G;Oliveira,PR; Centeno,DC; Santos,HP; Revers,LF;	Genomics, Molecular Genetics and Biotechnology
117	AGROBACTERIUM-MEDIATED TRANSFORMATION OF SOYBEAN VARIATED, BR16, GENE 35S:AREB1, ANALYSIS BY SOUTHERN BLOTING Giroto,L; Soldera,MCA; Marin,SRR; Kanamori,N; Fujita,Y; Yoshida,T;Marcelino-Guimaraes,FC; Yamaguchi-Shinozaki,K; Nepomuceno,AL;	Genomics, Molecular Genetics and Biotechnology
118	REGULATION OF RECEPTOR-LIKE KINASE (RLK) GENE FAMILY RESPONSIVE TO IRON EXCESS IN RICE Woyann,LG; Finatto,T; Tessmann,EW; Maia,LC; Costa-Oliveira,A;	Genomics, Molecular Genetics and Biotechnology
119	EVALUATION OF GRAPEVINE GERMPLASM UNDER TROPICAL CONDITIONS IN BRAZIL Maia,JDG; Camargo,UA; Machado,CAE; Ritschel,P;	Plant Genetic Resources
120	IN VITRO ESTABLISHMENT AND CONSERVATION OF GRAPEVINE GERMPLASM Dalbosco,D; Sinski,I; Comachio,V; Maia,JDG; Fajardo,TVF; Ritschel,PS; Quecini,V;	Plant Genetic Resources
121	ASSESSMENT AND UTILIZATION OF GENETIC DIVERSITY IN LOCAL LANDRACES OF MUNGBEAN (VIGNA RADIATA L. WILCZEK) OF ANDAMAN & NICOBAR ISLANDS, INDIA Singh,AK; Gautam,RK; Sigh,PK; Kumar,N; Kumar,K; Singh,DR;	Plant Genetic Resources
122	GENETIC VARIABILITY IN BRAZILIAN BARLEY FOR GRAIN PRODUCTION Cargnin,A; Minella,E; Santana,F;	Plant Genetic Resources
123	ANALYSIS OF GENETIC DIVERSITY WITHIN POPULATIONS OF RICE LANDRACES FROM YUNNAN USING MICROSATELLITE MARKERS Sun-Jianchang,SUNJIANCHANG; Tengqiong,Y; Cuifeng,T; Guilan,C; Furong,X; Longzhi,H;	Plant Genetic Resources
124	BIOENERGY CHARACTERISTICS IN FIFTY SWITCHGRASS CLONES GROWN ON MARGINAL AND PRIME LAND Cortese,LM; Bonos,SA;	Plant Genetic Resources
125	NITROGEN FERTILIZATION AND SEED PHYSIOLOGICAL QUALITY OF WHEAT Pereira,T; Coelho,CMM; Gmach,JR; Drum,G; Carvalho,CF; Souza,CA;	Seed Physiology, Production & Technology



Poster Session

09th

Friday

	Title and Authors	Area
126	TOLERANTE CULTIVARS TO WATER STRESS BY POLYETHYLENE GLYCOL Carvalho,CF; Coelho,CMM; Delgado,CML;	Seed Physiology, Production & Technology
127	ELECTRICAL CONDUCTIVITY IN SOYBEAN SEEDS WITH DIFFERENT OSMOTIC POTENTIALS Carvalho,CF; Coelho,CMM; Gmach,JR;	Seed Physiology, Production & Technology
128	COMPARATIVE ANALYSIS OF RESISTANCE TO MECHANICAL DAMAGE IN SOYBEANS WITH DIFFERENT COLORS OF TEGUMENT Andrade,ER; Fagioli,M; Pereira,EA;	Seed Physiology, Production & Technology
129	COMPARISON OF GERMINATION OF SEEDS OF SORGHUM BICOLOR IN DIFFERENT LOCATIONS OF MULTIPLICATION IN MINAS GERAIS Padilha,FA; Magalhães,KS; Netto,DAM;	Seed Physiology, Production & Technology
130	ISOZYME EXPRESSION IN SUNFLOWER SEEDLINGS UNDER WATER STRESS Dode,J; Chim,JF; Chaves,FC; Nora,L;	Seed Physiology, Production & Technology
131	THE INFLUENCE OF SPACING IN LINES AND OF COVERAGE NITROGEN FERTILIZATION IN PHYSIOLOGICAL QUALITY OF CORN SEEDS Santos,PJ; Andrade,ER; Sandim,MS; Fagioli,M;	Seed Physiology, Production & Technology
132	PERFORMANCE OF IRRIGATED RICE CULTIVARS IN RESPONSE TO IRON TOXICITY IN HYDROPONIC CULTURE Ahlert,RJ; Mesquita,R; Muller,C; Santos,FIC; Almeida,AM; Maia,LC; Oliveira,AC;	Seed Physiology, Production & Technology
133	AN ARTIFICIAL SOIL CRUST TO ASSESS SEEDLING EMERGENCE UNDER SOIL EROSION Gruber,S; Buehler,A; Claupein,W;	Plant Genetic Resources
134	EFFECT OF PLANT SENESCENCE INDUCTORS ON ELECTRICAL CONDUCTIVITY OF COMMON BEAN SEEDS Ataide,RCN; Souza,CA; Correa,C; Sponchiado,JC; Cechinel,MH; Werner,F; Zanesco,PR;	Plant Genetic Resources
135	COMMON BEAN LANDRACES UNDER COLD STRESS Prezzi,HA; Coelho,CMM; Polli,RG; Heberle,I; Souza,CA;	Plant Genetic Resources
136	EFFECT OF DROUGHT STRESS IN DIFFERENT WHEAT CULTIVARS IN THE UPPER PARANAÍBA REGION Desordi,R; Ribeiro,MDN; Kavalco,SAF; Pazza,R; Kavalco,KF;	Plant Genetic Resources
137	PHYSIOLOGICAL QUALITY OF SAFFLOWER AND CRAMBE SEEDS TREATED WITH BIOSTIMULANT Gonfio,FRP; Zucareli,V; Toledo,MZ;	Plant Genetic Resources
138	GROWTH REGULATORS AND PHYSIOLOGICAL QUALITY OF CRAMBE SEEDS Gonfio,FRP; Toledo,MZ; Zucareli,V;	Plant Genetic Resources
139	MINIMIZING PRE-HARVEST DESICCATION EFFECTS ON SOYBEAN SEED QUALITY WITH BIOESTIMULANTS AND MICRONUTRIENTS Toledo,MZ; Cavariani,C; Bennett,MA; Françaneto,JB;	Seed Physiology, Production & Technology



Poster Session

09th

Friday

	Title and Authors	Area
140	SEEDLING RESPONSE OF RICE PADDY BRAZILIAN CULTIVARS TO IRON PRESENCE Olivo,M; Kavalco,SAF; Baretta,D; Groli,EL; Santos,RL; Magalhães-Junior,AM; Oliveira,AC;Maia,LC;	Seed Physiology, Production & Technology
141	HERBS AND SPICES,ROSMARINUSOFFICINALIS, PIMPINELLAANISUM L., ORIGANUMVULGARE AND ARTEMISIA DRACUNCULUS L.WITH POTENTIALLY HEALTH-BENEFICIAL PHENOLIC CONTENT Dode,J; Chim,JF; Gandra,EA; Zambiasi,RC; Jacques,AC; Chaves,FC;	Biomedical, Health-Beneficial and Nutritionally Enhanced Plants
142	BIOFORTIFICATION OF MAIZE GRAINS WITH FOLIAR APPLICATION OF A NATURAL BIOSTIMULANT Messias,RS; Galli,V; Ávila,LO; Silva,SDA; Schirmer,MA; Rombaldi,CV;	Biomedical, Health-Beneficial and Nutritionally Enhanced Plants
143	COMPARATIVE STUDY OF PETIVERIA ALLIACEA L. AND PHYLLANTHUS NIRURI L. IN RELATION TO THEIR ANTIOXIDANT POTENTIAL Ferrari,AP; Silva,MGF; Bosse,MA; Haminiuk,CWI; Marchese,JA; Cabral,ISR; Carpesa,ST;	Biomedical, Health-Beneficial and Nutritionally Enhanced Plants
144	COMPARATIVE STUDY OF THE ANTIOXIDANT POTENTIAL OF TWO WEEDS Ferrari,AP; Silva,MGF; Bosse,MA; Haminiuk,CWI; Marchese,JA; Cabral,ISR; Carpes,ST;	Biomedical, Health-Beneficial and Nutritionally Enhanced Plants
145	COMPARATIVE STUDY OF THREE METHODS IN RELATION TO THEIR ANTIOXIDANT POTENTIAL OF QUASSIA AMARA L. Ferrari,AP; Silva,MGF; Bosse,MA; Haminiuk,CWI; Marchese,JA; Cabral,ISR; Carpes,ST;	Biomedical, Health-Beneficial and Nutritionally Enhanced Plants
146	DIVERSITY AND CHROMOSOMAL DISTRIBUTION OF LONG INTERSPERSED NON- LTR ELEMENTS (LINES) IN THE A GENOME OF ARACHIS SPECIES Samoluk,S; Carisimo,D; Robledo,G; Seijo,JG;	Plant Genetic Resources
147	DIFFERENTIALLY EXPRESSED GENES UNDERLYING DROUGHT TOLERANCE BETWEEN TWO ELITE RICE VARIETIES Zhang,HAIWEN; Pan,XIAOWU; Huang,RONGFENG;	Genomics, Molecular Genetics and Biotechnology



Tourism



Tourism

ABOUT BENTO GONÇALVES – HISTORY

In 1875, a wave of Italian immigration set the foundation for three colonies at the State's Northeast Upper Coast: Dona Isabel (today Bento Gonçalves), Conde D'eu (today Garibaldi) and Nova Palmira (today Caxias do Sul).

Dona Isabel colony was created in 1870, and became known as Regiao da Cruzinha (Little cross Region), due to a rustic cross stuck over the grave of an ancient tracer of commercial lands. It was barter times, a practice that consisted on the trade of merchandises. The Dona Isabel colony used to be a small trade assemble where the tracers would also rest.

In December 24th, 1875, new immigrants arrived at the Plateau regions and in March, 1876, the State Governor, Jose Antonio de Azevedo Castro, declared the existence of 348 lots of lands measured and marked and a population of 790 people, 729 of which were Italians. Simultaneously, pioneers coming from Austria and Veneto reached the esplanade where today still stands the Cristo Rei Church.

The trade and sale of products took place downtown the colonies, after long walks through the woods trailed by themselves. Carpenters, shoemakers, blacksmiths, tailors, skilled immigrants became able to fulfill the town's needs and established their own business. The expansion of houses, work tools and market development caused the development of the Dona Isabel colony. Due to the development, roads started to improve and the first trucks started to be used. In five years the population expanded to an extra 4 thousand people, including newborns and new immigrants.

In 1881, the first road was inaugurated connecting Dona Isabel colony with Sao Jose de Montenegro colony (today Montenegro). The settlement's beginning faced countless barriers. In 1877, Dona Isabel colony hosted 3 Commercial Houses, 2 Bakeshops, 1 Hat Factory, and 40 other commercial sites that offered many products and services.

The detachment of Dona Isabel colony from the city of Montenegro became official through the "Act" 474, of October 11th, 1890, signed by Candido Costa, which gave birth to Bento Gonçalves town. The town was named after General Bento Gonçalves da Silva, the Farroupilha Revolution's head that took place in Rio Grande do Sul from 1835 to 1845.

Bento Goncalves had its first real boost when 2 banks settled in. From 1919 to 1927 the electricity system was built and the hospital Dc. Bartholomeu Tacchini was inaugurated as well.

In 1950, the population was 22.600 habitants and the main economic activity was agriculture. Many industries were created, like accordions, furniture, leather, dairy, wineries and sulfate factories. In 1967, the city underwent a historical transformation.

The first Fenavinho, the National Wine Festival was made possible because of the support of dynamic leadership and the entire community. For the first time the city was visited by a President, Marshall Humberto de Alencar Castelo Branco.

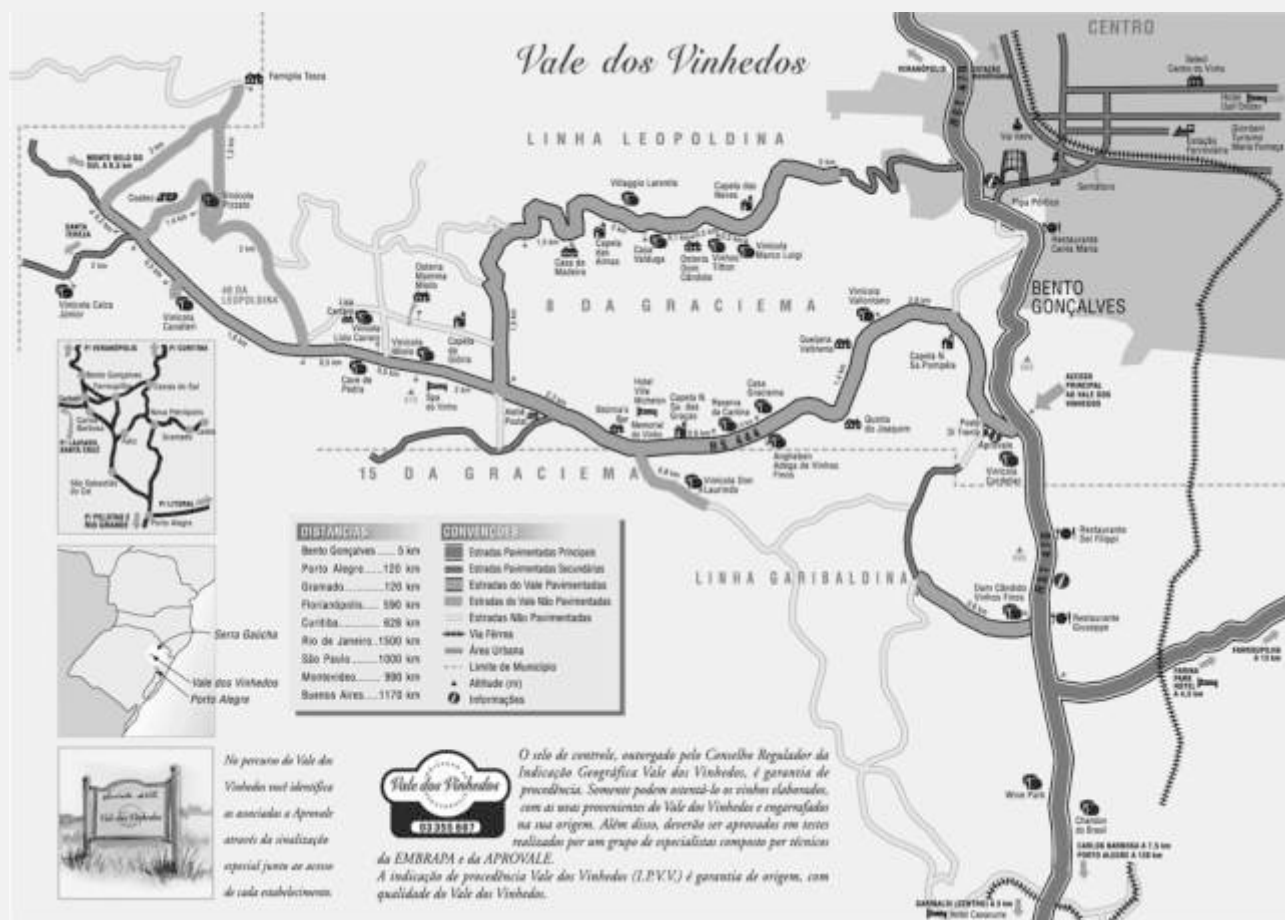
Currently, the town is known as one of the greater furniture poles from the country's south region. The main lodge at the Events' Park with 50.000m² all air-conditioned, is comparable to São Paulo's Anhembi Park. The town is now more than ever an able to host international events.





Tourism

BENTO GONÇALVES – Map





Abstracts



Oral Presentation



3085 - Plant Genetic Resources

Angela Rohr

GENETIC STRUCTURE OF POTATO BREEDING GERMPLASM FROM EMBRAPA

Rohr,A; Castro,CM; Pereira,AS;

UFPEl;

The potato (*Solanum tuberosum* L.) is one of the main staple food in the world. It is cultivated for direct consumption, as well as for processed food products. In potato breeding there is an ongoing challenge to search for cultivars that meet the needs from both markets. Thus, it is essential to potato breeding programs to explore efficiently the genetic variability found in the germplasm available to attend these demands. The objective of this work was to study the genetic structure present in the germplasm from the Embrapa work collection breeding program. One hundred and thirty-one genotypes were characterized with seven microsatellite (SSR) loci. This germplasm comprises cultivars and advanced clones from Brazilian breeding programs, as well as from others countries (Netherlands, Hungary, Argentina, Germany, United States, Peru, Ireland, Canada, India, Chile, France and Italy). In the molecular characterization a total of 28 alleles were identified. The average number of alleles per SSR locus was four, ranging from three to six. The analysis of principal coordinates, based on the dissimilarity matrix generated by the using Jaccard coefficient, showed the two first components explaining 17.03% of the total variation, respectively 10.54% and 6.49%. Although the dispersion of the 131 genotypes in the two first coordinates did not reveal clearly the formation of distinct groups, the cultivars released after 1990 by the Embrapa's potato breeding program were located in the lower portion of the graph, showing a tendency of isolation from the others genotypes. To verify if the genetic variability found in germplasm developed in Brazil is different from that of other countries, an analysis of molecular variance (AMOVA) was performed, which was not significant. It indicates that there is no subdivision in the potato germplasm that was analyzed according to its origin. Based on the results of this study, it can be concluded that although the germplasm of the Embrapa breeding program is not clearly subdivided, considering clustering of the recently released cultivars, there is a trend of narrowing the genetic base that is actually being used by the program.



2877 - Agronomy

Hanmin Yuan

SOIL ENVIRONMENT EFFECT ANALYSIS ABOUT DOUBLE-ZERO-TILLAGE-CROPPING WITH WINTER WHEAT-RICE ROTATION SYSTEM IN YELLOW RIVER NINGXIA BASIN, CHINA

Yuan,HANMIN;

Ningxia Academy of Agriculture and Forestry Sciences;

For the purpose of evaluating soil environment improvement from conservation tillage, soil nutrients, soil textures and diversity of soil microorganisms were tested by Conventional measure, Biology-ECO and Densitometer methods, respectively. The results showed that, compared with traditional farming (CK), soil organic matter, total nitrogen, total phosphorus, available nitrogen and available phosphorus increased 11.9%, 17.1%, 9.2%, 26.5% and 19.1%, respectively, within 0-40 cm depth soil layer after four year double-zero-tillage-cropping in succession with winter wheat-rice rotation system. Meanwhile, total potassium and available potassium decreased 0.9% and 10.2%, respectively. The proportion of clay soil particles increased but proportions of both silt particles and fine silt particles decreased, compared with CK. The metabolic diversity of microorganism function in the soil and its biological activity were significantly greater than under traditional farming. The changes based upon Shannon-Wiener, Pielou, Richness and Simpson measurements of metabolism diversity of microorganism function were consistent across soil layers 0-20cm and 20-40cm. The indices were higher at tillering and jointing stages of winter wheat for traditional farming treatment, whereas they were higher at heading and milling stages for four year double-zero-tillage-cropping treatment. The results also showed that the soil fertility of four year double-zero-tillage-cropping was distinguishably better than three year double-zero-tillage-cropping. In conclusion, four year double-zero-tillage-cropping benefited soil fertility, especially in the middle and late growth stages of winter wheat. Key words: Conservation agriculture; Double-zero-tillage cropping; Winter-rice rotation system; soil fertility



3248 - Crop Breeding & Genetics

Joana Liska Bock

INTERSPECIFIC CROSSES IN POTATO AND THE UTILIZATION OF THE 2,4-D AUXIN

Bock,JL; Savoldi,M; Suzin,M; Santos,CM; Grando,MF; Augustin,L;

Universidade de Passo Fundo - UPF;

The unilateral sexual polyploidization is a strategy used for transference of useful genes from diploid species into tetraploid cultivated potato. Aiming the adjustment of this technique, fruits and seeds formation were evaluated from Asterix, Hertha, BRS Ana, Chipsona, Macaca cultivars and the SMIJ464-1 clone, pollinated with diploid clones DLB1-140 and DLB1-150, using the application of synthetic auxin 2,4-D. The experiment was carried out in the acclimatized chamber with 16 hours light photoperiod and 20°C mean temperature. It were performed three consecutive pollinations in each flower, being the 2,4-D (0,1 mg.mL⁻¹) applied 24 and 48 hours after the first pollination, in the region just below the calyx. The number of fruits and seeds formed was evaluated in relation of the flowers pollinated. The influence of male and female genitor in frequency of fruits obtained was tested by Chi-square (X^2). Chromosome counting from root tip cells was accomplished to confirm the hybrid condition of seedlings. Total of 68 flowers pollinated (47 with DLB1-150 and 21 with DLB1-140), resulting in 16 fruits (23.5%) whereas 6 (37.5%) formed seeds. Valiati (2008) had 21.4% fruit formation in crosses 4x-2x with application of 2,4-D; without 2,4-D none fruit was obtained. In this experiment, 17 seeds was obtained, whereas 10 (58.8%) were fertile and germinated resulting in seedlings. There was influence of male genitor in frequency of fruits obtained ($X^2=7.29$), since DLB1-140 clone produced 42.8% and DLB1-150 clone 14.9%. To overcome the reproductive barrier among plants with different ploidy levels 4x-2x, there is need that the pollinators 2x produce unreduced (2n) pollen grains with a certain frequency. Rosa (2007) observed that the DLB1-140 clone showed a highest frequency of unreduced pollen grains than DLB1-150 clone. Also, the female genitors had influence in fruit formation ($X^2=14.64$). Asterix, Hertha, BRS Ana, Chipsona e SMIJ464-1 produced each one fruit and the cultivar Macaca produced 11 fruits. This cultivar is Brazilian and therefore more adapted and rustic than the others, and these aspects could explain this result. Eight plants were obtained: 7 from Macaca x DLB1-140 cross and one from SMIJ464-1 x DLB1-140 cross. The seedlings showed 48 chromosomes, confirming the true hybrids condition resulting from fertilization of unreduced pollen grains. Further studies may be carried out to improve the efficiency of unilateral sexual polyploidization technique in potato.



3373 - Plant Genetic Resources

Maarten van Zonneveld

UNDERUTILIZED CAPSICUM PEPPER DIVERSITY IN ITS ANDEAN CENTRE OF ORIGIN: ADVANCES IN HIGH VALUE DIFFERENTIATION

Van-Zonneveld,MJ; Ramirez,M; Williams,D; Petz,M; Meckelmann,S; Avila,T; Bejarano,C; Rios,L; Jager,M; Libreros,D; Amaya,K; Scheldeman,X;

Bioversity International, Regional office for the Americas; Bioversity International, Regional office for the Americas;

We aim to identify promising gene bank accessions to test the hypothesis that underutilized diversity from crops' centres of origin can provide unique opportunities for poor farmers to increase their income with the production of differentiated crop varieties for emerging markets of high value products. We focus on the genus *Capsicum* as a model gene pool because it is a highly diverse complex of domesticated and wild species offering abundant variation in its centre of origin and domestication, i.e. Bolivia and Peru. The Instituto Nacional de Innovación Agrícola (INIA) in Peru and the Centro de Investigaciones Fitoecogenéticas de Pairumani (CIFP) in Bolivia hold significant *Capsicum* collections. However, they have never been thoroughly characterized or evaluated. We report on advances in complementary collecting of *Capsicum* germplasm, taxonomic identification, initial biochemical characterization of the gene bank accessions, and selection of promising material. The CIFP collection now contains 492 accessions of the five cultivated species and seven wild species. The collection at INIA Peru now contains 711 accessions of the five cultivated species. These are the largest and most diverse *Capsicum* collections ever assembled in each country. Selection of promising material representative of *Capsicum* diversity in Peru and Bolivia is being achieved as follows: 1) Over 100 accessions representative of the different species and geographic distribution in each country were selected for biochemical screening to determine capsaicinoid content, polyphenols, antioxidant capacity, carotenoids, lipid content and colour in dry *Capsicum* samples; 2) A sub-set of accessions was selected from this group representative of the different species and variation in biochemical attributes; and 3) These accessions will be evaluated in different environments to identify in which agro-ecological areas they best express properties of commercial interest. According to the initial biochemical screening, *Capsicum* accessions from Bolivia and Peru have unique combinations of functional attributes confirming that a wealth of commercially valuable properties can be found in *Capsicum*'s centre of origin and domestication. This information will be provided to local multi-stakeholder platforms which are simultaneously being convened to strengthen *Capsicum* value chains, and look for specific seed material for different market opportunities.



2824 - Crop Physiology and metabolism

Adriana Graciela Kantolic

POST-FLOWERING PHOTOPERIODIC EFFECT ON SOYBEAN REPRODUCTIVE EFFICIENCY

Nico,M; Kantolic,AG; Miralles,DJ;

Facultad de Agronomia Universidad de Buenos Aires;

The objective of the present work was to assess the role of post-flowering photoperiod on soybean reproductive efficiency. Previous results have shown that less-inductive daylengths extended post-flowering phases and increased seed number. It is hypothesized that the increases in seed number, due to an extended post-flowering phase, are mediated by an enhanced crop reproductive efficiency. Field experiments were conducted at Buenos Aires, Argentina during 2009 (late sowing) and 2010/11 (early sowing), without limitation in nutrient, water or biotic stress. Treatments were a factorial combination of genotypes (maturity group IV and V), incident radiation (control and shade) and photoperiod regimes (natural and artificially extended) installed after beginning bloom (R1). Reproductive growth rate was estimated from R1 to R8 on a thermal-days basis. Reproductive efficiency was estimated as the quotient between final seed number and reproductive growth rate. Photoperiod extension prolonged the pod production phase but its effects on crop growth rate and partition were not significant. Seed number showed a positive linear relationship with the reproductive growth rate across genotypes and radiation levels, but different relationships were adjusted depending on the experiment and photoperiodic regime. At a given reproductive growth rate, plants exposed to extended photoperiod produced more seeds than those exposed to the natural photoperiod condition. Similarly, yield per unit of reproductive growth rate was higher under lengthened photoperiod, although the magnitude of the response was lower than those of seed number, because plants exposed to extended day length had smaller seeds. Reproductive efficiency showed a positive relationship with the mean photoperiod explored during the post-flowering phase. Interestingly, mean photoperiod value in the extended photoperiod regime in the late sowing experiment was similar to the natural photoperiod explored in the experiment sown earlier (14:55 and 14:30 h, respectively) and had similar reproductive efficiencies (487.8 and 489.2 grains g⁻¹ d m², respectively). These results suggest that the promotion of seed number establishment by extended photoperiods is given not only by lengthening the phase of pod production and growth, but also by an increment on the reproductive efficiency, accepting the postulated hypothesis.



3078 - Agronomy

Dr. Pisamai Chantuma

Decomposition and Carbon Cycling of Hevea Leaves in Thailand

Chantuma,PISAMAI;

Department of Aggieculture;

The study aims was assessed The decomposition of soil litter contributes to maintaining agricultural sustainability, since the nutrients released by microbial activity are determinants of the net productivity of the agroecosystem. The experiment was set up in Chachoengsao Rubber Research Centre (RRIT-DOA) and farmer plantations on clone RRIM 600 age vary from planting to falling or lifespan (0-3, 4-6, 7-9, 10-12, 13-15, 16-18, 19-21 and >22 years).The decomposition of rubber leaves (*Hevea brasiliensis* [Willd. ex A. Juss.] Mull. Arg.) located on the surface was studied, with emphasis on the production of carbonand other substances. *H. brasiliensis* leaves were de-foliaged which start from the beginning of December. Leaves falled 50% during 21-28±3 days and complete leaves fall after 42±3 days. Leaves litter mass varied from 2,609 to 5,688 kg/ha of rubber tree age 2-25 years. *H. brasiliensis* leaves also were release carbon 666-1,697 kg/ha, nitrogen 16.8-58.5 kg/ha, phosphorus 1.8-3.8 kg/ha and potassium 3.9-15.9 kg/ha.



3236 - Agronomy

Fahd Rasul

Phytohormones effect on the yield, quality and source-sink relationship of super hybrid rice (*Oryza sativa* L.)

Rasul,F; Tang,XR; Akhtar,M; Umer,M; Saleem,MF; Chaudhry,HJ;

Department of agronomy, university of agriculture faisalabad pakistan, south china agriculture university guangzhou china;

Phytohormones play an important role in growth and development of plants, specially flowering and seed development, to test different hormonal application effect on the yield, quality and source-sink characteristics of super hybrid rice experiments were conducted in field during early and late seasons of 2007 in rice double cropping area of south China. The different hormones were sprayed at full heading stage. The number of grains per panicle and 1000-grains weight in both early and late growing seasons 2007 were significantly affected by the application of different hormones depicting the role of hormones on seed formation and development. The seed setting rates in both early and late growing seasons 2007 were significantly similar and there were no apparent effect of these hormones on the seed setting rates of rice this exhibits the hormones role in fertilization is not significant and they affect the development of seed development after fertilization. The role of plant growth regulators to rice seed quality was non-significant and quality parameters like brown rice rate, milled rate, head rate, chalky rate etc all showed non-significant differences to the application of hormones except gel consistency. SOD in leaf showed significant differences only at 21 days after heading during the early growing season 2007 while it significantly differed in the late growing season at 7, 14 and 21 days after heading, this increase in SOD activity may be attributed to the production of ABA that regulate the defence mechanism of plant. The development of grain depends on the transfer of assimilates from leaf to seed (source-sink) that can be represented by the sucrose synthase enzyme activity which is regulated by these hormones, SS (Sucrose synthase)activity during the late growing season was significantly affected by the hormones application in the middle of the seed development including grain filling and ripening stage. The effect of hormonal spray of different kinds of hormones have significant effect on the yield components like 1000-grain weight, number of grains per panicle etc. but has less effect on final yield. Quality of rice grain is also not affected much except in the late growing season for milled rice rate and gel consistency in the early growing season 2007.



3166 - Agronomy

Rintaro Hattori

INFLUENCE OF EXCESS SOIL WATER DURING EARLY GROWTH STAGE ON GROWTH, NUTRIENT UPTAKE, AND YIELD OF SOYBEAN AND AM COLONIZATION AND BIOMASS

Rintaro-Hattori, RH; Atsushi-Matsumura, AM; Hiroyuki-Daimon, HD;

Graduate School of Life and Environmental Sciences, Osaka Prefecture University;

Arbuscular mycorrhizal fungi (AM) provides the host plant with nutrients, thereby improving plant growth. The growth of intraradical and extraradical hyphae of AM are affected by environmental factors. Such effect is a key factor in the nutrient dynamics of AM symbiosis. Therefore, it is essential to clarify the environmental effect on AM hyphal biomass and colonization in the plant roots. In Japan, more than 86% of soybean crops are cultivated in upland field converted from paddy. In such field, flooding injury occurs frequently at rainy season. We clarified the effect of excess soil water content on growth and nutrient uptake of soybean and hyphal biomass and colonization of AM. A field experiment was carried out at converted upland field in Osaka, Japan in 2010 and 2011. Seeds of soybean (cv. Fukuyutaka) were sown on 2 July (2010) and 15 June (2011). Two plots (wet plot and the control plot) were established. Wet plot are irrigated to the open ditch until 6 August (2010) and 21 July (2011). Shoot growth and total N and P contents were measured at early growth stage (V3~6) and reproductive growth stage (R2). At the sampling time, roots and soils were also sampled by a core sampling method (5 cm in diameter × 20 cm in depth). Soil cores were divided into two layers by soil depth. Roots were sorted out and root length density was measured with an image analysis system, and then a portion of roots was used to determine AM colonization ratio. To evaluate AM hyphal biomass, PLFA were extracted from the soils and analyzed by GC. During early growth stage, soil moisture contents were much higher in the wet plot. Shoot growth and total N and P contents in wet plot were significantly less than in the control plot. Root length density was higher in shallow layer at early growth stage in both plots. AM colonization ratio of the roots was markedly lower in wet plot, especially in bottom layer. AM hyphal biomass in wet plot was lesser than that in the control plot at early growth stage, especially in shallow layer. However, that was higher than in the control plot at R6 stage. Shoot and root growths and nutrient uptake of soybean were similar to those reported in the previous papers. When AM colonization ratio was suppressed at early growth stage under wet condition, it was still lower at reproductive growth stage. On the contrary, when AM hyphal biomass was suppressed by excess soil water, it didn't necessarily continue to be lower at reproductive growth stage.



3225 - Agronomy

Ariano Martins de Magalhães Júnior

RICE CROP UNDER SPRINKLER IRRIGATION

Magalhães-Jr, AM; Parfitt, JMB; Fagundes, PRR; Theisen, G; Nunes, CD; Franco, DF; Severo, ACM; Fonseca, GM; Streck, EA; Aguiar, GA; Lopes, JL; Oliveira, FA; Silva, DM; Silva, JT; Bretanha, G;

Embrapa Clima Temperado;

Rio Grande do Sul (RS) is the largest Brazilian state in rice production, accounting for about 65% of production in the country. Practically, its cultivation is carried out by the system of continuous flooding. The lowland areas traditionally used to this culture have diverse topography, ranging from very flat areas to areas more wavy. The continuous flooding system has some additional difficulties due the large amount of water necessary to irrigation and to build the levees for adequate water management. This system still causes problems to the cultivation of other crops. Another important aspects to be considered is that in a lot of regions where the rice is grown, the water availability combined with low efficiency of water use is a limiting factor to rice production. The efficiently use of water, by itself, is a great advantage of sprinkler system. The changing from the flood irrigation system to sprinkler causes big changes in the agronomic performance of Rice plant due the new environment. The changing in the performance of rice plant is not yet well known by the research. Thus, experiments were conducted during 2009/10, 2010/11 and 2011/12 seasons, in different regions of the state to evaluate the performance of rice cultivars under sprinkler irrigation. The experimental design was a randomized complete blocks with four replications. Each plot consisted of nine lines of five meters, the useful area being harvested four meters of central rows (4 m²). The variables analyzed were yield (kg ha⁻¹), 50% flowering - cycle (days), plant height (cm), lodging (rating scale), whole grain yield (% whole grains). The analysis of variance and the Tukey test (P).



2730 - Agronomy

Ashok K Alva

COVER CROPS IN IRRIGATED POTATO ROTATION SYSTEMS IN THE US NORTHWEST

Alva,AK;

USDA-ARS;

Potato acreage in the US Northwest is about 187,000 hectares (46% of US total potato acreage) with a total production of about 9.8 million metric tonnes (54% of US total Production). However, sandy soils are susceptible to erosion of topsoil during the off-season. Therefore, cover crops are important to minimize soil erosion, capture residual soil nutrients, and provide the nutrients for the subsequent crop in rotation. The objective of this study was to evaluate the potential benefits of different cover crops in an irrigated potato rotation system in the US Northwest. This four-year study was conducted in Washington State on Quincy fine sand under center pivot irrigation. The mean annual precipitation in this region is about 165 mm. The cumulative ET during the growing period is about 780-850 mm. Potato -Wheat - 2 years of sweet corn rotation was adapted. The treatments included: (i) fallow; (ii) fallow with fumigation; or the following fall-planted cover crops: either (iii) white mustard; (iv) winter wheat;(v) sudangrass; or (vi) hairy vetch/oats. The cover crops biomass followed the order: mustard > sudangrass > wheat > hairy vetch/oats across most years. The ranges of total N in the cover crop biomass before planting potato across 4 years were: 120-180, 60-90, 25-45, and 25-65 kg/ha for white mustard, sudangrass, winter wheat, and vetch/oats, respectively. The total tuber yields, mean across four years, were significantly greater under fallow/fumigated as compared to that under fallow or winter wheat or white mustard cover crops. The yield was much lower under sudangrass or vetch/oats cover crops. The proportion of large size tubers (>170 g/tuber) of the total tuber yields was much greater in 2003 and 2005 as compared to that in 2002 and 2004. This four year study revealed fallow/fumigated treatment supported the highest tuber yields. Perhaps, the decomposition of cover crops biomass may have impacted the timing of N availability in relation to critical N demand by the crop. This aspect of N dynamics in the soil with and without cover crops needs to be investigated. Furthermore, the physical and biological benefits of cover crops in relation to fallow soils need to be evaluated.



3336 - Forage & Grazing Lands

Eliana Vera Geremia

HERBAGE MASS AND MORPHOLOGICAL COMPOSITION OF ELEPHANT GRASS SUBJECTED TO STRATEGIES OF ROTATIONAL STOCKING MANAGEMENT

Geremia,EV; Da-Silva,SC; Pereira,LET; Paiva,AJ; Santos,TM; Vicente,SF; Oliveira,LP;

Escola Superior de Agricultura "Luiz de Queiroz";

The objective of this experiment was to evaluate herbage mass, morphological composition and vertical distribution of morphological components on elephant grass (*Pennisetum purpureum* Schum. cv. Napier) swards subjected to strategies of rotational stocking management. The experiment was conducted from January to March 2012, in Piracicaba, SP, Brazil (22°43'S, 47°25'W and 580m a.s.l.). Treatments corresponded to combinations between two pre-grazing (95% and maximum canopy light interception - LI95% and LIMax) and two post-grazing (35 and 45 cm) targets, and were allocated to experimental units according to a 2x2 factorial arrangement and a complete randomised block design, with four replications. Monitoring of canopy LI was performed using a canopy analyser LAI 2000. Measurements of herbage mass and morphological composition (leaf - L, stem - S and dead material - D) above post-grazing height were made harvesting all herbage within four 1.5 x 0.75 m metallic frames per paddock. Samples were divided up into three vertical strata (upper, intermediate and bottom) prior to hand separation into morphological components. These were dried in a forced draught oven at 65°C. Data were analysed using the Mixed Procedure of SAS®, means estimated using the "LSMEANS" command, and comparisons, when appropriate, made with Student t test with a 5% significance level. Herbage mass increased from the upper to the bottom strata regardless of the pre-grazing LI targets. Larger values were recorded on all strata of swards managed at LIMax relative to those managed at LI95%. On swards managed with LI95% there was no difference between targets of post-grazing height in herbage mass in any of the strata. The only difference was recorded on swards managed with LIMax, intermediate stratum, with larger %L for the 45 cm post-grazing height. Upper strata presented similar %L regardless of LI targets. For the intermediate and bottom strata, larger %L was recorded on swards managed with LI95%. The %S was larger on swards managed at LIMax in all three strata. LI95% resulted in accumulation of stems on the bottom strata, with increasing percentage recorded from the bottom to the upper strata for LIMax. Larger %D was measured in the bottom strata regardless of pre-grazing LI, with differences between LI treatments detected only in the bottom strata (lower values for LI95%). LI95% corresponds to an adequate pre-grazing target for managing elephant grass under rotational stocking management.



3198 - Agronomy

Gilberto Omar Tomm

WHICH IS THE LOWEST LATITUDE FOR CANOLA PRODUCTION?

Tomm,GO; Smiderle,O; Raposo,RWC;

Embrapa Trigo;

Brazil has millions of hectares in tropical areas where soybean and maize are cultivated in the summer, allowing a second crop, in the same year, during the months with lower temperatures. This could reduce the needs for expanding grain production in land currently under pastures and forests. Canola (*Brassica napus* L.), a temperate environment crop, has been developed at latitudes between 35° to 55° and information about the possibility to grow it at latitudes below 24° is decisive for expanding canola production towards the Equator. This study aimed at providing insights about the latitude and altitude limits of adaptation of the available canola hybrids. Data from a network of field trials, at locations in Brazil ranging from the Southernmost state (lat. 30°32'38"S, alt. 432 m) to the Northernmost state (lat. 2°49'11"S, alt. 85 m) along with observations in commercial fields of *B. napus* hybrids, during 8 years, provided the basis for this study. In addition, since 2003, the performance of canola hybrids has been evaluated in experiments and farmers fields at latitudes between 16 and 19°. Commercial production of canola in Central Brazil started in 2004 following promising experimental results. The average yield of eight genotypes at the lat. 18° 29' 59", alt. 815 m was 1,949 kg/ha. Samplings at a farmer's canola field that visually suggested higher yield potential, at the lat. 21° 47' 03", alt. of 442 m, reached 2,664 kg/ha. The lowest latitude at which promising performance was achieved is located in Northeastern Brazil (lat. 6°57'48", alt. 618 m) where the hybrids yielded up to 2,268 kg/ha. However, none of the *B. napus* hybrids produced grain at the latitude 2° 49'11", altitude 85 m, although plant development and flowering was adequate. Likely, the frequent temperatures above 27° C, affected pollen viability. These results suggest that the effect of higher altitude on environmental conditions can compensate for the lower latitudes to an extent that turns canola production agronomically viable with adequate low daylength sensitivity hybrids. The altitude of 600 m can be used as reference to increase research efforts at latitudes starting around 6 degrees, and to expand investigation and commercial production at latitudes as low as 17 degrees. There is much potential for yield improvements since the results were obtained without breeding and selection for these specific growing conditions, and research for adjusting management practices was scarce.



3151 - Genomics, Molecular Genetics and Biotechnology

Dong Xu

SOYBEAN KNOWLEDGE BASE (SOYKB) FOR SOYBEAN TRANSLATIONAL GENOMICS AND BREEDING

Xu,DONG;

University of Missouri;

Many genome-scale data are available in soybean including genomic sequence, transcriptomics (microarray and RNA-seq), proteomics and metabolomics datasets, together with growing knowledge of soybean in gene, microRNAs, pathways, and phenotypes. This represents rich and resourceful information, which can provide valuable insights if mined in an innovative and integrative manner and thus, the need for informatics resources to achieve that. Towards this we have developed Soybean Knowledge Base (SoyKB), a comprehensive all-inclusive web resource for soybean translational genomics and breeding. SoyKB handles the management and integration of soybean genomics and multi-omics data along with gene function annotations, biological pathway and trait information. It has many useful tools including Affymetrix probeID search, gene family search, multiple gene/metabolite analysis, motif analysis tool, protein 3D structure viewer and download/upload capacity for experimental data and annotations. It has a user-friendly web interface together with genome browser and pathway viewer, which display data in an intuitive manner to the soybean researchers, breeders and consumers. SoyKB has new innovative tools for soybean breeding including a graphical chromosome visualizer targeted towards ease of navigation for breeders. It integrates QTLs, traits, germplasm information along with genomic variation data such as single nucleotide polymorphisms (SNPs) and genome-wide association studies (GWAS) data from multiple genotypes, cultivars and G. soja. QTLs for multiple traits can be queried and visualized in the chromosome visualizer simultaneously and overlaid on top of the genes and other molecular markers as well as multi-omics experimental data for meaningful inferences. SoyKB can be publicly accessed at <http://soykb.org>.



2845 - Crop Ecology, Management & Quality

EVALUATING OF DISTINCTNESS, UNIFORMITY AND STABILITY FOR WHEAT (*Triticum aestivum* L.) CULTIVARS BASED ON MOLECULAR MARKERS

Wang,LIXIN; Li,HONGBO; Pang,BINSHUANG; Zhao,CHANGPING;

Beijing Academy of Agricultural and Forestry Sciences;

Evaluation of distinctness, uniformity and stability (DUS) is of great importance before the release determination of crop cultivars. The objective of this study was to figure out the feasibility and effectiveness of molecular markers in evaluating DUS of wheat cultivars or lines and establish more quickly and exactly methods to perfect actual field testing. Five hundreds and forty wheat lines, which under the examination of the National Regional Trials (NRT) from 2007 to 2010, were compared each other or with the released cultivars for genetic similarity coefficient (GS) using at least 100 molecular markers, tested the ratio of homozygous DNA locus (RHL) for assessment of the line's stability using 50 molecular markers, and tested seed purity (SP) using 30 molecular markers. The thresholds of DUS determination based on molecular markers for wheat lines of the trails were confirmed by comparing morphological traits between two cultivars or lines with high GS and observing uniformity and stability of the lines with lower RHL and SP in the field. Two cultivars or lines with GS 0.90 were distinct each other, otherwise they were similar possibly. The line with GS 0.90 to the others were about 95% among the lines of NRT. Only 5% should be tested in the field for distinctness determination. In the National Regional Trials, the lines with RHL 96% were about 80% and showed good performance on stability, whereas the lines with RHL 90% were about 10% and had obviously phenotypic segregation. The others with the ratio ranging from 90% to 96% were only about 10% and should be tested in the field for estimating the stability. The cultivar or line without stability should not possess uniformity. A cultivar or line with lower SP should not possess uniformity also. The crucial technique was distinguishing inhomogenous (wrong) seeds from sample when testing SP based on molecular marker. It was proved that the individuals with 3 different DNA loci comparing to the most individuals of the sample in 30 markers could be an index to estimate wrong seed for calculating seed purity. The uniformity of wheat cultivar (line) could be judged according to its RHL and SP. DUS of 90% of wheat cultivars or lines could be judged based on molecular markers. The national standard is going to be constituted according to above conclusions.



3370 - Crop Breeding & Genetics

Danielle Cristina Gregorio da Silva

CLASSIFICATION OF RESISTANCE TO PHAKOPSORA PACHYRHIZI IN SOYBEAN POPULATIONS POTENCIALLY SEGREGATING TWO RPP GENES

Silva,DCG; Camolese,AC; Botelho,L; Yamanaka,N; Pinheiro,M; Fraga,TR; Maia,MS; Rincão,MP; Novaes,RML; Arias,CAA; Abdelnoor,RV;

Embrapa Soja;

Embrapa's Soybean Breeding Program developed populations for stacking different combinations of Rpp genes for resistance to soybean rust in adapted materials. The objective of this work was to evaluate the reaction of those populations to rust infection, to determine the most promising to the development of resistant varieties in Brazil. The populations derive from crosses of Brazilian varieties and the following Plant Introductions (PIs): PI587880A and PI561356 (Rpp1), PI594538A (Rpp1b), PI197182 (Rpp2), Hyuuga (Rpp3), PI459025 A and B (Rpp4), and Shiranui (Rpp5). The crosses provided different two-Rpp combinations, and resulted in eight F5 populations. These populations and the sources of resistance were subjected to phenotypic evaluations for resistance classification, using as inoculum a population of *P. pachyrhizi*. The methods and criteria used were described by Yamanaka et al. (2010). The F5 populations were classified into two categories of resistance to *P. pachyrhizi*. CF10-03 was classified as 'resistant', the better performance of all populations, whilst all the remaining populations were classified as 'slightly resistant'. The F5 populations outperformed the corresponding sources of resistance in the indexes of resistance, suggesting that stacking of Rpp genes might have been effective. Among the PIs tested, Shiranui was classified as 'highly resistant'. PI561356 was classified as 'susceptible', demonstrating that its resistance has been broken by the inoculum. This explains why CF10-08, derived from this PI, presented the lower resistance values among all populations. The remaining PIs were classified as 'slightly resistant'. Although segregating the same gene, Rpp2, the populations CF10-01, 04 and 07 presented different resistance values, reinforcing that different genetic backgrounds can have divergent responses to the introgressed gene. The population CF10-03 showed the best combination of resistance characters and so is the choice for the development of resistant varieties against rust. The other seven populations showed intermediated resistance, requiring a refined classification to be distinguished and applied to breeding program. Marker-assisted selection would improve this classification and should be used in the future. Reference: Yamanaka, N. et al. Development of classification criteria for resistance to soybean rust and differences in virulence among Japanese and Brazilian rust populations. *Trop. Plant Path.*, 35:153-162, 2010. The authors declare no conflict of interest.



3222 - Forage & Grazing Lands

Renato Serena Fontaneli

SILAGE OF DUAL PURPOSE WINTER CEREALS AND BLACK OAT

Fontaneli,RS; Kaiper,E; Santos,HP; Fontaneli,RS;

Embrapa Trigo;

This study aimed at comparing the yield and nutritive value of oat, wheat, triticale, and black oat cultivars preserved as silage in Southern Brazil. The experiment was carried at Embrapa Wheat, in Coxilha, state of Rio Grande do Sul, during the cool season of 2010. Treatments consisted of 25 oat cultivars (*Avena sativa* L.), wheat 'BRS Umbu' (*Triticum aestivum* L.), triticale 'BRS Minotauro' (X Triticosecale Wittmack), and black oat 'Embrapa 139-Neblina' (*Avena strigosa* Schreb.), displayed in a randomized complete block design (RCBD), with three replicates. Plots had 5.0 m² (5 rows of 5.0 m long by 0.2 m apart). Sowing was done on June 4th, 2010 using a drill adjusted aiming at 300 plants m⁻². Fertilizer rate applied at seeding was 250 kg ha⁻¹ of 08-24-18 (N-P₂O₅-K₂O) and 40 kg N ha⁻¹ topdressed at the tillering stage. Plants were clipped at 5.0-cm stubble height, using a sickle-bar mower at the stage of seed filling, corresponding to about 30 to 35% dry matter (DM). Forage was weighted, samples were dried at 60°C during 72 h, and grinded to pass a 1-mm screen using a Willey mill. Concentration of N, NDF (neutral detergent fiber), ADF (acid detergent fiber), and digestibility, were determined using near infrared spectroscopy (NIRS). Experimental silos with 4.0 dm³ of capacity were filled with forage cut in pieces of 0.5-3.0 cm, and stored at room temperature during 60 days. The oat 'UPF 18' produced higher (P).



3335 - Genomics, Molecular Genetics and Biotechnology

Giovanni Orlando Cancino Escalante

EFFECTS OF TWO ORGANIC SUPPLEMENTS ON IN VITRO GERMINATION OF ENDANGERED NATIVE ORCHIDS IN COLOMBIA, SOUTH AMERICA

Cancino-Escalante,GO; Salazar-Mercado,SA;

Universidad de Pamplona;

Orchids are commercially grown as cut flower and potted plants and have in the past years held an average 8% share of worldwide floriculture trade. Due to its diverse colors, forms and shapes it is considered an exceptional ornamental plant. However, natural populations of some species have been strongly affected due to destruction of their habitat and excessive plant extraction. In particular, *Prosthechea vespa* and *Sobralia klotzscheana*, epiphytic orchids, endemic to Colombia, are considered to be endangered species under regulatory issues in Colombia. Their germination limitations in the wild have led to greater emphasis of the species conservation, therefore to preserve endangered orchids in vitro culture is an alternative tool. This research evaluated orchid seeds asymbiotic germination and seedling formation of *P. vespa* and *S. klotzscheana* species in Murashige and Skoog (MS) medium with two organic supplements (pineapple juice and coconut water). Mature capsules from *P. vespa* and *S. klotzscheana* species were collected in the Province of Pamplona, northeastern region of Colombia, and their viability with tetrazolium staining was determined. The seeds were disinfected and sown with the syringe method and the effect of the two organic supplements in MS on asymbiotic germination and seedling formations were assessed after 200 days. The seeds viability of the two species analyzed were 87.2% and 80.6%, respectively. The corrected percentage of viability compared to the germination was higher, between 2.8% (*P. vespa*) and 0.5% (*S. klotzscheana*). This study showed that MS medium supplemented with pineapple juice has a greater response to asymbiotic germination and seedling formation in *P. vespa* (22%) and *S. klotzscheana* (43%) with statistically significant differences (P Key Words: Conservation, Asymbiotic germination, Orchid, Viability, Tetrazolium).



3155 - Crop Breeding & Genetics

João Ricardo Bachega Feijó Rosa

ASSESSING LINKAGE DISEQUILIBRIUM AND POPULATION STRUCTURE IN THE SUGARCANE (*SACCHARUM SPP.*) BRAZILIAN GERMPLASM

Rosa,JRBF; Silva,RR; Pastina,MM; Barreto,FZ; Balsalobre,TWA; Souza,AP; Carneiro,MS; Garcia,AAF;

Department of Genetics, Luiz de Queiroz College of Agriculture, University of São Paulo;

Both linkage disequilibrium (LD) and population structure hold the key to association mapping and thus have been analyzed in many studies of humans and plants. In sugarcane (*Saccharum spp.*), a very important crop in Brazil, few papers involving that concepts were published to date. Here, we analyzed LD and population structure through 135 accessions belonging to the Brazilian panel of sugarcane varieties. This panel brings together important ancestral species, mostly used varieties as progenitors, promising clones at final stage of selection, most planted varieties and varieties from genetic mapping programs. A total of 1,474 polymorphic markers was scored from 86 EST-SSRs and 14 genomic SSRs, whose patterns were read as presence (1) or absence (0) due to highly polyploid genome of sugarcane. Based on these data, we calculated LD by Fisher exact test considering all the pairs of markers and corrected multiple tests with Bonferroni and False Discovery Rate (FDR). Furthermore, we verified LD decay using a previous genetic map, which provided distances between mapped and linked panel markers, after their detection in molecular patterns of the experimental population as well as their positions in the map. Population structure was assessed by no admixture model, implemented in STRUCTURE, and Neighbor-Joining algorithm, based on the dissimilarity matrix calculated by simple matching. Our results showed that 2.79% of associations (out of 1,085,601 Fisher exact tests) revealed LD with FDR threshold, a much higher proportion in comparison to other studies. Only 102 panel markers were detected in the reference map, of which 9 were involved in 5 significant associations between linked loci. Strong LD was observed up to 15 cM, mainly within the first 5 cM, suggesting a higher genome coverage with markers to increase mapping resolution. Nevertheless, LD was also detected between markers separated by 65 cM, an expected scenario considering the recent history of sugarcane breeding in Brazil under strong selection and recurrent crosses between related individuals. Four subpopulations were inferred in Brazilian panel by both STRUCTURE and Neighbor-Joining, which seemed to be in agreement to pedigree informations. Our results may provide important directions for actual studies of genetic mapping in sugarcane, which are already considering allele doses and thus its complex and highly polyploid genome.



3221 - Crop Breeding & Genetics

Karina Elizabeth D'Andrea

GENETIC VARIATION IN A MAIZE POPULATION OF RILS: I- HERITABILITY STUDY OF THE ECO-PHYSIOLOGICAL AND NUMERICAL DETERMINANTS OF GRAIN YIELD.

Dandrea,K; Seco,A; Galizia,L; Mandolino,C; Cirilo,A; Otegui,M;

FAUBA - CONICET;

Research on the physiological and numerical determinants of maize (*Zea mays* L.) grain yield is scarce in inbred lines as compared to hybrids, although these traits could improve selection efficiency. The development of maize germplasm with good performance under nitrogen stress implies a detailed knowledge of the physiological aspects involved, and of the interaction among promising traits and the target environment. The aim of this work was to study the genotypic variation for maximum leaf area (LAIMAX), fraction of radiation interception by the canopy (fIPAR), total shoot biomass, harvest index (HI), grain yield per plant (PGY), anthesis-silking interval (ASI), kernel number per plant (KNP), kernel weight and prolificacy. We phenotyped these traits for a collection of 180 recombinant inbred lines (RILs) derived from two contrasting parental inbreds (B100: American semident; LP2: Argentine flint). The collection, both parents and a tester line were grown under irrigation during two seasons (2009-2010 and 2011-2012). The experimental layout was a completely randomized block design with two replicates. The results showed that (i) there was significant genotypic variability (P.e.g. KNP) could be an advantage in less favorable environments, especially considering their early quantification as compared to grain yield. We identified lines of high and low grain yield (located on the topmost and bottommost 5% of the distribution). Inbreds in the uppermost 5% for PGY were those within the uppermost quartile for plant biomass, LAIMAX, HI and KNP. These results demonstrate the importance of enhanced light capture, achieved through a high LAI, in determining plant biomass at maturity and, therefore, PGY. This characterization is a starting point for genetic studies based on molecular marker associations.



3277 - Crop Breeding & Genetics

Rodrigo Gazaffi

OUTCROSSING/QTL: A NEW SOFTWARE TO PERFORM QTL MAPPING STUDIES IN OUTBRED SPECIES.

Gazaffi,R; Souza,LM; Mantello,CC; Garcia,D; Guen,V; Souza,AP; Garcia,AAF;

"Luiz de Queiroz" College of Agriculture/ ESALQ;

QTL mapping is an important approach to reveal the genetic architecture of quantitative traits, usually performed on experimental populations derived from inbred lines. For several species (e.g., rubber tree, eucalyptus, passion fruit, coffee, sugarcane and others) inbred lines cannot be obtained due to genetical or physiological limitations. For them, full-sib progenies are generally used as mapping populations, creating a complex scenario, since both markers and QTL alleles may have different segregation patterns, as well as different linkage phases. However, QTL mapping methods for outbred species are still scarce. In this work we present a software to perform QTL mapping for full-sib progenies using Composite Interval Mapping (CIM) approach on an integrated genetic map, with an example of usage on a rubber tree progeny. This software was implemented as a set of functions for the freely distributed R software. The method assumes multipoint probabilities to infer four QTL genotypes, and the statistical model considers three orthogonal contrasts to estimate additive (one in each parent) and dominance effects. Mixture models and maximum likelihood approach were used. EM algorithm was applied to obtain the estimates. Cofactors were also included in the model to control the variation caused by QTL located outside the mapping interval, increasing the statistical power. QTL mapping was defined as a two-step procedure: First, the genome is scanned to detect QTL. After, segregation pattern and linkage phases between QTL and markers are estimated. To exemplify the results obtained with this software, we performed QTL mapping on a rubber tree full-sib progeny. The mapping population consisted of 270 individuals, derived from the cross between PB217 (high latex yield potential) and PR255 (tolerance to injury and cold). The linkage map was obtained using Onemap software (based on HMM technology), consisted by 23 linkage groups with a total length of 2793 cM. Four phenotype measures were considered: height and circumference breast height (CBH), measured in the summer and winter periods. The analysis identified a total of 24 QTL, 14 for CBH (six in the summer and eight in the winter) and 10 for height (five in each season). The observed segregation patterns were: 1:1 (8 QTL), 1:2:1 (6) and 1:1:1:1 (10). Finally, 13 QTL showed dominance effect.



2804 - Agronomy

Hussein Fawzy Hussein Abouziena

COMPARISON OF NITROGEN FERTILIZERS, INDUCE AND ZINC ADDITION ON GLYPHOSATE EFFICACY ON THREE DIFFERENT WEED SPECIES

Abouziena,HR;

National Research Center;

Herbicides are often tank-mixed with fertilizers to save time, labour, energy, and equipment costs. However addition of some additives with glyphosate may result in reducing glyphosate efficacy. Therefore we evaluated the potential of three nitrogen sources (ammonium sulphate (AMS) at 2 or 4% w/v, ammonium nitrate (AN) at 1 or 2% w/v, urea at 1 or 2 % w/v), nonionic adjuvant (Induce at 0.05% v/v) and Zn at 250 g Zn/ha (1321 ppm) to enhance glyphosate efficacy on pig weed (*Amaranthus retroflexus* L.), crowfoot grass (*Dactyloctenium aegyptium* L.) and yellow nutsedge (*Cyperus esculentus* L.) under greenhouse conditions. The results indicated that there were variations in susceptibility of the three weeds to glyphosate+adjuvant treatments. Addition of AN at 2% reduced the efficacy of glyphosate on crowfoot grass. There was an antagonistic effect between glyphosate herbicide and Zn; the phytotoxic effect of glyphosate on the three weeds was less than 50 %. Zinc tank-mixed with glyphosate resulted in a greater number of tubers and shoots per plant than the untreated one. Addition of AN or urea at 2% reduced glyphosate efficacy by about 2.3 and 9 %, respectively, relative to their addition at 1%. Tankmixes of urea (1%), AN (1%), AMS (2%) and Induce adjuvant (0.05%) generally enhanced the efficacy of glyphosate (0.85 kg/ha), whereas the addition of Zn, as zinc sulphate, to glyphosate sprays adversely affected herbicide efficacy. Key words: adjuvant; *Amaranthus retroflexus*; *Cyperus esculentus*; *Dactyloctenium aegyptium*; herbicide; weeds



3156 - Agronomy

Jaikirat Singh Gill

GROWING SEASON RAINFALL INFLUENCES THE YIELD BENEFITS ASSOCIATED WITH SUBSOIL MANURING

Gill,JS; Sale,PWG; Peries,R; Tang,C;

Latrobe University;

Hard, dense, clay subsoils pose major restrictions to crop production under rainfed conditions in many parts of world. Our research has led to the development of a practice to ameliorate these subsoils. This is known as subsoil manuring and involves the incorporation of high rates (20t/ha) of organic manure into dense clay subsoils at depths of 30 to 40 cm. The practice resulted in a large grain yield increase of wheat of around 70% in a dry spring year. Subsoil manuring was evaluated in other regions over a three year period. Poultry manure was incorporated at rates of 10 and 20 t/ha. Fertiliser nutrients (N, P and K) equivalent to those in the 20 t manure application were also incorporated in the subsoil to evaluate the effect of nutrients only. Data are presented for two sites beginning in 2009. The average annual rainfall at the Derrinallum site is 650 mm and at the Penshurst site is 750 mm. In this paper we discuss the grain yield and yield parameters for the crops grown at the two sites. In 2009 at Derrinallum, the wheat yield was nearly doubled in the subsoil-manured plots receiving 20 t/ha of poultry manure, compared to control untreated plots. At Penshurst the wheat yield was 60% higher in 20 t/ha manured plot, than in control plot. The number of heads produced per square meter was the main driver for the increase in grain yield. The harvest index at Derrinallum was significantly higher in 20 t/ha poultry manure plots compared to untreated control. The 2010 season was a wet and canola crops at both sites were severely waterlogged. The 2011 results were interesting in an average rainfall year. The yield response in the 20 t/ha amended plots was much higher at the Penshurst site compared to Derrinallum. This was attributed to greater water extraction from the subsoil by the crop at Penshurst due to the drier finish to the season, than that which occurred at Derrinallum. The results in different years at the two sites showed that response to subsoil manuring was greater when there was less rainfall during the grain filling period as this led to increased extraction of water from the clay subsoil layers.



2849 - Crop Ecology, Management & Quality

Marcelo Sans Dodson

AGRICULTURAL PROJECT MANAGEMENT: SUGARCANE FARMING OPERATIONS CASE STUDY

Dodson,MS; Chavesjr,RA; Rodriguez,LH; Smith,VY; Wells,S;

Devry University;

The challenges to feed a constant growing world population are immense. Farmers must use the available knowledge to efficiently manage scarce resources, with profit and in a sustainable manner. On this scenario, the project management methodology can be used throughout the crop life cycle and increasing its operational performance. Therefore, this theoretical study has the objective to demonstrate the use of the project management standards described by Project Management Institute (PMI), in its "A guide to the project management body of knowledge (PMBOK® Guide), 4th edition", on sugar cane farming operations. A project plan was elaborated following the PMBOK® to implement a four year sugarcane crop cycle in 200 acres (80 hectares) in a hypothetical farm located in Southern part of the State of Florida, the United States. This plan included project scope, schedule, cost, quality, risk, human resources, and communication management plan. Machinery and equipment schedule and cost were estimated using Hanna (2002) and Edwards (2009) methodology, respectively. Microsoft Project was the software utilized to build project activities. The major findings of this case study are as follows. First, the results indicate that the work breakdown structure reduces the possibility of missing tasks and helps to elaborate more detailed costs, schedule, and resources management plans. Second, the MS Project provides the following benefits: the network diagram shows the project critical path, the Gantt chart presents a graphical visualization of the activities, it is possible to manage resources allocation, and the project baseline allows evaluating the activities performance using Earned Value Management. Third, the quality management plan provides statistical tools to measure variations from sugarcane agronomic specifications, at the activity level. Fourth, risk management plan addresses potential risks or benefits for the sugarcane crop and the risk register matrix integrates these risks which makes easier for the project team to monitor and control them. Finally, the case study showed that the project management methodology is applicable for sugarcane agricultural operations. Further studies on different crops are recommended in order to verify the methodology applicability and potential benefits.



3234 - Crop Breeding & Genetics

Biswanath Das

Breeding for low nitrogen tolerance in southern and eastern Africa: What's new?

Das,B; Tarekegne,A; Cairns,J; Babu,R; Vicente,FS; Crossa,J; Atlin,G;

CIMMYT;

Poor soil fertility is one of the principal abiotic constraints to maize production in eastern and southern Africa (ESA) where maize is the staple food and accounts for over 50% of daily calory intake. Average maize yields in the region have remained stagnant over the past 30 years at less than 2t/ha while fertilizer use has declined to 9kg/ha, amongst the lowest in the world. Genetic improvement of maize germplasm for low nitrogen tolerance (LNT) offers the most practical and accessible solution for small holder farmers, who produce over 80% of the maize in the region. A renewed emphasis on breeding for LNT in ESA, led by CIMMYT, is focusing on improved phenotyping and statistical methods, systematic identification of LNT donors and genome wide association studies (GWAS) to accelerate breeding gains. High levels of field variation under abiotic stress are often the primary constraint to phenotyping and breeding progress. The establishment of a characterized, regional 'low N' phenotyping network, consisting of over 60,000 plots in nitrogen depleted fields, in 15 locations within the target environment in ESA is offering unparalleled phenotyping opportunities. Multi-location testing in the low N network coupled with spatial analysis is consistently improving broad sense heritability of trials to above 0.5 under nitrogen depleted conditions. Intensive screening under nitrogen depleted conditions of line by tester trials and diverse germplasm in association mapping sets confirm that considerable genetic variation exists for LNT. Leading LNT donor lines that yield up to 50% higher in test crosses relative to current testers under severely depleted conditions have been identified and are being used aggressively in new hybrid combinations, pedigree starts and genetic studies. Some of these inbred lines have recently been released as international public goods. GWAS are being used to identify genomic regions of interest for potential development of molecular markers. Based on phenotype data from three low N sites in Africa, GWAS with high density based 'genotyping by sequencing' information in a collection of ~ 400 inbred lines identified three significant genomic regions on chr.9, chr.3 and chr.1 that coincided with MADS-box and cysteine synthase genes that have been previously implicated in positive responses under N-limiting conditions.



3309 - Crop Breeding & Genetics

Carlos Roberto Riede

BREEDING BIOFORTIFIED WHEAT CULTIVARS AT IAPAR ? BRAZIL

Riede,CR; Pavan,MA; Souza,RA; Gois,JF;

Agricultural Research Institute of Paraná - IAPAR;

The main objectives of the present work was to identify potential sources of important micronutrients Iron (Fe), Zinc (Zn) and Selenium (Se), in the Wheat Germplasm Bank of IAPAR and to incorporate them into more adapted and productive breeding materials, combining high grain yield, good industrial quality, and resistance to major diseases. Two sets of 265 and 126 entries of wheat genotypes were evaluated for Fe and Zn concentrations through an extraction of chemical elements from the seed flour using humid digestion with $\text{HNO}_3 + \text{HClO}_4$ (3:1) at the Soils Laboratory of IAPAR, in 2008 and 2009 seasons. One set of 33 selected genotypes were evaluate for Se concentration at UFSC Laboratory using an ICP-MS Nexlon 300D. Crosses were made between potential sources of micronutrients and adapted genotypes belonging to the wheat crossing blocks in different years. Segregating populations were developed and selection was made using mainly a bulk selection method. Some advanced lines are being evaluated in preliminary yield trials on the present 2012 cropping season. Among the evaluated genotypes, some cultivars or advanced lines presented higher levels of Fe, Zn and Se. The Fe concentrations varied from 7.36 to 118.70 mg.kg^{-1} and from 11.72 to 99.83 mg.kg^{-1} for Zn. Genotypes which showed high Fe and Zn simultaneously were: IPR 85, IPR 110, IPR 144, LD 072212, LD 082108 and LD 091204. Good for Fe concentration were: LD 092107, T 071018, T 071027, T 071049, T 071051, T 071052, T 071091, T 071125, T 071127, T 082001, T 082005 and T 082111. Those best for Zn concentration were: IPR 128, IPR 130, T 071030, T 071072 and T 071090. The Se concentrations varied from 0.02 to 0.17 mg.L^{-1} . Best genotypes for Se were: IPR 130, IPR 144, IPR Catuara TM, T 071018 and T 082142. Some of the above identified genotypes have been used in crosses in the last breeding seasons at IAPAR, to incorporate higher levels of Fe, Zn and Se into known high grain yield cultivars. The project received financial support from the Social Development Ministry (MDS) and from CNPq, to develop biofortified main food crops in Brazil. The main goal is to offer better quality food especially to the children and poor people. When different species were compared, oats (*Avena sativa* L) presented higher level of Fe, followed by wheat (*Triticum aestivum* L.) and at last position triticale (*xTriticosecale*). As for Zn concentration there was no significant differences among the three cereal species



3152 - Crop Breeding & Genetics

Cristiano Lemes da Silva

GAS EXCHANGE AND RELATIVE CHLOROPHYLL CONTENT AS SELECTION CRITERIA IN SPRING WHEAT POPULATIONS

Silva,CL; Beche,E; Ferrari,AP; Paladini,MV; Capelin,MA; Marchese,JA; Benin,G;

Universidade Tecnológica Federal do Paraná UTFPR;

Recent studies indicate that wheat yield potential can be increased through genetic improvement of the photosynthetic apparatus (Fischer, 2007; Reynolds et al., 2011). Moreover, recent advances in instrumentation in the area of plant physiology have made possible the rapid, non-destructive field assessment of physiological traits useful for selecting superior genotypes. The objective of this study was to evaluate heterosis of the relative chlorophyll content, gas exchange parameters and grain yield components in a full diallel cross of wheat. Four wheat cultivars were crossed in diallel form, disregarding reciprocal hybrids, totaling six combinations. In the 2011 crop season, the F₂ populations and parents were distributed in randomized block design, with three replicates. The following gas exchange readings were taken: CO₂ assimilation rate (PN), stomatal conductance (gs), and transpiration rate (E) using a portable gas exchange measuring instrument (LI-COR, Lincoln, Nebraska - USA). The chlorophyll contents were measured in flag leaves in the post-anthesis phenological phase using a electronic chlorophyll meter, model ClorofiLOG CFL 1030 Falker. The data were subjected to statistical analysis using the Genes statistical software (Cruz, 2006). Graph of the association between traits was constructed using the GGE Biplot software (Yan et al., 2001). There were high heterosis values for stomatal conductance (gs=32.69%), CO₂ assimilation rate (PN=13.21%), and transpiration rate (E=23.99%) (Figure 1). The crosses involving the Mirante parent exhibited superior performance for yield components and physiological traits, especially the hybrids BRS Tangará x Mirante and Mirante x Valente. The 1000-kernel weight was positively associated with CO₂ assimilation rate (PN= 0.76), transpiration rate (E= 0.65) and the relative chlorophyll contents "A" (0.64) and "A +B" (0.63), indicating that photosynthetic activity and chlorophyll content directly affect grain filling (Figure 2). The number of spikes per plant (0.89) and relative chlorophyll "B" content (0.87), were positively correlated with grain yield, which can be used as indirect selection criteria in wheat breeding programs.



3141 - Crop Breeding & Genetics

Euclides Minella

TROPICAL BARLEY: CHALLENGES AND PERSPECTIVES IN BRAZIL

Minella,E;

Embrapa Trigo;

Originating in Middle East, barley, *Hordeum vulgare*, proved poorly adapted to the acid, aluminum toxic soils and warm wet springs of Brazil. Fit these adverse conditions has challenged researchers since 1920. Increasing beer consumption has pushed domestic barley production since 1930. Varieties more tolerant to soil acidity in the 1950's, was a major achievement in establishing production in Brazil. Release of net blotch resistant Cevada BR 2 by Embrapa in 1990 was another major step to consolidate a malting barley industry. The switch the No Tillage Production System (NTPS) in mid 1990's, in subtropical areas, has significantly improved yield potential and stability, increasing its competitiveness against wheat. The better soil production capacity under the NTPS, called for more responsive varieties. The release of BRS 195, BRS Cauê, BRS Elis and BRS Brau varieties, revolutionized barley production. Widespread use of these modern genotypes boosted yield and malting quality, making barley even a more competitive crop. Since then, farm productivities over 6,000 kg/ha have been harvested, increasing the average yield from 1,500 in the 1980's to 3,500 kg/ha in the 2000's. Varieties BRS 180, BRS 195, BRS Sampa and BRS Manduri made production economically feasible also in tropical environments in the Southeast and Central West (cerrados) regions, under irrigation. There, yields over 7,000 kg/ha have already being obtained. However, the breakthroughs in yield, quality and disease resistance have not reduced to a satisfactory level, the yield/quality instability due to excessive rainfall at harvesting, in El Niño Southern Oscillation years. On average, around 20% of produced grain does not meet malting quality. Losses to PHS and scab (FHB and DON), are currently majors constraints to the sustainability of the malting barley industry.



3129 - Forage & Grazing Lands

Sanzio Carvalho Lima Barrios

RECIPROCAL RECURRENT SELECTION: A STRATEGY TO OBTAIN SUPERIOR APOMICTIC HYBRIDS IN BRACHIARIA DECUMBENS

Barrios,SCL; Valle,CB; Alves,GF; Simeão,RM; Jank,L;

Embrapa Beef Cattle;

Pastures of *Brachiaria decumbens* cv. Basilisk radically changed the scenario of central Brazil livestock production from the early 1970s and allowed the development of this vast region. Despite of the reasonable biomass yield and nutritional value, susceptibility to grassland spittlebugs limits its use nowadays. The breeding of *B. decumbens* was restricted to interspecific crosses using the cultivar Basilisk as pollen donor due to the lack of compatible sexual ecotypes within the species. Recently, with the chromosome duplication of a sexually reproducing diploid accession, it was possible to carry out intraspecific crosses. Four hundred and fifty seven intraspecific hybrids, obtained from crosses between three sexual plants artificially tetraploidized by colchicine and the apomictic tetraploid cv. Basilisk, compose the base population of this work. This paper reports part of the research to obtain superior apomictic hybrids in *B. decumbens* using reciprocal recurrent selection, a cyclic breeding strategy. The methodology involves progeny production through crosses; evaluation and selection of these progenies for agronomic traits, nutritional value and resistance to spittlebugs; recombination of selected progenies and identification of superior apomictic hybrids. Of the 457 hybrids in the base population, 153 had the mode of reproduction characterized. Of these, 80 were sexual and 73 apomictic, a result that is consistent with a monogenic dominant inheritance of apomixis. Crosses between the 80 sexual tetraploid plants and the apomictic cultivar Basilisk were performed in a crossing block scheme to obtain full sib progenies. These progenies will be evaluated in the next rainy season and selected for further recombination. In each selection cycle superior apomictic hybrids shall be identified to proceed to cultivar development in order to promote grassland diversification through the identification of improved cultivars.



2892 - Crop Breeding & Genetics

Yoseph Beyene Aydagn

Testcross performance and genetic distance among doubled haploid inbred lines derived from tropical backcross maize populations

Beyne,Y; Mugo,SN; Semagn,K;

CIMMYT;

In contrast to conventional inbreeding that takes up to seven generations to develop inbred lines, the doubled haploid (DH) technology allows production of inbred lines in two generations. The objectives of the present studies were to evaluate testcross performance of 504 DH lines derived from 10 backcross (BC1) populations, and to assess the genetic distances and kinship coefficients among the DH lines using 179,059 SNP markers generated using genotyping-by-sequencing (GBS). The 504 DH testcrosses were divided into six sets, with each set containing from 84 to 126 DH testcrosses and six commercial checks. The trials were evaluated at three optimum rain-fed sites and a managed drought-stress site in 2010 using alpha lattice design with three replications. Testcrosses of the DH lines showed significant differences in grain yield and other agronomic traits. In the combined analysis across the three optimum locations, about 65% of testcrosses yielded more than the mean of the commercial checks, and the top 10% testcrosses produced up to 2 t/ha higher grain yield than the mean of the commercial checks. Under managed drought condition, 60% of the DH testcross produced 11 to 122% higher grain yield as compared to the mean of commercial checks. The best testcrosses were similar to or better than the commercial checks for other agronomic traits as well. Genetic distance from pairwise comparisons of the 504 DH lines ranged from 0.01 to 0.48 with the overall mean distance of 0.34. Most of the distances (92.5%) fell between 0.30 and 0.40. Relative kinship coefficients between pairs of lines varied from 0 to 1.96, with an overall average of 0.56, but most (65.4%) values were < 0.500. These results clearly show the variability and uniqueness of the lines for use in maize breeding programs. Thirteen of the best DH hybrids are currently in National Performance Trials (NPT) testing, an important step towards commercialization in Kenya, Tanzania and Uganda. The best DH lines identified in the study could be used in maize breeding programs in eastern and southern Africa for improving yield and disease resistance



3120 - Crop Physiology and metabolism

Camila Pegoraro

MPG1 PROTEIN IMMUNODETECTION IN GENETICALLY MODIFIED MELON

Pegoraro,C; Chaves,FC; Simionatto,S; Dalcero,J; Borsuk,S; Oliveira,AC; Rombaldi,CV;

Plant Genomics and Breeding Center at Federal University of Pelotas;

Due to high ethylene production, Charentais melon (*Cucumis melo* L. var. cantalupensis N.) exhibits a rapid decrease in flesh firmness, rendering the fruit susceptible to mechanical damage, which limits transport, storage, and shelf-life. Biochemical mechanisms controlling changes in flesh firmness involve solubilization of cell wall polysaccharides by polygalacturonases (MPGs). Reduction in ethylene production in melon has been achieved by genetic modification using antisense ACC oxidase gene. However, the behavior of MPG1 during ripening of transformed melon has not been investigated. In order to evaluate MPG1 protein expression, transformed (AS3, Silva et al., 2004) and non-transformed melons (NT) were harvested and treated with ethylene (500 $\mu\text{L L}^{-1}$). Immunodetection of proteins was performed by Western blotting using mouse polyclonal antibodies produced against the recombinant protein MPG1. Antibody preparation followed protocol described by Pegoraro et al. (2010). Protein was extracted from frozen melon flesh using specific buffers and quantified according to Bradford's method. Equal amounts of total protein were loaded per gel slot onto a denaturing polyacrylamide gel. Proteins were then transferred to a nitrocellulose membrane, which was incubated for 1 h at room temperature (RT) with primary antibodies diluted in TBST at 1:2000 (anti-MPG1). Membranes were washed and incubated for 1 h at RT with a 1:50000 dilution of the peroxidase-labeled rabbit anti-mouse antibody. Washed membranes were then developed using the GE Healthcare Kit. NT and AS3 fruit 24h after harvest had only a slight decrease in flesh firmness. At 48h after harvest, NT fruit showed a drastic decrease in flesh firmness while AS3 fruit despite ethylene supply was significantly less soft. Western blotting results demonstrated that AS3 fruit at harvest had lower MPG1 content than NT fruit, possibly due to higher ethylene production in NT. In AS3 fruit, MPG1 production was markedly induced upon exposure to exogenous ethylene (24 and 48h) and decreased at 120h after harvest when fruit were at an advanced maturity stage. In NT fruit at harvest, endogenous ethylene production was sufficient for high MPG1 accumulation. MPG1 content in NT fruit was lower than in AS3 fruit at 48h after harvest likely because NT fruit were already senescing due to accelerated ripening induced by endogenous and exogenous ethylene. Thus, the MPG1 seems to be ethylene partially-dependent.



3385 - Genomics, Molecular Genetics and Biotechnology

Felipe Klein Ricachenevsky

COUPLING ARABIDOPSIS HETEROLOGOUS EXPRESSION, IONOMICS PROFILING AND SYNCHROTRON RADIATION-BASED TECHNIQUES FOR RAPID CHARACTERIZATION OF METAL-RELATED GENES FROM RICE (ORYZA SATIVA)

Ricachenevsky,FK; Punshon,T; Lahner,B; Yakubova,E; Lee,S; Salt,DE; Guerinot,ML; Fett,JP;

Centro de Biotecnologia, Universidade Federal do Rio Grande do Sul, Brazil;
Department of Biological Sciences, Dartmouth College, USA.;

Iron (Fe) and zinc (Zn) are essential for plant growth, but become toxic when in high concentrations in the cell. The amount of Fe and Zn absorbed by plants also impacts human nutrition. Important genes related to metal homeostasis have been described in the genetic model *A. thaliana*, but functional characterization of orthologs in crop species is comparatively slow. Alternative approaches for molecular characterization would help translation from model systems to crops. We describe the ionomic analysis of 50 *A. thaliana* lines heterologously expressing rice (*Oryza sativa*) full-length cDNAs (FOX lines) in order to identify metal homeostasis-related proteins. Leaves of soil-grown plants were analyzed by ICP-MS to determine the concentration of 18 elements and compared to those of wild type (WT) plants. Two lines expressing a putative ZIP transporter (OsZIP-OE lines) showed 25% increase in Zn concentration in leaves. Expression of this transporter resulted in increased Zn sensitivity. Yeast complementation experiments with the OsZIP gene showed rescue of the Zn-uptake mutant *zrt1zrt2*. OsZIP YFP-tagged was transiently expressed in *A. thaliana* protoplasts and co-localized with a plasma membrane marker. We analyzed metal distribution via Synchrotron X-ray Fluorescence (SXRF) microtomography of mature, unsectioned seeds. OsZIP-OE seeds had twice the Zn abundance of WT. We used SXRF 2D mapping to determine changes in Zn distribution in leaves. Leaves of OsZIP-OE plants growing in control conditions showed a punctate pattern that was not seen in WT. When growing in 50 μ M or 100 μ M Zn, both WT and OsZIP-OE lines showed the same pattern, although OsZIP-OE leaves had higher amounts of Zn. Overlapping Zn and calcium maps showed that the Zn spots occur around the base of trichomes. High-resolution 2D maps show that Zn is localized in a ring around the base of trichomes. To understand the role of trichomes in whole leaf Zn accumulation, we mapped leaves of 16 natural accessions with either high Zn or low Zn. We found good correlation between whole leaf Zn and Zn accumulation at the base of the trichome, indicating that the genotypic leaf Zn variation is mainly contained in trichomes. Thus, we have in vivo evidence that this rice ZIP gene encodes a Zn transporter, which leads to Zn over accumulation and alters Zn distribution when heterologously expressed in *A. thaliana*. This work highlights a good framework for characterization of metal-related genes. Support: CNPq, NSF.



3386 - Genomics, Molecular Genetics and Biotechnology

Felipe Klein Ricachenevsky

EVOLUTION OF VACUOLAR IRON TRANSPORTER 1 (VIT1 PROTEINS IN PLANTS AND FUNCTIONAL CHARACTERIZATION OF RICE PARALOGS

Ricachenevsky,FK; Menguer,PK; Lopes,KL; Turchetto-Zolet,AC; Margis,R; Fett,JP;

Centro de Biotecnologia, Universidade Federal do Rio Grande do Sul, Brazil;

Iron (Fe) is essential for many processes in plants. However, Fe can be toxic when in high concentrations inside the cell, meaning that Fe concentrations have to be tightly regulated. In humans, Fe deficiency affects 2 billion people, being the most prevalent micronutrient disorder. Rice is basic to the diet of nearly 3 billion people; however, it is a very poor source of minerals, especially Fe. To date, very little is known about which genes are involved in localization of Fe in plant seeds. One of the few examples is VIT1 from *Arabidopsis thaliana*, a vacuolar transporter highly expressed in seeds that controls localization of Fe to the provasculture of embryos. So far, homologs of this gene have not been described in crops. We identified two genes with high similarity to VIT1 in the rice genome, OsVIT1 and OsVIT2. Using RT-qPCR, we observed that under control conditions OsVIT1 is expressed in roots, while OsVIT2 transcripts are found in leaves. Interestingly, OsVIT1 expression is highly induced in shoots upon excessive Fe conditions. To understand the evolution of the VIT family, we carried out similarity searches for VIT1 homologs across 23 plant genomes. We found striking conservation between VIT sequences. Interestingly, 15 plant species show two VIT paralogs, while six have only one and another two have three. All five monocots and most eudicots have two copies, while *Arabidopsis* have only one. Our phylogenetic analysis of VIT family in plants clearly shows that independent duplication events resulted in the observed two copies of VIT genes. The monocots and eudicots gene copies are grouped in separate clades. The VIT1 and VIT2 genes grouped separately within each monocots and eudicots clades. Synonymous to non-synonymous substitution ratio (Ka/Ks) revealed that, although highly conserved, VIT1 and VIT2 groups in monocots show sites under positive selection, which is not observed in eudicots. By analyzing synteny between the chromosome regions where VIT gene copies are located, we proposed an evolutionary model consistent with eudicots paralog copies being less likely to show positive selection, even the species harboring a more ancient duplication event. We are characterizing the molecular function of rice OsVIT1 and OsVIT2 proteins by heterologous expression in yeast and GFP fusions for subcellular localization. These results will help understand the role of VIT proteins in Fe homeostasis in rice plants. Support: CNPq, CAPES.



2826 - Genomics, Molecular Genetics and Biotechnology

Sinara Artico

ISOLATION AND CHARACTERIZATION OF FLOWERS TISSUE SPECIFIC PROMOTERS IN GOSSYPIUM HIRSUTUM FOR CONTROL OF THE COTTON BOLL WEEVIL (*ANTHONOMUS GRANDIS*)

Artico, SINARA; Lambret-Frotté, JULIA; Alves-Ferreira, MÁRCIO;

UFRJ;

The cotton boll weevil (*Anthonomus grandis*) is one of the most important plagues that causes damage to the crop of cotton (*Gossypium hirsutum*). This insect attacks fruits and flower buds, mainly the 6mm diameter ones, the preferred stage for their feeding and breeding. In addition to usual techniques of control, the development of transgenic plants expressing toxins to insects has been extremely successful in combating plagues. The most successful example is plants expressing Cry proteins from *Bacillus thuringiensis*. However, the development of plants resistant to insects not only depends on the identification and characterization of toxins, but also in characterization of plant promoters. Therefore, it is crucial the identification of new promoter regions with strong promoters but also tissue specific activity. The goal of this work is isolate and functionally characterize the adjacent sequence to the coding region of genes characterized as flower specific in *G. hirsutum*. In silico analysis were performed from available information on Cotton Genome EST Database, to identify highly expressed genes in libraries of flowers, fruit or ovule. Three genes were selected for expression analysis by qPCR. The expression analysis of the putative flower specific genes revealed that they all are highly expressed in flower compared with other plant organs (leaf, root, stem, fruit and branch) and both showed high expression in the buds 6 to 12 mm, and mainly in stamens, petals and carpel. The regions upstream of validated ESTs were isolated through Genoma Walker kit and fragments of 1639pb (GhPGFS1), 383pb (GhPGFS4) and 514pb (GhPGFS8) were obtained. Several putative regulatory cis-elements were identified the promoter regions, including elements involved in controlling tissue specific expression in pollen grains and fruits. In vivo analyses of these sequences were performed in transgenic *Arabidopsis* plants by fusing them with the uidA (GUS). GUS staining in *Arabidopsis* was restricted to stamens, petals, carpel and in the apical portion of the siliques and quantitative fluorometric assays showed high activity in flower bud. These promoters fused to GUS were tested in transient expression assays using flower bud of *G. hirsutum* showing to be stamens specific. Because of the activity in floral tissues, such promoters may be an important tool for controlling the cotton boll weevil when used together with genes that encode toxic proteins in transgenic plants in *G. hirsutum*.



3116 - Crop Physiology and metabolism

Guillermo Ariel García

NIGHTTIME TEMPERATURE INCREMENT REDUCES GRAIN YIELD IN WHEAT AND BARLEY: A FIELD STUDY

García,GA; Dreccer,MF; Serrago,RA; Miralles,DJ;

Universidad de Buenos Aires - CONICET;

Climate models predict reductions in the diurnal temperature range as consequence of greater nighttime minimum temperatures without an equivalent change in daytime maximum ones. A better understanding of the impact of nighttime temperature increment (NTI) on the processes affecting wheat and barley grain yield (GY) and quality would lead to improved simulation capability in crop growth models and informed development of adaptation strategies. The objective of this field study was to analyse the impact of a NTI during the critical period on GY and its numerical and physiological components in wheat and barley. The field study combined (i) two crop species: a bread wheat and a two-row malting barley, with (ii) two nighttime temperature regimes: a control (natural temperature) and an increment of ca. 5°C from jointing to 10 days post-anthesis. Crops were modern high-yielding cultivars with similar flowering time, grown in the field at FAUBA,(34°35'S, 58°29'W, 26masl) during 2011 without water, nutritional or biotic constraints. The NTI was achieved using transparent polyethylene chambers (2x2x1.5m) with an iron frame, equipped with electric heaters automatically controlled to increase inside temperature as a differential from outside one, which were placed on the crop at 8pm and removed at 8am. Heat chambers maintained a NTI of 4.6±0.1°C during the treatment period. GY was reduced in both species (13% in wheat and 18% in barley) due to NTI, as consequence of a minor biomass accumulation (17% in wheat and 21% in barley) without changes in harvest index. NTI reduced the critical period duration (ca. 5 days in both species) without important differences in radiation interception efficiency, determining lower intercepted accumulated radiation (16% in wheat and 21% in barley). Radiation use efficiency was differently affected by NTI during this period; it was increased in wheat (18%) but reduced in barley (5%). Grain number per unit of area (GN) was reduced by NTI in a similar proportion than biomass accumulation while grain weight remained relatively constant. GN reduction was associated with a minor spikes number ($r^2=0.71$ in wheat and $r^2=0.63$ in barley). In conclusion, a NTI of ca. 5°C during the critical period reduced GY associated with (i) a diminished capacity for biomass production as consequence of an accelerated development and (ii) a reduced spike establishment probably due to enhanced tiller mortality.



3173 - Crop Physiology and metabolism

Gustavo Ariel SLAFER LAGO

IS FLORET DEATH TRIGGERED BY THE DEVELOPMENTAL STAGE OF THE MOST ADVANCED FLORETS IN DURUM WHEAT?

Slafer,GA; Ferrante,A; Savin,R;

ICREA & University of Lleida;

Yield of wheat is usually related to the number of grains, which is the final outcome of developmental processes related to the generation and degeneration of floret primordia. Survival of floret primordia is more relevant than the maximum number of primordia in determining number of fertile florets -and grains- (JXB 61, 4351 & 62, 4889). Understanding what determines the onset of floret mortality (and later what regulates the rate of floret death) is critical to potentially identifying opportunities to further rising wheat yield. In theory, it could be expected that the mortality of the florets be a process regulated by the availability of assimilates (FCR 100, 125). However, the dependence of floret mortality on growth has been recently challenged (FCR 110, 44) indicating that floret mortality was triggered by the onset of a particular stage of floral development of the most proximal florets of central spikelets. Using a wider database, it has been provided further evidences supporting the relationship between floret death and spike growth (JXB 62, 4889). In this study we analysed to what degree the onset of floret death is related to development of the most advanced florets for crops exposed to a wide range of environmental conditions and different cultivars which would have modified growth and development independently. Briefly, experiments were carried out during 4 growing seasons. Treatments changed among experiments but all in all included different cultivars, unfertilised or N-fertilised and rainfed or irrigated. From terminal spikelet to anthesis, one plant per experimental unit was dissected to count the total number of primordia and to determine their stage of development twice or thrice a week within basal, central and apical spikelets. Although the dynamics of floret primordia generation-degeneration was very similar between seasons, spikelets, cultivars and N x water treatments, there was not a clear developmental stage of the most proximal floret of central spikelets that was synchronic with the onset of floret death across the range of variation explored. The stage of development (AnnBot 51, 119) of the most proximal florets of central spikelets at the timing of the onset of floret death ranged between rather distinct stages of development (W6-W8). Furthermore, the variation in stage of development at which floret death started did not seem related to growing conditions (it was not related to resource availability).



12048 - Genomics, Molecular Genetics and Biotechnology

Jean-Philippe Ral

TOWARDS AN UNDERSTANDING OF THE ROLE OF STARCH PHOSPHORYLATION IN CEREALS

Ral,JP; Bowerman,AF; Cavanagh,CR; Howitt,CA; Morell,MK;

CSIRO Food Future National Flagships;

Australian National University;

Phosphorylation is a critical element of transitory starch metabolism in plants. A key enzyme involved in starch phosphorylation is glucan, water dikinase (GWD), which catalyses the transfer of the β -phosphate from ATP to a glucosyl residue. Phosphate groups increase the starch solubilisation at the granule surface and facilitate access to degrading enzymes, which in turn release maltose and glucose from the chloroplast into the cytosol for further metabolism. Arabidopsis mutants lacking functional GWD display a starch excess phenotype, along with reduced growth. While the role of phosphorylation in transitory starch metabolism is well understood, its importance in cereal endosperm starch remains unclear. To investigate the effect of reducing the starch phosphate content in the endosperm, we have used RNAi to suppress expression of GWD in an endosperm specific manner in wheat. Here we report the results of this study, including the impact on the starch degradative pathway and the unexpected consequences on plant growth.



2895 - Agronomy

Sabine Gruber

DORMANT CANOLA SEED ? STILL A SLEEPING BEAST?

Gruber,S; Weber,EA; Claupein,W;

University of Hohenheim;

Background Shed seeds of canola (*Brassica napus*) can fall dormant in the soil and cause volunteer plants in following crops. In this way, GM (genetically modified) traits and genes can persist in the environment by hybridization with other plants or by admixture with seeds from conventional crops. Many consumers in the EU are concerned about GM crops, and strategies are needed to confine genes and traits in the original crop. Aim of the study was to select canola genotypes with low seed dormancy and to assess volunteer emergence by a modelling approach which includes pre-existing cropping data. Common German winter canola varieties (open pollinated) were tested (2 locations, 2 seasons) for secondary dormancy by a standard test. The self-fertilized offspring of randomly selected plants of each variety was then grown in the field in small plots, and again tested for dormancy to detect the heritability of the trait. A selection for low dormancy in an originally high-dormancy variety was performed in the greenhouse over three generations. The data was used to update a modelling approach which also includes cropping data (such as tillage and crop rotation) to calculate volunteer density in practical farming. Dormancy ranged from 2% to 90% dormant seeds across the varieties in the field, and correlated significantly between the two locations and two seasons ($R^2=0.93$). All varieties were composed by plants with individual levels of dormancy. The trait turned out to be heritable as the offspring of low-dormancy plants from a low-dormancy variety had similar dormancy as the parental variety. Furthermore, three steps of selection for low dormancy in an originally highly dormant variety (78% dormant seeds) in the greenhouse resulted in an offspring with about 1% dormancy, when all generations were grown together in the field in the same year. These results corroborate with the recent discovering of QTL for dormancy of canola seeds. Varieties with low dormancy resulted in the model and in practice in a clearly smaller soil seed bank and lower infestation of the following crops with volunteers. The heterogeneity of canola varieties and the heritability of the trait "dormancy" allows to breed low-dormancy genotypes which can be used as confinement system. The combination of appropriate genotype and cropping system would well reduce gene escape by volunteers from GM and conventionally bred varieties.



3211 - Agricultural Extension and Economics

Senthold Asseng

THE AGMIP WHEAT PILOT STUDY: A SENSITIVITY ANALYSIS WITH 27 CROP MODELS.

Asseng,C; Ewert,F; Rosenzweig,C; Jones,JW; Hatfield,JL; Ruane,A; Boote,KJ; Thorburn,P; Rotter,RP; Cammarano,D; Brisson,N; Basso,B; Martre,P; Ripoche,D; Bertuzzi,P; Steduto,P; Heng,L; Semenov,MA; Stratonovitch,P; Stockle,C; Oleary,G; Aggarwal,PK; Nareshkumar,S; Izaurralde,C; White,JW; Hunt,LA; Grant,RP; Kersebaum,KC; Palosuo,T; Hooker,J; Osborne,T; Wolf,J; Supit,I; Olesen,JE; Doltra,J; Nendel,C; Gayler,S; Ingwersen,J; Priesack,E; Streck,T; Tao,F; Muller,C; Waha,K; Goldberg,R; Angulo,C; Shcherbak,I; Biernath,C; Wallach,D; Travasso,M; Challinor,A;

Agricultural & Biological Engineering Department, University of Florida, Gainesville, FL 32611, USA;

The Agricultural Model Intercomparison and Improvement Project - AgMIP (www.agmip.org) aims to provide more robust estimates of climate impacts on crop yields and agricultural trade, including estimates of associated uncertainties. In the AgMIP Wheat Pilot Study, 27 wheat crop simulation models were tested with quality-assessed field experimental data from four contrasting environments from The Netherlands, Argentina, India and Australia using standardised protocols to study the role of crop model-based variability in projections of climate change impacts. The environments represent major wheat-producing regions of the world. A standardised sensitivity analysis was carried out with each model for each of the environments with a range of temperature and CO₂ changes and seasonal variability in rainfall indicating strengths and weaknesses across crop models. Results from the model intercomparison will be presented. Implications for model applications to climate change and global food security studies, for model improvement and for needed field experiments are discussed.



2887 - Agronomy

Thin Mei Choo

EARLY PLANTING MITIGATES THE LEVEL OF DEOXYNIVALENOL CONTAMINATION OF BARLEY IN EASTERN CANADA

Choo,TM; Martin,RA; Savard,ME; Blackwell,BA;

Eastern Cereal and Oilseed Research Centre;

Fusarium head blight, principally caused by *Fusarium graminearum*, is a destructive disease of barley in many countries. *Fusarium* species produce mycotoxins such as deoxynivalenol (DON) in the grains. An integrated management strategy is needed to mitigate the level of DON contamination in barley. Therefore, a study was initiated to determine if early planting and earliness can be used to avoid severe contamination of DON under natural infection conditions in Eastern Canada. Twelve six-row barley cultivars were planted in a split-plot design with two planting dates (early vs. late) as main-plot units and cultivars as sub-plot units in Prince Edward Island for four years (2007, 2008, 2010, and 2011). Among these 12 cultivars, two (OBS4714-1 and Nordbec) were early heading, five (AC Alma, Chapais, Brucefield, AC Vision, and AC legend) were medium heading, and five (AC Klinck, Stander, AC Westech, Encore, and Synasolis) were late heading. Data for grain yield, heading date, and DON content were collected for each plot. Early planting resulted in less DON than late planting in 2007 (0.9 vs. 1.7 mg/kg), in 2008 (1.7 vs. 3.8 mg/kg), and in 2011 (4.0 vs. 9.9 mg/kg). But the DON content in 2010 was similar between the two planting dates (10.2 vs. 9.6 mg/kg). The reason for this could be due to an abnormally high rainfall in June 2010 (156 mm), which was twice or three times the amount of June rainfall in the other three years (51 - 85 mm). For the majority of the 12 cultivars, early planting resulted in less DON contamination in comparison with late planting. But some cultivars contained the same level of DON in early planting as in late planting. Days to heading was positively correlated with DON content at late planting in 2007, indicating that early heading cultivars might have escaped the heavy infection of *Fusarium* head blight. No such correlation was found in the other three years. Early planting also results in higher yield than late planting in 2008 (3.1 vs. 0.8 t/ha) and 2011 (3.6 vs. 3.0 t/ha). The results of this study suggest that six-row barley should be planted early in Eastern Canada to avoid a high level of DON contamination and a reduction in grain yield.



3170 - Agricultural Extension and Economics

Wei-li LIANG

A LOT MORE WITH LESS: IMPROVING PROFITABILITY OF THE WHEAT-MAIZE PRODUCTION IN THE NORTH CHINA PLAIN WITH BETTER FIELD MANAGEMENT AND RATIONAL INPUT

Yang,RUIHUA; Liang,WEILI; Wang,GUIYAN; Lv,HONGZHAN; Xia,AIPING;

China Agricultural University;

Wheat-maize double cropping is the most important system producing staple food grains, animal feed and raw industrial materials in the North China Plain and in China. It has been proved that an approximate 30% increase in annual productivity of the system can be achieved by eliminating the 'easy to overcome' problems. However, a big concern has been the profitability of such a 'great leap' of productivity. Analysis in this paper uses the data from a survey covering 389 farmer households at 18 villages in 6 counties of Hebei province in North China Plain, and data from maximum yield demonstration plots in the same counties in the same year in 2006. A partial budget was built to compare average production in farmers' fields to maximum yield production in demonstration plots. Average maximum yield and the average yield in farmers' fields of winter wheat (*Triticum Aestivum* L) are 9.1 ton ha⁻¹ and 6.6 ton ha⁻¹ respectively in the six counties, while the average maximum yield and average yield in the farmers' fields of maize (*Zea Maize* L) are 10.5 ton ha⁻¹ and 7.3 ton kg ha⁻¹ respectively, that produce the maximum and the average farm yields of the cropping system as 19.6 ton ha⁻¹ and 13.9 ton ha⁻¹ respectively. These data indicate that the current farm yield is 71% of the maximum annual yield. This means that annual productivity of the cropping system could be increased with currently available techniques by 29%. Problems limiting crops yields in farmers' fields include: Confusion in variety use, unsatisfactory land preparation before wheat sowing, over seeding of wheat and under seeding of maize, untimely sowing, unbalanced nutrient application, poor irrigation practice, untimely and improper pest and diseases control, too early harvesting of maize, etc. The result of the partial budgeting reveals that 29% increase of annual productivity of the wheat-maize system obtained with improved field management and rational input reduces total cost (fertilizer on wheat, irrigation frequency and seed cost) by 478.5 Yuan RMB ha⁻¹, adds a total value (wheat and maize grain yields) of 10 696 Yuan RMB ha⁻¹. With a slight fertilizer cost increase on maize (664.5 Yuan RMB ha⁻¹), the yield 'leap' results in a net gain of 111 74.5 Yuan RMB ha⁻¹. This result indicates that, with currently available knowledge and technology, a much greater profit can be obtained with a little less cost in the wheat-maize cropping system in the North China Plain.



3307 - Crop Physiology and metabolism

Ignacio Alzueta

GRAIN NITROGEN PERCENTAGE IN WHEAT AND BARLEY GROWN UNDER A WIDE RANGE OF YIELDING CONDITIONS AND IN RESPONSE TO POST FLOWERING DEGRAINING

Alzueta,I; Serrago,RA; Abeledo,LG; Miralles,DJ; Savin,R; Slafer,GA;

Facultad de Agronomía, Universidad de Buenos Aires;

Wheat and barley are the main small-grain crops. Due to industry requirements, grain nitrogen percentage (GNP) must be kept within certain limits (>1.7% in bread wheat and 1.6-1.9% in malting barley). GNP is the end result of the dynamics of carbon (C) and nitrogen (N) accumulation. Not only are these dynamics different but also C accumulation seems mostly sink-limited whilst N accumulation seems mostly source-limited (depending largely on remobilization of vegetative N, absorbed before flowering). However, there is debate in the literature on the appropriateness of generalizations of these limitations. We evaluated how changes in the source:sink ratio during the grain filling period affect GNP in wheat and barley through three experiments, one in Argentina (Buenos Aires) and two in Spain (Agramunt and Giménez); all in all combining (i) different genotypes, (ii) low and high input levels, and (iii) different source:sink ratios during post flowering (control and hand-trimming the spikes removing 50% of the spikelets 7 days after flowering). The range of yield explored across the environmental conditions was 3.1 to 9.9 Mg ha⁻¹. Across this range, wheat showed higher GNP and N content (mgN grain⁻¹) than barley. Trimming the spikes determined higher increases in N than in dry weight of the grains (c. 20 vs. 5 %, respectively). Thus, overall conditions, there was a much greater N than C source-limitation. Response to trimming was also generally sharper in wheat than in barley, though the magnitude of the response showed interaction between genotypes, level of inputs and sites. Differences in the absolute N content in the grains between species were explained by the proportion of vegetative N remobilized to the grains, which was higher in wheat than in barley. There was a negative relationship between the grain N percentage and the proportion of biomass and N partitioned to the grains (HI:NHI ratio) and the physiological nitrogen use efficiency (NUE). Barley showed higher values of both variables and consequently lower GNP than wheat. In conclusion, we observed a generalized higher N than C source-limitation during grain filling across rather different growing conditions, and that constitutive differences between species in final GNP seemed explained by their differences in HI:NHI ratio and NUE.



3301 - Agronomy

Marcos Lima Campos do Vale

DYNAMICS OF AMMONIA VOLATILIZATION FROM APPLIED UREA EVALUATED BY ADJUSTED PARAMETERS OF A LOGISTIC FUNCTION

Vale,MLC; Sousa,RO; Scivittaro,WB;

Eliseu Maciel Agronomy College, Pelotas Federal University;

Urea is the nitrogen source most affected by ammonia volatilization losses. The relevance of this process is related to the potential reduction of urea efficiency as nitrogen fertilizer. Even though the mainly strategies taken for data analysis have been producing important results on ammonia volatilization loss studies, they provide few details about process behavior. One way for a more detailed study of the variable behavior is the investigation of its characteristic curve, through which the functional relation between the ammonia volatilization and a single or a set of factors can be observed. The purpose of this study was to evaluate the behavior of cumulative ammonia volatilization losses from urea applied, affected by two different soil classes (Vertic Argiaquolls and Typic Albaqualf) and the amount of urea applied (50, 100 and 150 kg ha⁻¹ urea nitrogen), with or without N(n-butyl) thiophosphoric triamide urease inhibitor. To test our hypothesis, we have adjusted the cumulative ammonia volatilization dataset to a logistic function and adopted its function parameter values as an indirect response variable. The logistic function used, $P(t-t_0) = B/[1-e^{-A(t-t_0)}]$, was the result of the separation of variables, partial fractions and substitution integral techniques applied to a modified Verhulst differential equation $dP(t-t_0)/d(t-t_0) = A\{1-[P(t-t_0)/B]\}P(t-t_0)$, where "P" is the population size, t is the time unit, "t₀" is the reference time, "A" is the rate of population growth and "B" is the maximum population size under self-limiting conditions. Univariate and multivariate analyses of variance were performed. These analyses have shown a major effect of soil class factor, which indicate a greater relevance of the adsorption potential on ammonia losses, and that the urease inhibitor had no effect on ammonia total losses. The evaluation of ammonia volatilization characteristics curves is a simple way to provide details about the variable behavior which can be used to develop more accurate techniques to increase the efficiency of urea as nitrogen source for crops.



2813 - Crop Ecology, Management & Quality

Mikhail Semenov

MODELLING PREDICTS THAT HEAT STRESS, NOT DROUGHT, WILL INCREASE VULNERABILITY OF WHEAT IN EUROPE

Semenov, MA;

Rothamsted Research;

New crop cultivars will be required for a changing climate characterised by increased summer drought and heat stress in Europe. However, the uncertainty in climate predictions poses a challenge to crop scientists and breeders who have limited time and resources and must select the most appropriate traits for improvement. Modelling is a powerful tool to quantify future threats to crops and hence identify targets for improvement. We have used the Sirius wheat simulation model combined with local-scale climate change scenarios based on the CMIP3 multi-model ensemble of global climate model future projections to predict impacts of heat stress and drought on wheat in Europe. Despite the lower summer precipitation predicted for 2050s across Europe, relative yield losses from drought is predicted be smaller in future, because wheat will mature earlier avoiding severe drought. By contrast, the risk of heat stress around flowering will increase, potentially resulting in substantial yield losses for heat sensitive cultivars commonly grown in northern Europe.



3196 - Seed Physiology, Production & Technology

Emanoella Lima Soares

PROTEOMIC ANALYSIS OF DIFFERENT REGIONS IN THE INNER INTEGUMENT OF JATROPHA CURCAS L. SEEDS

Soares,EL; Shah,M; Rocha,AJ; Nogueira,FCS; Carvalho,PC; Soares,AA;
Domont,GB; Campos,FA;

Universidade Federal do Ceará;

In order to understand the biochemical and physiological events which characterize the programmed cell death in the inner integument of *Jatropha curcas* seeds a detailed proteomic analysis was undertaken in different regions of this tissue. The regions from the inner integument were dissected using a binocular microscope and were separated according to the proximity with the embryo. They were named proximal and distal if were close or distant of that tissue, respectively. A LC/MS/MS analysis of these two regions resulted in the identification of 759 proteins, in which 148 were unique from the proximal region and 245 were unique from the distal region. The gene ontology annotation and functional classification of the identified proteins from these two regions indicates that, the protein expression profile was different. In the proximal region, hydrolases, especially proteases, and proteins involved in cell wall degradation were prevalent compared with the proteins identified in the distal region. This suggests that the process of programmed cell death in the inner integument starts in the nearest region of the embryo consistent with the role of this maternal tissue to providing nutrients to the developing embryo. In the distal region, a significant number of the proteins identified were related to amino acid and protein synthesis machinery of cells showing a prevalent anabolic process in this region in contrast to the prevalent catabolic process in the proximal region. In conclusion, this study provides important information for the better understanding of the mechanism involved in programmed cell death of the inner integument of *Jatropha curcas* seeds.



2830 - Crop Physiology and metabolism

Emi Kaburagi

PHYSIOLOGICAL REASONS OF SALINITY TOLERANCE AND SODICITY TOLERANCE

Kaburagi,E;

Tottori University;

Salt-affected soils cause problems in arid land agriculture and are divided into saline soil and sodic soil. Saline soil mainly inhibits water absorption by plants due to low soil osmotic potential. Sodic soil causes Na toxicity and disturbs the homeostasis of essential cations such as K, Ca, Mg, and microelements. According to Maas (1984), barley is tolerant to both saline and sodic stresses, spinach is sensitive to saline stress and moderately tolerant to sodic stress, and kidney bean is sensitive to both stresses. Most plant species have a same tolerance to both stresses. However, alfalfa is classified as sensitive to saline stress, but as tolerant to sodic stress. The physiological reasons for the classification are not clear. The purpose of the present study is to elucidate the physiological reasons for the classification. The four plant species were grown in PEG6000 (PEG) solution whose osmotic potential was equal to that of 80mM NaCl. Dry weight, water content, and water absorption of plants were determined. In saline stress, dry weight of four species supported the Maas classification. PEG did not affect growth and water content of barley, but decreased water absorption. In other species, PEG decreased growth and water content. It is interesting that the water content of alfalfa was extremely decreased in PEG. This shows that the classification of salinity tolerance is related to the osmotic adjustment and stomatal adjustment. The four species were grown in a sodic soil (SO; pH 8.2, SAR 43.5) and a high pH soil (PH; pH 7.8, SAR 4.6), and were artificially made from Tottori dune soil. Dry weight and contents of Na, K and Fe of plants were determined. The growth of alfalfa was not affected by SO treatment but that of barley and spinach was significantly decreased. Under SO treatment, barley and spinach accumulated Na in shoot, whereas alfalfa accumulated it in root. Barley and spinach accumulated more Na than K in shoot, although alfalfa accumulated more K than Na. This shows that the classification of sodicity tolerance is related to the ability of the species to inhibit Na translocation to shoot and to maintain a low Na content and a high K content in shoot. The Fe content of spinach and alfalfa was not affected by SO treatment. Na raises soil pH and induces the deficiency of essential microelements. Thus, the absorbing ability of microelements can be another index of the sodicity tolerance of plants.



3249 - Crop Ecology, Management & Quality

Koki Homma

EVALUATION OF RICE PRODUCTIVITY WITH RICE GROWTH SIMULATION MODEL IN SANKER RIVER BASIN, CAMBODIA

Homma,K; Tsujimoto,K; Hirooka,Y; Koike,T; Tamagawa,K; Aida,K;

kyoto university;

In order to develop the strategy to overcome food crisis and climate change, the evaluation of crop productivity is firstly recommended. Since the water availability fundamentally affects the crop productivity, it is better to develop the strategy on the unit of water basin. This study focused on the Sanker river basin, where the information of crop productivity is quite limited. Since rice is the main crop in the area, we evaluated weather condition for rice production by using a simulation model. Weather data in the area was obtained from Global Land Data Assimilation System (GLDAS) in NASA. Original data is 0.25° mesh, but was resized to 0.1° mesh for future study. A rice growth simulation model, SIMRIW-rainfed developed by Homma and Horie (2009), was used for the evaluation of crop productivity. Cultivar parameters that imitate IR 64 (improved type indica) and KDML 105 (traditional type indica in Thailand) were prepared. Field parameters such as nitrogen supply rate and soil moisture at field capacity were generated from soil texture derived from Land Data Assimilation System at the University of Tokyo (LDASUT, Lu et al. 2009). The simulated results show that the rice productivity is strongly restricted with soil moisture content and has great possibility to be improved by upgrading irrigation network. KDML 105 sometimes shows higher yield than IR 64 because of its longer growth duration, but IR 64 has the possibility of double cropping even though under rainfed condition. The field investigation to validate simulation results will be conducted in next study. Cultivar parameters for Cambodian rice cultivars are also necessary for further study. We now try to combine the simulation model to Water Cycle Integrator (WCI, Koike 2011) to calibrate weather data from GLDAS and to incorporate irrigation management.



2908 - Biomedical, Health-Beneficial and Nutritionally Enhanced Plants

Sang-Soo Kwak

TRANSGENIC SWEETPOTATO WITH ENHANCED CONTENT OF CAROTENOIDS

Kwak,SS; Kim,SH; Jeong,JC; Lee,HS;

Environmental Biotechnology Research Center, Korea Research Institute of Bioscience and Biotechnology (KRIBB);

Sweetpotato (*Ipomoea batatas* (L.) Lam) ranks seventh in annual production among food crops in the world. It is also an alternative source of industrial materials such as starch, ethanol and antioxidants including carotenoids. Moreover, it does not require large amounts of fertilizer and pesticides for cultivation and is rather tolerant to some environmental stresses. Its wide adaptability on marginal land ranging from tropical to temperate zones and rich nutritional content provide a high potential for preventing malnutrition and enhancing food security in the developing countries. The nonprofit Center for Science in the Public Interest (CSPI) designated the sweetpotato as one of ten super foods for better health, since it contains high levels of antioxidants, potassium and fibers. Recently, sweetpotato is very popular as the well-being food in the developed countries. Antioxidants have been attracted special attention because they can protect human body from oxidative stress, which may promote aging and many diseases including cancer. The oxidative stress is one of the major damaging factors reducing plant growth and productivity. Despite the importance of sweetpotato as the well-being food source, relatively little research has been carried out on sweetpotato antioxidants at the molecular level. In this respect, we are trying to generate transgenic sweetpotato with high yields of β -carotene by down-regulation of β -carotene hydroxylase (CHY-b) and lycopene ϵ -cyclase (LCY- ϵ). Our results indicated that down-regulation of gene expression of both *l*bCHY and *l*bLCY- ϵ by RNAi technology increase the content of carotenoids including β -carotene and enhance tolerance to oxidative stress in transgenic sweetpotato cells. In addition, we have recently isolated *l*bOrange gene responsible for carotenoid accumulation from the orange-fleshed sweetpotato. Transgenic sweetpotato calli overexpressing *l*bOrange gene showed a distinctive yellowish color with high levels of carotenoids compared to control cells. In the presentation, further characterization on down-regulation of *l*bCHY and *l*bLCY- ϵ , and *l*bOrange gene will be introduced in terms of the content of carotenoids and oxidative stress tolerance. We anticipate that rational metabolic engineering of carotenoids will lead to development of eco-friendly industrial sweetpotato plants with enhanced content of carotenoids on marginal land.



3361 - Genomics, Molecular Genetics and Biotechnology

Anderson Luis Nunes

THE RELATIONSHIP OF THE OSCPL1 GENE WITH THE SEED SHATTERING

Nunes,AL; Bispo,NB; Delatorre,CA; Merotto-Júnior,A;

Instituto Federal do Rio Grande do Sul;

Better understanding of seed shattering regulation in red rice can be used to develop biotechnological procedures to reduce the problems of this weed. The objective of this study was to characterize the expression and nucleotide composition of OsCPL1 gene in rice genotypes with contrasting seed shattering. The analysis was performed by real-time RT-PCR. The high-abscission genotypes selected were red rice ecotypes AV 31 and AV 60 and low seed shattering genotypes were Batatais and Lacassine. The RNA extraction was carried out using Trizol ten days after pollination from tillers with panicles pollinated naturally. Each genotype had three biological replicates and each biological replicate had four technical replicates. The endogenous control was performed by expression of the 28S rRNA gene. The relative expression analysis was performed using the Dussault & Pouliot formula (2006). In red rice ecotypes which have abscission, gene expression was higher in respect of the crops that have a lower seed shattering. Thus, OsCPL1 gene expression was related to the activation process of abscission. The OsCPL1 expression pattern was detailed by the generation of transgenic plants expressing the GUS reporter gene under the control of gene promoter OsCPL1 (Ji et al., 2010). Histochemical analysis showed expression of OsCPL1 in the region surrounding the abscission layer. Furthermore, it was noted that higher expression levels induced lower levels of seed shattering. This pattern of expression demonstrates that the OsCPL1 is involved in repression of development of the abscission layer. Thus, the relationship between the expression and the level of seed shattering in AV 60, AV31, Lacassine and Batatais was contrary to what was expected. Because in these genotypes the OsCPL1 expression was related to the presence of seed shattering and not with the suppression of dehiscence as observed by Ji et al. (2010). The explanation for the difference observed may be in the nucleotide composition of gene OsCPL1. At the end of intron seven Ji et al. (2010) found a SNP (A to T) at position 5498 of the gene causing a 15-bp deletion of its mRNA as a result of altered splicing making the present seed shattering. However, none of the genotypes in this study showed the SNP expected. Moreover, in the exon six was observed by the Ji et al. (2010) three mutations that were not found. Therefore, the differentiated nucleotide composition of the OsCPL1 may explain the result obtained.



3387 - Genomics, Molecular Genetics and Biotechnology

André Luiz de Lima Passianotto

MAPPING RR TRAIT IN SOYBEAN GENOME BY GENOTYPING BY SEQUENCING METHODOLOGY

Passianotto, ALL; Belzile, FJ; Sonah, H; Ilquira, E; Abdelnoor, RV;

Empresa Brasileira de Pesquisa Agropecuária - Embrapa Soja;

Genotyping by sequencing (GBS) has become an important approach to identify SNPs and has been very useful to population studies, germplasm characterization and also mapping of specific traits in plants. This work aimed to characterize soybean cultivars and to identify the location of the Roundup Ready (RR) by GBS. In order to be suitable for sequencing, the DNA from 90 soybean cultivars were purified with the DNeasy Plant Mini Kit from Qiagen, and digested with ApeKI, a type II restriction endonuclease that recognizes a degenerate 5 bp sequence. Barcode adapters were added to the fragments, allowing the discrimination of the soybean cultivars sequences. To minimize the possibility of misidentifying samples, all pair-wise combinations of barcodes differed by a minimum of three mutational steps. To avoid the potential loss of sequence quality due to phasing errors caused by reading through a non-variable restriction site prior to the twelfth base, barcode lengths were modulated from 4 to 8 bp and care was taken to maximize the balance of the bases at each position in the overall set. Preparation of Libraries for Next-Generation Sequencing up to 96 DNA samples can be processed simultaneously. Samples are then digested with ApeKI and adapters are ligated to the ends of genomic DNA fragments, appropriate primers with binding sites on the ligated adapters are added and PCR is performed to increase the fragment pool. The libraries were sequenced using Solexa technology. In the standard protocol, we identified 46,651 SNPs. After to remove the SNP loci with less than 20% missing data in order to exclude sites on the basis of the proportion of missing data we obtained 19,392 SNPs, to perform the association mapping the filter chosen was 0.1, meaning the minimum frequency of the minority polymorphisms for the site to be included in the filtered data set, generating 7,103 SNPs. Using the TASSEL program, we performed an whole genome scan of the Roundup Ready trait. Utilizing the kinship and Principal component analysis we identified, by the mixed linear model, the region of chromosome 2 contains SNPs with p-value in the range of 3,6E-6 to 9,8E-5 highly associated with the RR characteristic. The use of restriction enzymes to reduce the complexity of GBS is an advantage to eliminate repetitive regions, and prioritize important regions of the genome. This technology proved to be competent to identify regions linked to specific traits.



3107 - Crop Physiology and metabolism

Bárbara França Negri

ROOT TRAITS ANALYSIS OF RECOMBINANT INBRED LINES TO IMPROVE PHOSPHORUS ACQUISITION EFFICIENCY IN MAIZE

Negri,BF; Azevedo,GC; Matos,FM; Magalhães,KS; Guimarães,CT; Sousa,SM;

Embrapa Milho e Sorgo;

Phosphorus (P) is essential macronutrient for plants, which is acquired from the rhizosphere solution as phosphate (Pi), primarily in the form of $H_2PO_4^-$. The concentration of Pi in the soil solution is often low, therefore the supply of Pi to the root surface by diffusion is slow. Hence, P is one of the least available mineral elements in the soil and frequently limits plant growth. Crop production always requires P fertilizers to maintain yield and quality. An alternative to ameliorate this problem is to explore the genetic diversity available in plants and breed more Pi-absorption efficient cultivars in combination with soil management practices. This study aimed to analyze maize root traits that could be involved in P acquisition efficiency. We used a paper pouch system with Magnavaca's nutrient solution (low P - 2.5 M) under a controlled environment to evaluate four root traits (length, volume, diameter and volume of fine roots) in a population of 145 recombinant inbred lines (RILs) derived from a cross between maize genotypes L3 and L22, which have contrasting adaptation to low P availability in the field. High heritability (79.1 to 86.1%) and low coefficient of variation (7.1 to 22%) were detected for the root traits. Additionally, Principal Component Analysis (PCA) enabled us to differentiate contrasting maize RILs based on the selected root morphology traits. The first principal component (PC1) explained 66.2% of the variation while the second principal component (PC2) explained 31.2%. PC1 had positive eigenvector coefficients for all variables, except for root diameter. PC1 was explained most by root volume and PC2 was explained mostly by root diameter, allowing identification of the lines with contrasting root system traits. These phenotypic results will be used in the discovery of root morphology QTLs that are also involved on P acquisition efficiency in maize.



3169 - Agronomy

weijian zhang

RESPONSES AND CONTRIBUTIONS OF RICE CROPPING SYSTEM TO CLIMATE CHANGE: EVIDENCES FROM FIELD EXPERIMENTS IN CHINA

Zhang,WJ;

Chinese Academy of Agricultural Sciences;

To learn the responses and contributions of rice cropping system to climate change in China will greatly enhance our understanding of the impacts of global warming on food security, and will significantly benefit the strategy decision and technology selection of future crop production. We, therefore, have conducted a series of field experiments since 2004 to investigate the impacts of (1) high temperature on rice growth; (2) nighttime warming on rice production; (3) rice cropping on greenhouse gases emissions; and (4) rice cropping on soil organic carbon sequestration. The main results of our ongoing researches are partially summarized as follows. High temperature significantly decreased rice yield and grain quality, and there were large differences in heat injury among rice varieties. Significant difference in rice canopy temperature existed among the fertilization and irrigation regimes under same temperature background. The impacts of nighttime warming on rice productivity depended on the cropping patterns and regions. Negative effects existed on the early rice yield of double rice cropping system in South China and the single rice yield of rice-wheat cropping system in East China, while significantly positive effects on the later rice yield of double rice cropping system in South China and the rice yield of single cropping system in Northeast China. Great positive effects of nighttime warming were found on the total annual yields of all rice cropping systems in China. Nighttime warming may benefit crop production in China if suitable cropping adaptations are taken. There were large differences in the greenhouse gases emissions among rice cropping patterns. Rice variety selection and field water management showed great potential to mitigate the emissions of greenhouse gases. Crop residue recycling with water-saving irrigation pattern can not only enhance system productivity but also decrease the total emissions of greenhouse gases. Rice cropping for high-yield and low-emission can be integrated into one aim. Rice cropping significantly increased the content of soil organic carbon. There was no significant effect of no-tillage on soil organic carbon in paddy field, while crop straw recycling and cropping patterns showed great positive effects on soil organic carbon sequestration.



3300 - Plant Genetic Resources

Chang Hyu Bae

GROWTH AND GENETIC DIVERSITY ANALYSIS OF GENUS TARAXACUM ACCESSIONS COLLECTED IN KOREA

Ryu, JAIHYUNK; So, HYUNSU; Choi, GAMLIM; Bae, CHANGHYU;

Sunchon National University;

Genus *Taraxacum*, a perennial plant in the family Asteraceae, has been widely utilized for medicinal and edible purposes. In order to develop useful genetic resources characteristics of growth, and genetic diversity and relationship were evaluated by using *Taraxacum* accessions collected from various regions in Korea. Flowering was twice per year in Korean native species (*T. mongolicum*, *T. coreanum* and *T. coreanum* var. *flavescens*), however, many times in Korean naturalized species (*T. officinale* and *T. laevigatum*). The number of peduncle and the annual seed yield of the naturalized species were 5 to 11 times higher than that of the Korean native dandelion. The genetic diversity and the genetic relationship by using 32 accessions of five *Taraxacum* species (*T. mongolicum*, *T. coreanum*, *T. coreanum* var. *flavescens*, *T. officinale* and *T. laevigatum*) were evaluated by using ISSR markers. A total of 142 ISSR loci detected overall were all polymorphic loci (100%) among the five species of *Taraxacum*. According to the clustering analysis, the three native species were divided into 4 independent groups and the two naturalized species were classified into 3 independent groups except 2 accessions. When the genetic variations of trnL-trnF region were evaluated using 23 accessions, nucleotide lengths of the trnL-trnF region ranged from 929 to 930 bp in the native dandelions, but those of the naturalized dandelions ranged from 910 bp (*T. officinale*) to 975 bp (*T. laevigatum*). Insertion, deletion and transposition of DNA sequence of the trnL-trnF region were occurred in 47 sites among the individuals, showing 11 classification sites of DNA sequence between the native and the naturalized dandelions.



3281 - Crop Physiology and metabolism

Felicity Harris

THE RELATIONSHIP OF DEVELOPMENTAL GENES, GROWTH HABIT AND SEEDLING VIGOUR OF WHEAT

Harris,FAJ;

Charles Sturt University;

Early vigour in wheat increases water use efficiency, improves weed suppression, provides a grazing opportunity while crops are vegetative and may lead, in some circumstances, to increased biomass at flowering which has been correlated with grain yield. In other circumstances rapid early growth may lead to excess water use and reduced yield when water is limiting. There are some published observations that early maturity in wheat is associated with increased seedling vigour. Three field experiments were conducted between 2010-2011 in southern Australia observing differences in the early vigour and growth habit of a series of genotypes. The selected genotypes consisted of doubled haploid lines derived from the cross between cv. Janz and cv. Diamondbird and possessed allelic variance for Vrn-A1, Vrn-B1, Vrn-D1 and Ppd-D1. Results of the three field experiments consistently indicated genotypes responsive to vernalisation (winter wheats) showed significantly greater prostrate growth habit than the mostly spring genotypes which had an erect growth habit.



3167 - Crop Ecology, Management & Quality

kwang soo kim

USE OF CLIMATE DATA TO PREDICT YIELD OF MISCANTHUS IN SOUTH AMERICA

Kim,CY; Kim,KS;

Seoul National University;

Use of climate data to predict yield of Miscanthus in South America Introduction Simulation models for Miscanthus have been developed to predict temporal growth pattern as well as potential yield. These growth simulation models would help identify the optimal site for Miscanthus production. The objective of this work was to develop a simple yield prediction model for Miscanthus based on monthly climate data, and identify suitable production areas of Miscanthus in South America. Materials and Methods The Miscanthus Mapping (M2) model was developed to provide qualitative yield prediction assessing climate conditions in relation to growth of Miscanthus. Growing degree day, precipitation, and number of hours in a specific range were used as input variables. Yield of Miscanthus, Y , was estimated as follows: $Y = DD \cdot G_m$, where DD and G_m represent a seasonal growth condition and a growth condition in a month m , respectively. DD was defined as follows: $DD = \sum D$ (GDD), where GDD and DD indicate growing degree day above base temperatures of 10°C and its membership function, respectively. G_m was defined as follows: $G_m = \sum T(T_m) \cdot \sum P(P_m) \cdot \sum X(P_X)$, where $\sum T$, $\sum P$, and $\sum X$ are membership function of temperature, and monthly precipitation and extreme precipitation. T_m indicate the average number of hours between 11-16°C in a day. P_m and P_x represent total precipitation in m. Iterative process were performed to determine the parameters of M2 model. A set of parameters were used to predict yield in Europe using the M2 model. Then, predicted yield from M2 model was compared with that of MISCANFOR, which is a Miscanthus growth model in Europe to select the optimum set of parameters. Results Under current climate condition, the M2 model predicted that high yield of Miscanthus could be obtained in Southern Brazil, Uruguay, areas near Santiago, Chile. High yield of Miscanthus was also predicted in mountain areas in Peru using the M2 model. Discussion By combining yield prediction under current climate as well as future climate, it would be possible to identify suitable area for Miscanthus production. The M2 model would make it easy to predict yield potential under climate change conditions because future climate datasets are monthly data. Currently, no phenology is considered in the M2 model, which merits further improvement of the M2 model for accurate prediction in tropical areas, e.g., northern South America.



3124 - Genomics, Molecular Genetics and Biotechnology

Wesley T Barber

GENETIC VARIATION FOR RETROTRANSPOSON DERIVED SMALL INTERFERING RNAS

Barber,WT; Li,Q; Hudson,ME; Moose,SP;

University of Illinois at Urbana-Champaign;

At the DNA level, transposable elements (TEs) have shaped plant genomes by expanding their size, disrupting collinearity and creating genetic variation. At the RNA level, TEs influence the growth and development of plants through their generation of small interfering RNAs (siRNAs) that act in cis on the TE source or in trans on other TEs and genes. We have previously shown that maize possesses a novel source of genetic variation for regulating both TEs and genes at a genomic scale in the form of 21-22-nt siRNAs derived from retrotransposons, which may contribute to the species' high degree of observed heterosis. To describe the sRNA biology of TEs of the species, we are characterizing the variation in retrotransposon derived siRNAs across 36 maize inbred lines using sRNA sequencing. We are mining this data to identify variation for post-transcriptional regulation of genes that is mediated by retrotransposons. We are estimating genetic relatedness of the inbreds based on their siRNA profiles to determine if this information can predict hybrid performance. This research will enhance crop improvement strategies by demonstrating how to leverage high-throughput sequencing technologies to document functional variation in an important but often overlooked portion of plant genomes, the TEs. This research also has broader impacts beyond crop improvement because it addresses why retrotransposons are expressed in dividing tissues.



Plenary Talks



Plant Breeding in the New Millennium: Priorities and Prospects

Chittaranjan Kole

Clemson University, Clemson, South Carolina, USA

The new millennium is expected to witness several challenging problems including increasing rate of human population, incidence of fatal diseases and malnutrition, depletion of fossil fuels, genetic erosion of biodiversity, and drastic effects of climate change and global warming. Such changing scenarios will require employment of pragmatically improvised plant breeding strategies and tools for developing crop varieties with strikingly augmented yield of food, feed, fiber, fuel, etc. At the same time attempts should be made for breeding functional food and feed varieties with improved content of nutritional and nutraceutical compounds. Special emphasis should be laid upon breeding varieties with genome plasticity and genome elasticity for wider adaptability over diverse agricultural conditions and geographical regions. Above all, the future crop varieties should meet multipurpose economic needs. For these proposes, one of the potential breeding strategies should include genetic treasuring of primary, secondary and tertiary gene-pools, particularly indigenous varieties and wild crop relatives. Many of such genotypes are rich in several potential donor genes underlying biotic and abiotic stresses, content of nutritional and nutraceutical compounds and even yield. Genetic characterization of such genetic resources employing comparative genomics and genotyping-by-sequencing; and utilization of selected donor genotypes through molecular- and sequence-assisted breeding will be highly useful. Broadening of genome plasticity through gene pyramiding and gene staking using marker-assisted backcross breeding and transgenic, preferably cisgenic, breeding will play a pivotal role in future plant breeding programs. Association mapping and fast-track breeding will facilitate breeding of varieties in many fruit, plantation and forest tree crops that are constrained with long juvenile period. Molecular pharming will deserve more attention for production of nutraceuticals and pharmaceuticals at commercial scale. Besides these well-established strategies, nanobiotechnology has recently emerged as a promising tool for elucidation and improvement of crop genomes. These concepts, strategies, tools and methodologies for future plant breeding will be deliberated with examples from major crops. A model for 'new crop-new trait-new strategy' will be presented with recent results from an orphan cucurbit crop, bitter melon, for which varieties and advanced breeding lines have been developed that could produce higher fruit yield, content of anticancer and antidiabetic phytochemicals and biomass yield.



GLOBAL ADOPTION, IMPACT AND FUTURE PROSPECTS OF BIOTECH/GM CROPS

Dr. Clive James,

Founder and Chair, ISAAA Board of Directors, Cornell University, Ithaca, NY USA.

In the early 1990s, some were skeptical that genetically modified (GM) or transgenic crops, now more often referred to as 'biotech crops' could deliver improved products and make an impact at the farm production level. There was even more skepticism that developing countries could access and adopt biotech crops. The first decade of commercialization of biotech crops, 1996-2005, witnessed unprecedented rapid global adoption in both industrial and developing countries including the lead countries of USA, Canada, China, India, Brazil, Argentina, and South Africa. 2011 was the sixth year of the second decade of commercialization of biotech crops (2006-2015). The adoption of biotech crops, in 2011 and the sixteen year period 1996 to 2011 is reviewed, within a broad framework that addresses their adoption and impact (economic, environmental and humanitarian) and their contribution to food, feed, and fiber security on a global basis. The potential contribution of biotech crops to the goals of the Millennium Development Goal (MDG) Year of 2015 is discussed, as well as their potential contribution to mitigating some of the challenges associated with climate change. The future prospects of biotech crops are summarized, in the context of a world that must double affordable food, feed and fiber production sustainably, on less resources by 2050.



Crop Science Research to Assure Global Food Security--Part 2

Kenneth G. Cassman, Robert B. Daugherty

Daugherty Professor of Agronomy, University of Nebraska, USA

In a proceedings paper from that talk, I began: "The research agenda for crop science in the 21st century will depend largely on whether policy makers believe that present conditions of global food surplus will continue, or food scarcity recurs. Accurate prediction of food supply and demand is therefore pivotal to prioritization of research." The paper went on to describe how research prioritization would differ under two scenarios: (1) adequate food supply and continuing trends of low food prices, or (2) food supply shortfalls and increasing food prices. At that time, most crop scientists, economists, policy makers, and research administrators believed that maintaining adequate food supply at reasonable prices was not a major challenge. The reason for such optimism was 30-yrs (1970-2000) in which global crop production stayed ahead of demand and optimism that new science would propel yields ever higher. We now know the optimistic scenario did not come to pass: crop production has falling behind demand and grain prices have tripled. What derailed this optimistic scenario? The optimism was largely based on predictions from econometric models that estimate future food demand based on expected population and income growth and food production capacity as determined by amount of arable land and expected growth rates in crop yields based on historical rates and investment in agricultural research. But the models underestimated food demand by a large margin because economic growth in developing countries was much faster than anticipated. Likewise, the models overestimated crop yield gains because good quality arable land is in short supply and assumptions about yield increases were too optimistic. Indeed, rate of return from global private-sector investment in agricultural research has decreased by about 50% since 1994 because research investment has doubled while rates of crop yield gain remain linear. Linear growth rates mean that relative rates of gain continually decrease, and they are now well below rates needed to meet expected grain demand without major expansion of crop area. It is now apparent that the scientific challenge to meet future food demand without exhausting natural resources or damaging environmental quality is the single greatest challenge facing humankind. We must accelerate crop yield gains and reduce the environmental footprint of food production well below current levels. While the challenge is large, it can be met if we focus research investments on achieving *ecological intensification* that ensures adequate rates of yield gain without negative environmental outcomes. It is no longer relevant to fund research that seeks to increase yields without regard to environmental impact, or research that seeks to avoid negative environmental consequences without producing higher yields. Future crop scientists must be interested in contributing to both goals. Current global concern about high food prices provides a "teachable moment" to attract the needed funding from both public and private sectors. The race is ours to win!



Development of a Science-Based, Advanced Tropical Agriculture in Brazil

Mauricio Antonio Lopes, PhD

Executive Director of Research and Development, Brazilian Agricultural Research Corporation - Embrapa

Brazil is one of the largest countries in the world, with an extensive surface of continuous land, a large supply of fresh water, abundant solar energy, and a rich biodiversity. The wide range of climatic conditions, from temperate to tropical, together with advanced capacity in technology development, allowed considerable diversification of agricultural systems, making Brazil one of the world's largest producers of food, feed, fibers and renewable fuels. The country is today the acknowledged world leader in generation and implementation of modern, tropical agricultural technology. Responding to increasing concerns over agriculture's footprint on its natural resource base, the agricultural research system in Brazil has taken important leaps, in a short period of time, towards development of innovations for increasingly safer and sustainable agricultural systems. The country is a leader in crop management based on minimum and no tillage systems, which significantly helps decrease erosion and improve general soil quality and groundwater recharge. Biological nitrogen use, through inoculation techniques with nitrogen fixing bacteria, has led to a significant decrease in the amount of chemical fertilizers applied to crops such as soybean. This, in turn, has significantly reduced environmental impacts such as water resources contamination with nitrates or other harmful elements. Biological control, regularly used in a number of crops such as soybean, sugarcane, cotton and fruit crops, has also reduced the need for chemical pest and disease control in several management systems, which have a positive impact on the environment, rural workers' quality of life and product safety and quality. Over the last decades, plant breeding programs have allowed development of cropping systems to a wide variety of environmental conditions in the country. This has been achieved by incorporating adaptation to different latitudes, tolerance to acid soils—especially to toxic aluminum, increased efficiency in nutrient use (like phosphorus and nitrogen), as well as resistance and tolerance to biotic factors, that are especially severe in tropical regions. These and many other innovations incorporated by Brazilian agriculture allowed increased resource use efficiency, higher productivity and intensified use of land, reducing drastically the environmental costs of farming. These technological advances have made Brazil a leader in production of agricultural goods and one of the largest producers and users of green energy. A striking example of the country's success in energy security is the ethanol production chain. The production and use of ethanol from sugarcane in Brazil is a global model for bioenergy production, distribution, and use, and is recognized as one of the most efficient in the world. Like ethanol, biodiesel is also receiving increased attention in Brazil, with development of new source materials, production and industrial technologies. This presentation will review in detail the pathways of agricultural development in Brazil in the past decades, as well as prospects, key drivers and expected developments in coming years.



Molecular Genetics, Genomics and Genetics of Symbiotic Nitrogen Fixation Supports Sustainability of Food and Biofuel Production

Peter M. Gresshoff

ARC Centre of Excellence for Integrative Legume Research; and SAFS; and QAAFI, The University of Queensland, St. Lucia, Brisbane QLD 4072, Australia

Presenting author: p.gresshoff@uq.edu.au; www.cilr.uq.edu.au

Crop plants require reduced nitrogen compounds to build the biochemical machinery for growth and development, as well as production of harvestable end products (seeds, biomass, fodder, biofuel). Commonly nitrate, whether soil-derived, or applied as industrial fertiliser satisfies this requirement. But decreasing natural fertiliser supply, increasing energy prices for industrial production and escalating global demand together with environmental concerns (run-off, N₂O production, ground water contamination, CO₂ release in production) detract from its long-term sustainability and economic benefit. Accordingly alternative strategies are being developed focusing either on increased Nitrogen Use Efficiency (NUE) or optimisation of the natural Symbiotic Nitrogen Fixation process. Nitrogen fixation itself occurs only in prokaryotes and is optimal when in symbiosis with legume plants such as soybean, bean or peanuts. Nitrogen gas from the atmosphere is converted to ammonia, which in turn is assimilated to amino acids for synthesis of proteins, nucleic acids and metabolites. The process occurs in specialised root organs called nodules, induced by compatible soil bacteria broadly called 'Rhizobium'. Advances over the last two decades have defined genetic components of the bacterium and the plant that facilitate the process. Key regulatory control points affected by internal (Nod factor perception, Signal transduction, Autoregulation of Nodulation) and external signals (e.g., nitrate, soil acidity) have been defined and now are open for genetic improvement through modern methods aided by functional genomics, biochemistry and plant breeding. The presentation will feature two fields of research and application, namely the current status of genetic knowledge of nodule induction and regulation, and efforts of translational biology where advanced technology and knowledge from crop legumes, such as soybean (*Glycine max*) are applied to the biofuel feedstock legume *Pongamia pinnata*. Significantly, optimising symbiotic nitrogen fixation under stress conditions will increase the sustainability of future food and biofuel production, by lessening the energetic, economic and environmental footprint of nitrogen fertiliser supply.



Rice biotechnology: how can we feed the billions?

Qifa Zhang

National Key Laboratory of Crop Genetic Improvement, Huazhong Agricultural University, Wuhan 430070, China (Email: qifazh@mail.hzau.edu.cn)

Rice is the main staple food for a large segment of the world population. In the last half century, rice yield has undergone two big leaps, primarily as the result of genetic improvement: increasing harvest index by reducing plant height making use of the semidwarf gene and utilization of heterosis by producing hybrids. Consequently, rice yield has more than doubled in most parts of the world and even tripled in certain countries. However, rice production is facing even greater challenges in the next half a century because of high demands in both quantity and quality, and ever increasing pressures on resources and environments. At the same time, advances in genomics, biotechnology and genetic studies have brought about unprecedented opportunities for crop genetic improvement. In my presentation, I will address the main issues that we have encountered as challenges, describe the demands for increased production for future needs, present current understanding on the progress in the researches in relevant areas, and provide prospect how the advance in research can be translated into technologies and activities for rice genetic improvement.



Drought, the New (old?) Challenge for Agriculture: What Role for Genomics-Assisted Breeding?

Roberto Tuberosa (roberto.tuberosa@unibo.it), Silvio Salvi, Marco Maccaferri, Pierangelo Landi, Silvia Giuliani, Marta Graziani, Simona Corneti, Sandra Stefanelli, Maria Corinna Sanguineti

Department of Agroenvironmental Sciences and Technology, University of Bologna, Viale Fanin 44, 40127-Bologna, Italy

Crop productivity is increasingly threatened by drought. Although conventional breeding has effectively raised yield under drought conditions, a more widespread adoption of genomics-assisted breeding (GAB) procedures will be instrumental to reach the yield gain required to ensure food security while enhancing sustainability. Unveiling the genetic basis of crop response to drought is an essential prerequisite to improve drought tolerance via marker-assisted selection and/or genetic engineering. Hundreds of quantitative trait loci (QTLs) for yield under water-limited conditions have been described in biparental mapping studies. More recently, association mapping has offered a new paradigm for gene/QTL discovery, greatly facilitated by the availability of SNPs and sequence information. Nonetheless, except for some notable examples, the elusive and unpredictable nature of QTLs limits the impact of QTL discovery on the release of drought-tolerant cultivars. Accordingly, only few drought-adaptive QTLs have shown consistent effects across genetic backgrounds and/or environments. Examples in cereals will be presented and critically appraised. From a selection standpoint, simulation studies have indicated genome-wide selection as the best option to improve quantitative traits controlled by many QTLs with minor effects. While QTL mapping will continue to shed light on drought tolerance, phenotyping of drought-adaptive traits remains a major limiting factor, particularly for root traits. Automated, high-throughput platforms help us to collect the large amount of data required for mapping and cloning QTLs. More recently, a growing interest has been devoted to modelling drought-adaptive traits and yield based on QTL effects. A promising and equally challenging topic for a deeper understanding of the functional basis of drought tolerance is the regulation of gene expression via RNA interference and DNA methylation. Although significant progress has been reported in the study of the epigenome, little is presently known on how drought influences epigenetic variation and its effects on traits plasticity and ultimately yield. This notwithstanding, the major challenge is how to best integrate GAB procedures in extant breeding projects. Adequately meeting this challenge will require a deeper understanding of Genotype x Environment x Management interactions and a closer collaboration among soil scientists, agronomists, crop physiologists, molecular geneticists and breeders.



Poster Session



Poster Session

Agricultural Extension and Economics



3294 - Agricultural Extension and Economics

Wei-li LIANG

DOES CROP INSURANCE POLICY PERFORM EFFICIENTLY??AN ASSESSMENT WITH THE CASE OF WHEAT CROP IN HENAN PROVINCE IN CHINA'S MAJOR GRAIN-PRODUCING AREA

Yang,RUIHUA; Liu,SHENG; Ju,RONGHUA; Xian,ZUDE; Liang,WEILI;

China Agricultural University;

In China, grain crop farming is the major enterprise for 93% of rural households in the Major Grain-Producing Areas (MGPA), which brings a highly spatial risk aggregation of natural disasters. Higher fluctuation in grain production often causes vulnerable livelihood in farming families in these areas. Henan province is the largest area of MPGA in central China and gives approximately 1/4 of the national annual wheat production. Since the year of 2009, premium subsidized wheat insurance pilot program began to be performed under voluntary principle. In this program, the insurance policy of single premium has been adopted, and the premium has been set at 6% of the material cost-based insured quantity, which is equivalent to only 38% of the normal wheat yield, while the catastrophic risk fund has not yet been established in Henan. To identify the efficiency of the wheat insurance system, we linked MCMC (Markov chain- Monte Carlo) model with GPD (Generalized Pareto Distribution) model to actuarially estimate wheat yield risk (probability of wheat yield loss) and basic premium in 17 districts and catastrophic insurance premium at provincial level of Henan. The model estimations prove that: (1) The wheat yield risk decreases while proposed yield loss level increases from 20% through 25% to 30% , and approaches to zero when the proposed yield loss level is above 40%. In other words, though the risk of wheat yield loss is high in Henan?the probability of obtaining a wheat yield lower than 70% of normal is very small; (2) In terms of basic premiums with operating expenses, the minimum is 0.88% and the maximum is 5.42%, with a variance coefficient up to 58% across the 17 districts, indicating a high heterogeneous risk; (3) With the GPD model, a catastrophic loss threshold of 438.84 kg/ha is identified, at which the catastrophic insurance premium under 100% insurance guarantee reaches 10.39%. Comparing model estimations to the practical insurance policy, we find that risk sharing is not actuarially fair in the current system, and the crop insurance policy designed upon voluntary principle is inefficient. Possible ways to improve the wheat crop insurance system, as suggested by the outputs of a questionnaire survey covering 312 rural households in Henan, include risk zoning of the target area to match premium level to risk level in various zones, and increasing coverage level of insurance to guarantee a 50-70% gain of normal production.



Poster Session

Agronomy



3272 - Agronomy

Adilar Chaves

PRODUCTION AND DRY MATTER PARTITIONING IN SOYBEAN CULTIVARS DUE TO PLANT POPULATIONS AND SOWING DATES

Chaves,A; Rizzardi,MA; Pires,JLF; Boller,W;

Universidade de Passo Fundo;

The objective of this work was to assess the accumulation and partitioning of dry matter (DM) on soybeans stem and branches under two sowing dates (12/11 and 14/12), four cultivars NS 4823 RR ("1"), NA 5909 RG ("2"), A 6411 RG ("3") and BR SUL LA ("4") and five populations (10, 17, 24, 31 and 38 plants m⁻²) in Passo Fundo/RS State, Brazil. The experimental design was randomized complete block in a split-split-plot arrangement, with sowing dates on main plots, cultivars on subplot and populations on sub subplots. At the R5 stage, was quantified the DM apparent on stem and branches without leaf blades and the DM of leaf blades located on stem and branches, and at harvest, the DM of grains and waste produced on stem and branches. At the R5 stage, cultivar "4" showed DM of stem higher than other cultivars on both sowing dates. The cultivar "2" showed DM of branches higher than others cultivars on both sowing dates. The differences between cultivars increased on sowing of 12/11 more than 14/12 with increased populations. The DM from the leaf blades on stem was higher in cultivar "4" and lower in the "2". The apparent DM at R5 stage on "1" and "4" cultivars was higher on sowing of 12/11 while on "2" was higher on 14/12 and did not differ between sowing dates on cultivar "3". At harvest, the "2" and "3" cultivars produced DM of grains on branches more than "1" and "4" cultivars, while they produced DM grain on branches more than "2" and "3" cultivars on both sowing dates. The cultivar "2" produced DM of grains on stems at sowing on 14/12 more than on 12/11, while the cultivar "3" did not differ between sowing dates and "1" and "4" cultivars produced on sowing on 12/11 more than on 14/12. Sowing on 12/11 resulted in higher yield and lower harvest index than sowing on 14/12. The waste DM of stem and branches in the sowing on 12/11 was higher than on 14/12 and "1" and "4" cultivars produced more waste from the stems while the "2" and "3" more waste DM of branches. The differences in DM accumulation due sowing date, cultivars and plant populations occur mainly on branches and the adequacy of the populations can compensate the differences between cultivars.



3275 - Agronomy

Adilar Chaves

VERTICAL DISTRIBUTION OF YIELD COMPONENTS IN SOYBEAN CULTIVARS OF INDETERMINED GROWTH HABIT UNDER PLANTS ARRANGEMENTS AND SOWING DATES

Chaves,A; Rizzardi,MA; Ramos,HS; Ulrich,VR;

Universidade de Passo Fundo;

The objective of this work was to evaluate the effect of plant arrangements and sowing dates in the vertical distribution of yield components of indeterminate growth soybean. Spacings of 34 and 50 cm between rows, populations of 10, 17, 24, 31 and 38 plants m⁻², NS 4823 RR ("1") and NA 5909 RG ("2") cultivars sown in 28/10 (I) and 15/12 (II) were used in Sertão/RS State, Brazil. The experimental design was randomized complete block in a split-split-plot arrangement. Each sowing date was considered an experiment. In sowing date I, "1" and "2" cultivars showed 28% and 19% of the reproductive nodes (RN) on the basal third (BT), and 38 and 51% on the medium (MT) respectively. In sowing date II, the percentages were 26 and 7% on BT and 39 and 56% on MT, in the "1" and "2" cultivars, respectively. The percentage on upper third (UT) in I was higher in "1" in populations smaller than 31 and equaled among cultivars on the 38 plants m⁻². In sowing date II, the percentage of RN on UT decreased linearly with increasing populations, with no difference between spacing and cultivars. The percentage of pods (%P) on BT in the season I was higher on "1", which did not differ between population and row spacing. Was higher on "2" in the spacing of 34 than 50 cm. On MT did not differ between populations in the spacing of 50 cm and increased in quadratic function up to 24 plants m⁻² in the 34 cm at the season I; on season II, was 42% and 54 on "1" and "2" cultivars, respectively, without differences between population and spacing. The %P in the UT did not change in sowing date. The number of grains per pod (NGP) in BT decreased in logarithmic scale with the increase of population on I and did not differ among cultivars, population and row spacing on II. On MT, the NGP was higher in "1" than "2" cultivar on I and did not vary on II. On UT, decreased linearly on I, and on II, only on cultivar "2" with the increase of population, with no other differences in both seasons. The weight of 100 grain did not change on TB and TM on "1" and "2" cultivars and increased in linear and quadratic function to 31 plants m⁻² on sowing date I and II, respectively. Cultivars and sowing times affect the vertical distribution of grain yield components more than plant arrangement, and the most affected components are the number of RN and pods.



3276 - Agronomy

Adilar Chaves

YIELD COMPONENTS IN THE STEM AND BRANCHES OF SOYBEAN CULTIVARS AFFECTED BY PLANT POPULATIONS AND SOWING DATES

Chaves,A; Rizzardi,MA; Boller,W; Pires,JLF;

Universidade de Passo Fundo;

The objective of this work was to quantify yield components on the stem and branches at the R5 stage and harvest of soybean under different sowing dates and plant populations. We used the cultivars NS 4823 RR ("1"), NA 5909 RG ("2"), A 6411 RG ("3") and BR SUL LA ("4"), with sowing in 12/11 (sowing I) and 14/12 (sowing II) on populations of 10, 17, 24, 31 and 38 plants m⁻² in Passo Fundo/RS State, Brazil. The experimental design was randomized complete block in a split-split-plot arrangement, with sowing dates on main plots, cultivars on subplots, and plant populations on sub subplots. The number of branches per plant at harvest was lower than at R5 stage in larger populations, especially in the sowing date I. The number of reproductive nodes on branches (NRB) was higher on season I (27 NRB) than II (22 NRB) and in the average of sowing dates. Cultivars "2" and "3" did not differ and exceeded "1" and "4" that did not differ too; the increase in the population reduced the number of NRB on logarithmic scale at both sowing dates; the number of reproductive nodes on stem (NRS) was higher on cultivar "1", with no difference between other cultivars on both sowing dates, and on "1", "3" and "4" cultivars was higher in sowing date I, while in "2" was greater on II. The number of pods on branches (NPB) did not differ among "2", "3" and "4" cultivars, which surpassed the "1", respectively with 56; 60; 50 and 38 pods plant⁻¹. The number of pods on stem (NPS) was higher on "1" and "4" cultivars that did not differ and exceeded the "2" and "3" that also did not differ, with 41, 40, 21 and 30 pods, respectively. At harvest, the number of NRB differed between sowing dates, cultivars and populations, with interaction of factors. The number of NRS differ between cultivars and populations with interaction of season and cultivars. The NPB differ between sowing dates, cultivars and populations, with interaction of cultivars and populations. The NPS differed between cultivars and populations with interaction of cultivars and sowing dates and cultivars and populations. The number of grains per pod (NGP) on branches was higher on cultivar "1" and decreased linearly with increasing populations. On stem the NGP varied seamlessly with sowing dates, cultivars and populations. The yield at harvest is less than the potential yield at R5 and the reduction is greater in smaller populations and sowing later. The yield potential of branches reduces more than the stem.



3257 - Agronomy

Adriana de Andrade Figueiró

DETECTION OF RALSTONIA SOLANACEARUM IN POTATO TUBERS

Figueiró,AA; Duarte,V;

UFRGS;

The bacterial wilt, caused by *Ralstonia solanacearum*, is considered the most important disease of potato (*Solanum tuberosum* L.), particularly due to the status of quarantine pest in countries like Canada and the USA. *R. solanacearum* is a broad host range pathogen and able to remain at low levels in symptomless seed tubers. Certification programs of seed potato tubers is the essential step toward the bacterial wilt management, but depends on specific and sensitive methods of detection of this pathogen. In this context, bacterial cell suspensions and macerated potato tissues with known amounts of bacterial cells were spotted on Whatman FTA. DNA from cards was eluted according to Whatman's instructions. To cellular lyse, the potato tuber tissue (100µL) was heated for 4 min at 96° C. To determine the detection threshold in Whatman FTA Cards, *R. solanacearum* was grown in nutrient broth for 24 h at 28° C. The bacterial cell concentration was estimated by spectrophotometry (OD600 = 1, 0.5, 0.25, and 0.1). Serial dilutions were obtained until 10⁻¹⁰, from OD 600 = 0.1. Ten microliters of each suspension were transferred to SPA medium, for counting cells, or cards, and these were subjected to cell lysis by heating for comparing the detection limit. Discs of the card and 1 L of DNA extracted by heating were used in PCR with the primers OLI1 and Y2 in qualitative PCR. The same suspensions in the cards were tested with primers RSI and RSII by qualitative and quantitative PCR. The quantitative PCR was performed using SYBR Green for absolute quantification. The FTA card method was more sensitive to obtain DNA from potato tissue than by heating cellular lyse. The presence of *R. solanacearum* in potato tubers was not detected by PCR (OLI1/Y2), on samples submitted to DNA extraction through FTA card method or heating cellular lyse. However, the detection in the FTA cards was possible when RSI/RSII was used; the PCR sensitivity increased from 10⁶ to 1 CFU/mL. PCR results with DNA eluted from FTA cards were similar, allowing the use of the DNA from the FTA card in quantitative PCR. Quantitative PCR (RSI/RSII primers) confirmed the presence of *R. solanacearum* in all symptomless potato tuber samples. Thus, with the standardization of the FTA method, the detection process becomes faster, allowing to get the DNA without is not necessary to extract the DNA, and its use in conjunction with the primer RSI and RSII, both qualitative and quantitative PCR have great potential.



2821 - Agronomy

Adriana Graciela Kantolic

A FUNCTIONAL AND QUANTITATIVE APPROACH FOR ESTIMATING YIELD LOSSES DUE TO LATE DEFOLIATION IN SOYBEAN

Enrico, JM; Kantolic, AG; Bodrero, M;

INTA Oliveros - Santa Fe;

The objective of this work was to obtain a quantitative estimation of yield losses due to late defoliations in different genotypes of soybean, based on the functional bases that define seed growth. Field experiments were performed during three seasons manipulating source level (i.e. defoliation: 0, 33, 67 and 100%) and sink level (depodding: 0 and 40%). Treatments were applied 15 (season 1 and 2) and 20 days (season 3) after R5 stage. Total defoliation reduced seed number up to a 38%; 67% defoliation produced milder effects (9 to 17% of reduction respect to the control), while 33% of defoliation only decreased seed number in 2 of 10 comparisons. Partial defoliations decreased seed weight by a 5 to 21%; when leaf area was completely removed, seed weight was reduced ca. 40% (season 1 and 2) and 22% (season 3), respect to the control. Depodding increased seed weight from 6 to 13%, depending on the cultivar and independently of the level of defoliation. Across treatments, seed weight was more related to variations in seed growth rate than to the duration of the seed filling period. The seed water concentration at physiological maturity was similar among treatments (ca. 56 % $\pm$ 0.3 %), regardless of the source or sink level; a strong relationship between maximum water content and final seed weight ($r^2=0.97$) was observed throughout treatments and cultivars. Nineteen to 52% of seed weight came from remobilized biomass, depending on the cultivar and year; however, we did not find any evidences that reserves can act as moderators for sustaining seed weight when partial defoliation was applied. In summary, late defoliations reduced soybean yield components without altering the normal progress of seed water relations and without substantial increment in remobilization from vegetative organs. Thus, yield should be directly related with the canopy photosynthesis during seed fill. We found that predictors of the ability of the crop to produce assimilates, like Leaf Area Index (LAI) or the proportion of radiation intercepted by the crop (R_i) provided adequate quantifications of changes in relative yield. As depodding increased maximum seed weight, correcting LAI or R_i by the level of sinks did not provide a better estimation of relative yield loses. The most simple and accurate model predicted that yield will be maximized when R_i 15-20 days after R5 stage remains around 95%, and the relative yield will decrease 0.77% per unit of reduction in R_i .



3205 - Agronomy

ANA CLAUDIA PEDERSEN

CANOLA YIELD, PROTEIN AND OIL CONTENT UNDER DIFFERENTS DENSITITES AND ROW SPACING

Pedersen,AC; Santos,FL; Rodrigues,VM; Astolfi,E; Tomm,GO; Chavarria,G;

Universidade de Passo Fundo;

Canola is a winter oilseed developed from the genetic improvement of rapeseed. Because of interest in the proteins and oil production of high quality its area has been increased. Chemical properties of canola can vary based on environmental factors and genetics. Varieties grown in Brazil have shown about 40-46% oil and 34-38% protein. The arrangement of plants is an important aspect to improve the use of light, water and soil nutrients. Therefore, the present study was conducted to determine the effect of different row spacing and densities on yield and oil and protein content of canola cultivar Hyola 61. Field experiment was conducted in Passo Fundo/RS/Brazil, in a randomized block design arranged in split plot, row spacing (17, 34, 51 and 68 cm) in main plots and densities (15, 30, 45 and 60 plants m⁻²) in the subplots, four replications. In order to determine grain yield, each subplot were harvested, weighed and converted into kg ha⁻¹, when 40-60% of the seeds have changed from green to brown-black. A sample after weighing was taken from each subplot and oil and protein content was determined. The oil content was determined by Soxhlet extraction with hexane and protein content by Kjeldahl method with a catalyst (potassium sulfate + copper sulfate), both analyzes were made in triplicates. The data obtained were statistically analysed using analysis of variance and means were compared by using Tukey test at 5% of probability. The treatments showed no significant differences in oil and protein content, with an average of 17.36% and 9.24% respectively. The row spacing significantly affected yield, the spacing of 17 cm showed an average yield of 1041.33 kg.ha⁻¹. The plant arrangement on canola has no effect on the protein and oil content. The yield of canola is higher when the plant is subjected to the spacing of 17 cm between rows.



3210 - Agronomy

Anderson Santi

WHEAT GRAIN YIELD VARIABILITY IN CROP SYSTEMS IN A LONG-TERM EXPERIMENT

Santi,A; Dalmago,GA; Wuttke,D; Pires,JLF; Santos,HP; Cunha,GR; Fochesatto,E;

EMBRAPA - EMBRAPA TRIGO;

The need to increase world food production to attend a growing population demands is one of the great challenges for agricultural scientific research. In this scenario, wheat crop plays a critical role, since it corresponds to more than 30% of the grain produced worldwide. Nevertheless, in Brazil the wheat production meets only 50% of its needs. Aspects related to production systems may contribute to increase crop productivity and provide a solution for some problems. The objective of this work was to evaluate the effect of four cropping systems on wheat yield in long-term experiment carried out at Embrapa Trigo (National Center for Wheat Research) in Passo Fundo, RS/Brazil. Experiment started 1980 aiming to determine the influence rotation on wheat yield. The treatments consisted of three crop rotation systems (System I: radish-wheat/soybean, black oat/corn, barley/soybean and oat/black beans; System II: vetch/corn, oat/soybeans and wheat/soybean, System III: wheat/soybean, white oat/soybean, and wheat/soybean) and a continuous double cropping (wheat/soybean). The experiment, was outlined in a randomized block design with four replications. The wheat yield was evaluated from 2008 to 2011 period, under randomized block design with factorial arrangement (4 years x 4 systems) in four replications. We performed analysis of variance, and the results were tested for interaction and the averages were compared by Tukey test.



3259 - Agronomy

Arata TARUI

Cutting the aboveground parts of hairy vetch enhances N uptake of the mixed-cropped oat grown as green manures

Arata-Tarui,AT; Atsushi-Matsumura,AM; Hiroyuki-Daimon,HD;

Graduate School of Life and Environmental Sciences, Osaka Prefecture University, Japan;

In general, cereal crops in mixed-cropping with legumes absorb more N than in sole cropping due to transfer of rhizodeposited-N of legume to the associated crop. In the mixed-cropping, cutting the legume may increase N transferred from legume through turnover of roots and root nodules. In the present study, we investigated the effects of N released from belowground parts of hairy vetch (*Vicia villosa* Roth) on the growth and N uptake of mixed-cropped oat (*Avena sativa*) grown for green manure production. The experiment was carried out in 2010/2011 at the experimental farm of Osaka Prefecture University, Japan. The treatments were as the follow; sole cropping of oat (A); sole cropping of hairy vetch (V); mixed-cropping (M); mixed-cropping under cutting hairy vetch (MC); sole cropping of oat under cutting the half of oat (ACH). The seeds were sown on 29 November 2010 with seeding rates of 4.3 g/m² (A and ACH) and 2.9 g/m² (V). To estimate N transfered from hairy vetch, 15N-labeled ammonium sulfate was applied at the rate of 3 gN/m². The cutting treatment for MC and ACH was conducted on 21 April 2011 and the shoots were removed. Oat and hairy vetch were harvested on 22 May 2011, and total N contents were determined. In spite of half seeding density of oat in mixed-cropping under cutting hairy vetch (MC), the shoot dry weight of oat in MC was 68% in sole cropping (A). Cutting the hairy vetch markedly increased relative amounts of accumulated solar radiation at interrow, resulting that newly emerged tillers grew vigorously. Total N content of shoot of oat considerably increased after cutting of hairy vetch. According to 15N dilution method, an amount of N transferred from hairy vetch was calculated as 38% of total N accumulated in oat plants in MC. On the other hand, cutting the half of oat plants in sole cropping plot (ACH) had no effect on total N content of the residual oat. These results suggest that cutting hairy vetch at blooming stage results in higher tiller number and total N content of associated oat due to transferring a large amount of N from hairy vetch and removing light interception by hairy vetch vines to oat shoots. This experiment demonstrates that comparatively rapid decomposition of oat green manures could be achieved by the mixed cropping with hairy vetch cutting at blooming stage. Analysis of growth and N uptake of the succeeding corn are now in progress, especially from the viewpoints of different C/N ratios of those green manures.



3311 - Agronomy

Bianca Silva Fernandes

CYTOTOXICITY OF AQUEOUS EXTRACT OF TROMBETEIRA ANTHERS ON LETTUCE SEEDS

Silva-Fernandes,B; Auler,PA; Soares-Lopes,MR; Saleh-Ribeiro,M; Gomes-Rocha,BH;

Federal University of Pelotas;

The Trombeteira (*Brugmancia suaveolens* Willd.) is a shrubby plant with outstanding flowers, having intense secondary metabolism, such as other species of Solanaceae. Substances present on this family are known to have cytotoxic effects. Seeds are excellent organisms for bioassays because when they are rehydrated, they come into the germination process, undergoing fast physiological changes and becoming sensitive to environmental stress. Thus, this study aimed to evaluate the cytotoxic effect of aqueous extract of trombeteira anthers on lettuce seeds (*Lactuca sativa* L.). Therefore, the aqueous extract was prepared from anthers dried by refluxing, at concentrations of 1%, 2%, 3% and 4%, from a stock solution at 5%, and distilled water (DW) as control. The seeds were placed in germination boxes containing germitest paper moistened with 10 mL of extracts and DW, maintained at 20° C. To determine the mitotic index (MI) it was used the technique of crushing, in which lettuce roots were collected, fixed in Carnoy (3:1), hydrolyzed in HCl (5N), colored with acetic orcein 2% and viewed by an optical microscope with a 40 x objective and analyzing 2000 cells per treatment through the scanning technique. The MI was obtained by dividing the number of mitotic cells by the total number of cells observed and multiplied by 100. The results were subjected to analysis of variance and means were compared by Duncan test with a probability of error of 5% using the software WinStat. There were no statistically significant differences in all treatments analyzed of the MI variable. No evident cytotoxic effect of aqueous extracts of anthers of the trombeteira on lettuce seeds were found.



3371 - Agronomy

Cacilda Marcia Duarte Rios Faria

INFLUENCE OF SUBSTRATE DRAINED OF AGARICUS SP MEAL CINNAMON SEEDS AND FRUIT ON MELOIDOGYNE JAVANICA

Faria,CMDR; Pereira,SGM; Dallemole-Giaretta,R; Botelho,RV; Mateus,MAF;

Unicentro;

The nematodes of the genus *Meloidogyne* are causing yield losses in many crops. The objective of this study was to evaluate the effect of substrate depleted of *Agaricus* sp and flour seeds and fruits of chinaberry (FSFC) in the control of *Meloidogyne javanica*. To obtain the FSFC, seeds and fruits of chinaberry were collected and dried at 40 ° C for 48 hours and oven and then crushed in a mill. The experiment was carried out in vessels of 0.5 kg of polypropylene of capacity, containing a mixture of soil and sand (2:1, v: v). In each vessel were placed 5 g of substrate separately drained of *Agaricus* sp. FSFC of 2 g or 5 g 2 + g, respectively, of exhausted substrate *Agaricus* spp. and FSFC. Then, the soil was infested with eggs and 4.000 *M. javanica*. In the treatment, control, only the soil was infested with nematodes. After 15 days, transplanted to a change of tomato in each pot. The trial was conducted in a greenhouse in a completely randomized design with eight replicates per treatment. The numbers of eggs and galls / root system were evaluated 45 days after transplanting the tomato plants. None of the treatments controlled the nematode galls. It was found that only 1 treatment increased by 48% the number of galls. And the treatments 2 and 3, respectively, increased by 36% and 31% the number of nematode eggs. Further studies should be performed for these organic compounds are best investigated for their potential in controlling nematode galls.



2836 - Agronomy

Choi Hong Jib

COMBINED EFFECT OF MEPIQUAT CHLORIDE AND TRINEXAPAC-ETHYL ON OIL COMPOSITION, SEED YIELD AND ENDOGENOUS GIBBERELLIN IN FLAX

Kim,SANGKUK; Choi,HONGJIB;

Gyeongsangbuk-do ARES;

Flax (*Linum usitatissimum* L.) which is used for fiber and edible oils is an annual crop belonging to the family Linaceae. In Korea, recently, there has been some interest in seed flax as a health food because of its amount of polyunsaturated fatty acids including phytochemicals known as lignan specially SDG(secoisolariciresinol diglucoside) in seed oil. The objective of this study was to determine flax plant response to mepiquat chloride (MC) and trinexapac-ethyl (TE) at during seed development. The MC concentration of 300 and 600 ppm was combined with TE at 100, 200, 300ppm, respectively. Flax plant foliage was sprayed with the combination of MC and TE at 50 days after seeding. Growth characteristics and seed yield were measured at harvesting time. Composition of fatty acid, oil, lignan and endogenous gibberellins were also determined from flax seeds. Plant height was clearly reduced by the increased combination of MC (600ppm) and TE (100, 200 and 300ppm) compared to the combination of MC (300ppm) and TE (100, 200 and 300ppm). Otherwise, ripened seed rate, 1,000-seed weight and seed yield were increased in the combination of low MC (300ppm) and TE (100, 200, and 300ppm). Among these combined treatments, the MC 300ppm and TE 300ppm treated flax plants had a greatest seed yield and ripened seed rate than plants treated with TE 100 and 200ppm. Highest oil and SDG content was only observed at the combination of MC 300ppm and TE 300ppm. In the change of unsaturated fatty acids, linolenic acid content was increased by the combination of MC 600ppm and TE 100ppm. In particular, the increased TE concentrations caused decreased linolenic acid content. Bioactive gibberellins, GA1 and GA4, were more decreased in MC 600ppm than in MC 300ppm. Furthermore, an increased TE combination did not affect bioactive gibberellin contents. We conclude that the combination of two plant growth retardants, MC 300ppm and TE 300ppm will be useful for increasing oil and lignan content in flax plants.



3382 - Agronomy
Christian Bredemeier

ESTIMATING WHEAT GRAIN YIELD POTENTIAL AT DIFFERENT GROWTH STAGES USING AN ACTIVE REFLECTANCE SENSOR

Bredemeier,C; Variani,C; Almeida,D; Perin,J; Schmitz,JF; Rosa,AT;

Universidade Federal do Rio Grande do Sul;

Nitrogen fertilization in spring wheat in southern Brazil is based on grain yield potential, soil organic matter content and previous crop. These variables are not precise and subjected to errors, resulting on N losses and yield potential reduction. Moreover, yield potential definition is difficult, since it is affected by weather conditions that are variable between years. The development of proximal remote sensing sensors based on canopy NDVI (normalized difference vegetation index) evaluations is an approach for site-specific nitrogen fertilization in field crops. The Greenseeker is an active reflectance sensor that utilizes light diodes to generate red as well as near infrared light. The emitted light is reflected by the canopy and detected by photodiodes in the equipment's front part. In Brazil, the use of sensors for N fertilization is still incipient and the increasing use of precision agriculture practices shows that this technology must be adapted to the production conditions in southern Brazil. In this sense, the objective of the present work was to study the variation of normalized difference vegetation index (NDVI) during crop development in four wheat cultivars as affected by N availability at emergence and at 6-leaf stage and its relation to grain yield. The experiment was carried out at field conditions in Eldorado do Sul (State of Rio Grande do Sul, Brazil) in 2009 and 2010. Treatments consisted of different N rates applied at plant emergence and at the 6-leaf-stage. NDVI in different growth stages using an active sensor and wheat grain yield were evaluated. NDVI measured was efficient to detect growth variability generated by N availability and correlated well with grain yield for all cultivars tested, indicating that yield potential can be estimated by NDVI evaluations during crop ontogeny. Highest values of NDVI were observed at booting. Grain yield increased with increasing NDVI due to the increasing nitrogen availability. One single model for the relationship between NDVI and yield potential can be used considering the cultivars used in this work. Our results indicated that NDVI measurement by an active sensor is an efficient tool to evaluate N nutritional status. This information can be used for site-specific variable N fertilization, according to spatial variability within a field.



3095 - Agronomy

Conceição Aparecida Cossa

BIOSTIMULANT AND COMMERCIAL INOCULANT IN THE GLYCINE MAX PRODUCTION

Cossa,CA; Sorace,MAF; Osipe,R; Campos,FG; Camolese,AC; Villela,TT;
Castro,IR; Troost,ME; Tashima,H;

UENP-CLM;

Currently, the soy is one of the cultures that greater presents relevance in world-wide the agricultural scene, not only for the rude value of its grains, but, over all, for the value of the aggregate products. In Brazil, the soy is cultivated in an area of 15 million hectares, being responsible for a production of more than 40 million tons of grains, what it becomes the Country as the bigger producer of the world. Its culture demands each time more, on the part of the agriculturist, the use of technologies that bring increase of income of the culture. In such a way, the biostimulant use as agronomic technique to optimize the productions in diverse cultures is each more common. In Brazil, some cultures already had reached high technological levels and high productivity and they are not conditional for limitations of nutricional or hídric order, what it has led to the use of biorregulators, that can be compensating beyond economic. The isolated effect of plant hormones sufficiently had been studied and already known, being presented positive and negative effect in accordance with the applied amounts, periods of application, region of application and cultures. However, the effect of combined use of hormones is unknown, requiring further study. The objective this work was to test the influence of the treatment of seeds with a commercial mixture (CM) composed for plant regulators and mineral nutrients compared with the commercial inoculant for soybean in the production. The experiment was in conditions of field in the UENP-CLM in Bandeirantes-PR. Seeds of soy cv. Brasmax had been submitted the treatment with a CM of plant regulators (AIB, GA, kinetin), mineral nutrients (B, S, Cu, Zn, Mn, Mo) and thiamin. The statistical design utilized was entirely casualized and the means were compared by the Tukey test 5%. The concentration of the CM and the commercial inoculant was the recommended one for the manufacturer. The variables evaluated in end of de cycle had been: dry mass of root, shoot and string beans. For the evaluated parameters, it did not have significant differences, what it indicated that the soy production it is not modified by the different treatments of the seeds. Acknowledgements: Fundação Araucária



3094 - Agronomy

Conceição Aparecida Cossa

EFFECT OF THE INOCULATION IN THE INITIAL DEVELOPMENT OF SOYBEAN (GLYCINE MAX)

Cossa,CA; Sorace,MAF; Osipe,R; Campos,FG; Camolese,AC; Villela,TT; Castro,IR; Troost,ME;

UENP-CLM;

Few works approach physiological aspects of the plant of soybean related to the application of plant regulators that are a promising handling for this culture. Information on the effect of these products in the soybean could provide basic elements for posterior studies on the agronomic use of the plant regulators. The plants are modified morphologically by the application of biostimulants, of form that the growth and the development of them are promoted or inhibited. The biostimulants are part of the called group of plant hormones, and can be cited: the auxin, the kinetin, the gibberillin, the inhibitors and the ethylene. The classification of the Stimulate (product of consecrated use) was made by Castro et al. (1998), as being a biostimulant that contains fitoregulators. The basic composition of this biostimulant contains acid indolbutírico (auxin), kinetin (kitocinina) and acid gibberellico (gibberellin), being the same components of the Commercial Mixture (CM) used in this work and this still contening: B, S, Cu, Zn, Mn and Mo and the thiamin. Additionally, the action of plant hormones is changeable in agreement the development stadium, being more effective in the emergency of seedlings and the initial development. The objective of the present work was to test the influence of the treatment of seeds with the CM composed for plant regulators and mineral nutrients compared with the commercial inoculant for soybean in the vegetative development of soy plants. The experiment was conducted in conditions of field in the UENP-CLM in Bandeirantes-PR. Seeds of soy cv. Brasmax had been submitted the treatment with the CM of plants regulators and mineral nutrientes. The statistical design utilized was entirely casualized and the means were compared by the Tukey test 5%. The concentration of the CM and the commercial inoculant was the recommended one for the manufacturer. The variables evaluated in intervals of 15 days had been: number of nodules, dry masses of root and shoot, length of root, diameter and height of the shoot, length, width and dry mass of leaflet. For the evaluated parameters, it did not have significant differences, what it indicates that the soybean, in its initial development, did not replied to the treatment of the seeds with the biostimulant. Acknowledgements: Fundação Araucária



3093 - Agronomy

Conceição Aparecida Cossa

TREATMENT OF SEEDS OF ZEA MAYS WITH VEGETAL REGULATORS AND MINERAL NUTRIENTS

Cossa,CA; Sorace,MAF; Osipe,R; Campos,FG; Camolese,AC; Villela,TT;
Castro,IR; Troost,ME;

UENP-CLM;

The agriculture evolves constantly and with the sprouting of new technologies the employment of the "technological packages" where the plant regulators are being used in order to increase or to improve the culture of the plants and consequent to increase the production of the same ones. Inside of this new gamma of products, many mixtures are gifts in the market, each one with its particularity. But in a general way, all possess in its composition necessary hormones and nutrients to the plants. As well as the macronutrients, the micronutrients and elements trace its possess effects in the vegetal cycle. The nutrients can be placed in some functions in the plant, such as energy storage, to compose the cellular wall, to compose clorofila and many other functions. But one of most important is to compose vegetal hormones, among them the auxin, gibberellin, kinetin, ethylene and some others. The objective of the present work was to test the influence of the treatment of seeds with a commercial mixture (CM) composed for nutrientes and plant regulators in the vegetative development of maize plants. The experiment was conducted in conditions of field in the UENP-CLM in Bandeirantes/Paraná. Seeds of maize cv 2B710Hx had been submitted the treatment with a commercial mixture (CM) of plant regulators (AIB, GA, Kinetin), vegetable nutrients (B, S, Cu, Zn, Mn and Mo) and thiamine. Statistical design utilized was entirely casualized with 2 treatments and 10 repetitions and the means were compared by Tukey test 5%. The concentration of the CM was the recommended one for the manufacturer and the not treated seeds had been considered the control treatment. The variable evaluated in intervals of 15 days had been: dry masses of root and shoot, length of root and shoot, stem diameter, length and width of the first leaf expanded. For the parameter dry mass of shoot the treatment with the CM was significantly minor than witness. For the other evaluated parameters it did not have significant differences what it indicates not the necessity of the treatment of the seeds of maize with this CM. Acknowledgements: Fundação Araucária



2876 - Agronomy

Cynthia Grant

Canola response to N fertilization as affected by preceding crop and location

Grant,CA; Gao,X; Odonovan,JT; Zebarth,B; Blackshaw,RE; Lafond,GP;
Harker,KN; Johnson,EN; Gan,Y;

AAFC Brandon Research Centre;

Excess N application is a major cause of poor N use efficiency (NUE), contributing to negative Field studies were conducted at 6 sites across western Canada to assess effects of preceding crop, soil characteristics and environment on yield response of canola to N fertilization and to evaluate the effectiveness of various soil tests and modelling approaches in predicting optimum N fertilization rate. The study consisted of a two year crop sequence with preceding crops (fababean grown for seed, fababean used as green manure, and pea, lentil, wheat and canola grown for seed) grown in the first year and canola grown in the second year. Nitrogen fertilizer was applied to the canola as urea, banded at the time of seeding at 0, 30, 60, 90 and 120 kg N ha⁻¹. A split-plot design with four replicates was used with preceding crop as the main plot and N rates as sub-plots. Crops were harvested at maturity and analysed for seed and tissue N. Total soil nitrate-N in the upper 60 cm was highest after fababean green manure in half of the sites, but soil nitrate-N was not consistently higher after pulse crops than after canola or wheat. Total canola seed yield and the yield increase with N application varied substantially with location and preceding crop. Seed yield was consistently higher after fababean green manure than wheat or canola, regardless of N fertilizer input or effect on soil nitrate, indicating both a nitrate-based and a non-nitrate-based benefit. Seed yield of canola and the yield response to N application was related to soil nitrate-N concentration to some extent, but there were discrepancies. For example, soil nitrate-N at Beaverlodge and Lacombe was low compared to that at Brandon, yet the canola seed yield was as high or higher in the unfertilized check and response to fertilizer application lower at these two sites than at Brandon. This may indicate high levels of mineralizable N at the Beaverlodge and Lacombe sites. Several mineralization tests are currently being evaluated for their ability to more accurately predict plant-available N and potential response to N fertilization at these field locations. Fababean green manure provided both nitrogen and non-nitrogen benefits to the following canola crop. Soil nitrate-N provided an approximate indication of plant-available N and yield response to N application, but better prediction is needed to more accurately determine fertilizer N requirements.



2875 - Agronomy

Cynthia Grant

Cd and Zn concentration in flax and durum wheat are affected by long-term phosphorus fertilization and soil characteristics

Grant,CA; Gao,X; Flaten,DN; Tenuta,M; Akinremi,W; Malhi,SS;

AAFC Brandon Research Centre;

Phosphorus fertilizer contains Cd and Zn as contaminants that can influence the accumulation of these trace elements in soils and crops. Phosphorus fertilization can also influence accumulation of Cd and Zn in crops indirectly by effects on soil chemical reactions, rhizosphere interactions, nutrient translocation within the plant and biological dilution related to increased crop yield. These effects may be moderated by soil characteristics. Field studies were established in 2002 at 7 sites across the Canadian prairies to evaluate the impact of repeated applications of 0, 20, 40 and 80 kg P ha⁻¹ of monoammonium phosphate (MAP) fertilizer containing 0.38, 70 or 210 mg kg⁻¹ of Cd on crop concentrations of Cd and Zn. The sites were planted each year, following a durum wheat-flax cropping sequence. In 2010, after 8 annual fertilizer applications, P fertilization was terminated and crops were grown in 2010 and 2011 with no further P input to determine the attenuation in trace element availability over time. Seed Cd and Zn concentration was measured each year and the concentration of DTPA-extractable soil Cd and Zn in the 0 to 7.5 and 7.5 to 15 cm soil depths was measured after the final application of P fertilizer and annually thereafter. The DTPA extractable soil Cd and Zn in the surface 7.5 cm depth increased with application of MAP containing moderate or high concentrations of Cd, but concentration in the 7.5 to 15 cm depth only increased with the high-Cd MAP. Cadmium and Zn concentration of flax and durum wheat varied substantially from location to location, indicating the importance of soil characteristics in influencing crop trace element concentration. Cadmium concentration in both durum wheat and flax increased with increasing input of Cd in P fertilizer, but the magnitude of the effect varied with soil characteristics and was not consistently related to DTPA-extractable soil Cd. In contrast, Zn concentration in durum wheat and flax seed decreased with P application in spite of increased soil Zn concentrations, reflecting P inhibition of Zn uptake and translocation in the plant. As with Cd, the effect of P on Zn accumulation in crops varied with soil. Since the effect of MAP fertilizer on both DTPA-extractable Cd and Zn and seed Cd and Zn concentration is affected by soil, it is important to consider soil characteristics when assessing the impact of fertilizer inputs on trace element accumulation in crops and soils.



3327 - Agronomy

DANIEL FERNANDO CALDERINI ROSSO

DOUBLE HAPLOID LINES COMBINING HIGH GRAIN NUMBER AND WEIGHT ARE PROMISSORY TO INCREASE YIELD POTENTIAL OF WHEAT

Calderini,DF; Hasan,AK; Bustos,DV; Moure,S;

Universidad Austral de Chile;

World yield rates have markedly slowed in the last decades, while world population is expected to reach 9.1 billion in 2050. The challenge of satisfy the future food demand without increasing the price of commodities like wheat imply a quantum leap of farm output during the first half of the 21 century. Therefore, the assessment of strategies aimed at boosting yield potential of wheat has become crucial. One of them is to try to combine high grain number and weight in the same genotype. The objectives of this study was to evaluate grain yield performance of double haploid lines derived from the cross between a high grain number and high grain weight cultivars and to identify promising physiological traits explaining high yield performance under the high yield potential environment of southern Chile. Three experiments were carried out at the Experimental Station of the Universidad Austral de Chile (39°38'S) in Valdivia from 2008 to 2011. Two double haploid (DH) populations were evaluated: Bacanora x Weebil (106 lines) and Bacanora x Kambara (210 lines) together with the parent cultivars and a Chilean high yielding cultivar as check (Pandora INIA). Different Source-sink ratios during grain filling were also assessed. Experiments were conducted under yield potential conditions. Grain yield, biomass and other traits were measured at harvest and radiation interception and radiation use efficiency (RUE) were measured or calculated in experiment 2. In this experiment the dynamic of growing flowers was also assessed up to anthesis. DH lines over-yielded both parents and the Chilean check up to 50%, reaching the DH lines 16 ton ha⁻¹. Most of the higher yield reached by DHs was explained by higher RUE (up to 4 mg MJ⁻¹) but also improved harvest index was found. DHs showed a wide range of grain number and more than 10 of them achieved higher grain number (up to 36200 m⁻²) than the parents and the Chilean cultivars (ranging between 20000 and 29000 grains m⁻²). The improvement of grain number was bases on the improved floret dynamic of DH lines. Although grain number was higher in DH these lines showed a better balance between grain number and weight than the cultivars, which is supported by the source-sink manipulation. This results seem to be promising for increasing grain yield of wheat and to deal with the trade off between grain weight and grain number.



3419 - Agronomy

deivid luis vieira stefen

ALTERATION IN THE CRUDE PROTEIN OF WHEAT GRAINS DUE TOPDRESSING NITROGEN ASSOCIATED WITH PLANT GROWTH RETARDANT

Stefen,DLV; Souza,CA; Cechinel,MH; Ataide,RCN; Tormem,ME; Zanesco,PR;

Santa Catarina State University (UDESC);

The objective of this research was to evaluate the crude protein content of wheat grains after use of topdressing nitrogen applied on tillering or at tillering plus filling grains stage associated with distinct plant growth retardants. The experiment was carried out at field conditions, in 2011 growing season, at Lages-SC, using seeds of wheat cv. Mirante. The assay was in a randomized complete block design with four replications under incomplete factorial design 2x7, consisted two levels of N topdressing (once N topdressing plus once plant growth retardant spray and; twice N topdressing e twice plant growth retardant spray). The plant growth retardant were applied at 31 and 32 stages of Zadoks code and, two control (control 1, N applied at tillering stage and control 2, N applied at tillering and filling grain stage too).The retardant used were mepiquat chloride, chlormequate chloride, chlorocholine chloride, ethyl-trinexapac, prohexadine-Ca and ethephon. The crude protein was determined using NIRS-System (near infrared spectroscopy), in 500g samples of grains. The data were submitted to variance analysis and the averages of treatments compared by Duncan test (P). The topdressing N during filling grain provided an addition 1.8% in the crude protein content of grains. When applied two doses of nitrogen and two doses of prohexadine-Ca retardant crude protein content was increased (13.6 x 12.7%). The mepiquat chloride retardant promote higher crude protein content (14.2 x 13.8% from control). The same effect occurred with only once nitrogen and once prohexadine-Ca levels that show crude protein content lower (11.7% x 12.7% of control 1; control 1 was once N topdressing applied at tillering stage). In conclusion, N topdressing at filling grain stage contributes to increase crude protein content of wheat grains and the plant growth retardant did not affect the crude protein content of grains, except the prohexadine-Ca that decreased protein content in both the treatments (low and high N topdressing).



3418 - Agronomy

deivid luis vieira stefen

EFFECT OF NITROGEN TOPDRESSING ASSOCIATED WITH THE PLANT GROWTH RETARDANT ON YIELD OF WHEAT CV MIRANTE

Stefen,DLV; Souza,CA; Cechinel,MH; Ataide,RCN; Tormem,ME; Werner,F;

Santa Catarina State University (UDESC);

The objective of this work was to evaluate the topdressing nitrogen associated with plant growth retardant and its effect on plant height, yield components and yield of the wheat. The experiment was carried out at field conditions, at 2011 growing season, at Lages-SC, using seeds of wheat cv. Mirante. The assay was in a randomized complete block design with four replications in incomplete factorial design 2x7, consisted two levels of N topdressing (twice growth retardant spray) of and six plant growth retardant (applied at 31 and 32 stages of Zadoks stages) and two control (control 1, N applied at tillering stage and control 2, N applied at tillering and filling grain stage too). The retardant used were mepiquat chloride, chlormequate chloride, chlorocholine Chloride, ethyl-trinexapac, prohexadine-Ca and ethephon. The characteristics evaluated were plant height (pre-harvest): grains number per ear (GNE), grain weight per ear (GWE), thousand grains weight (TGW), hectoliter weight (HLW) and yield (GY). The data were submitted to variance analysis and the averages of treatments compared by Duncan test (P). The plant height did not differed between treatments. The topdressing N at twice associated with twice consecutive retardants application lead to plant height of 77 cm against 80 cm with only one nitrogen dose and only one retardant application. The ethyl-trinexapac applied at one time associated with one N level of retardant provided more shorter plants (70 cm x 82 cm of control 1) and when twice nitrogen and twice retardant too, the ethyl-trinexapac (62 cm) and prohexadine-Ca (66 cm x 87cm of control 2) were the retardants that provided the more shorter plants. On these growing season did not observed problem with plant lodging. The grain weight per ear, thousand grain weight and hectoliter weight were increased due twice N topdressing, however these traits did not differed due and between retardants applied. In conclusion, the ethyl-trinexapac and prohexadine-Ca, decrease the plant height and, the nitrogen application at filling grain stage did not affect grain yield.



2598 - Agronomy

Dr. Stanford Blade

BUILDING ALBERTA'S BIOECONOMY: USING BIOMASS IN INNOVATIVE WAYS

Blade,SF;

Alberta Innovates Bio Solutions/University of Alberta;

The agriculture and food sector in the province of Alberta (Canada) is a \$25B industry. Investment in innovation by Alberta Innovates Bio Solutions is resulting in new opportunities for crops and livestock through research programs in the strategic areas of sustainable production, food for health and prion research. Examples of new initiatives in oilseed and livestock genomics, unique food processing techniques and protein-misfolding research will be discussed. Alberta is also uniquely positioned to grow its biorefining capacity through the combined strengths of its large energy industry (hydrocarbon-based) and its wealth of agriculture and forestry resources. Alberta has committed US\$700+ million to support bioeconomy initiatives in the areas of feedstock improvement, biomass conversion and product development. The talk will describe several examples of Alberta investment in technology innovation and commercialization which have resulted in new bio-opportunities in transport fuels, heat, electricity, chemicals, materials and food. New technologies and economies of scale are creating exciting opportunities for how the agriculture, forestry and energy sectors use their resources and integrate their efforts to produce the sustainable products and services that will be available to meet the growing global demand.



3233 - Agronomy

Fabiano Daniel De Bona

MAIZE AND BRACHIARIA INTERCROPPING FOR IMPROVING NO-TILL SYSTEMS IN BRAZILIAN SUBTROPICAL REGION

De-Bona,FD; Denatdin,JE; Faganello,A; Silva-Júnior,JP; Santi,A; Dalmago,GA;

National Wheat Research Center - Embrapa Trigo;

After 40 years of no-till adoption in the subtropical region of Brazil, physical and chemical soil degradation has been observed. This condition has increased the occurrence of water deficit by rainfall shortage. The reason of this problem is attributed to no-till adoption without considering important principles of Conservation Agriculture. One of the biggest problems that cause soil degradation is the use of poor crop diversification that produce low plant biomass for the maintenance or increment of the soil fertility. Then, the challenge is to develop new crop production systems that promote the plant diversification and also produce economic benefits. This study aims to evaluate an intercropping system composed by maize (*Zea mays*) and *Brachiaria* spp. as an intensive grain and pasture production model that may allow the use of two or three crops per year in the same crop field. The experiment was carried out in the research station of Embrapa Trigo, in Coxilha (RS). Single maize and maize intercropped with *Brachiaria* spp. as crop system treatments were studied on a randomized complete block design, with four replicates, during six cropping seasons (2005 to 2011). The trial was established, every year in the beginning of spring season. Considering single crop and intercropping, maize grain productivity ranged between 6.3 to 18.0 Mg.ha⁻¹. The main variation in maize yield was related to different annual rainfall distribution. *Brachiaria* spp. intercropped with maize also was affected by water availability and the shoot dry matter varied from 0.9 to 4.0 Mg.ha⁻¹. *Brachiaria* spp. affected the maize yield in a unique cropping season. Nevertheless, in this cropping season the yield of maize cultivated together with *Brachiaria* spp. reached value above 14.0 Mg.ha⁻¹. *Brachiaria* spp. is used for cattle grazing or silage production, and the biomass produced has promoted improved physical and chemical soil attributes. Intercropping maize and *Brachiaria* spp. seems to be a promising crop system for enhance the plant biodiversity in no-till system areas of Brazilian subtropical region, increasing the biomass production, improving the soil fertility and farmer's profit.



3355 - Agronomy

Fábio Andrade Padilha

DESCRIPTION OF THE DIFFERENT STRUCTURES USED IN THE CULTIVATION OF VEGETABLES IN PROTECTED ENVIRONMENT

Padilha,FA; Magalhães,KS; Pedrosa,JA;

UFSJ/ Embrapa Maize and Sorghum;

The growing demand for high quality vegetables on offer throughout the year has contributing to investments in new cropping systems which allow production adapted to different regions and adverse environmental conditions. The main objectives of protected cultivation is protection against climatic factors and soil leaching, reduced fertilizer use, cleaner products, increased productivity, greater stability of supply and quantity of products. The main structures built today in Brazil for the production of vegetable crop are: greenhouse model chapel, which is usually the first model built by the producer who is initiating the activity, and model bow which offers greater resistance to wind tunnels and forced cultivation. The present work was carried out in order to describe the main structures used in the cultivation of vegetables in protected environment. We described the greenhouse structures of model chapel arch with wooden frame and bow with galvanized structure, both with 210m²; a greenhouse for seedlings, model chapel, with a size of 48m²; and the forced cultivation tunnels: tunnel up and down to the size range 105 and 36m². The descriptions of the prices of materials were made in shops located in Diamantina - MG during 2007, and in the company AGRISTUFA ® (São Paulo - SP). Chapel was the greenhouse model that had the lowest amount, R\$ 2,702.18, folloed by the greenhouse model bow with wood and structure such as galvanized (R\$ 3944.80, and 9184.60 respectively). This is the one that best adapts to the Diamantina region, as a region with an incidence of high winds, and the tunnels of cultivation, which had cost R\$ 867.84 for the high tunnel and the tunnel down to R\$ 351.10. Chapel was the greenhouse model that showed the lowest value among the greenhouses described with a value of R\$ 2.702 m⁻². The Arch model, both in wood and galvanized structure was one that offers greater wind resistance, so this is the best model to be deployed in areas with high incidence of strong winds. The greenhouse with galvanized structure presented the highest value, however it showed longer lifetime. The tunnels had forced cultivation construction for low values of m², so until it can be deployed by small producers, achieving gains in productivity and better quality products compared to open field production. Supported by UFSJ, CNPq, UFVJM.



3358 - Agronomy

Fábio Andrade Padilha

Production of tomato seedlings in different substrates

Padilha,FA; Pedrosa,JA; Magalhães,KS;

UFSJ/ Embrapa Maize and Sorghum;

The tomato *Lycopersicon esculentum* is a crop of great economic importance, since it represents a raw material for industry, being the second most produced vegetable crop in Brazil. The success of agricultural production begins by obtaining the tomato seedlings, constituting one of the most important stages of the production system, since it determines the final performance of the plants in the production beds, from a nutritional standpoint, time needed to production, and consequently the possible number of production cycles per year. This work aimed to evaluate different substrates for the production of tomato seedlings in trays. The experiment was conducted at the Federal University of Vales do Jequitinhonha and Mucuri in the glasshouse industry of Vegetable Crops. The experimental design was completely randomized (CRD), containing six treatments and four repetitions, with a total of 24 plots. The substrates were: Plantimax[®], humus, compost, soil / humus (1:1), soil / compost (1:1) and soil / manure (1:1). We evaluated the number of leaves (NL), root length (RL), shoot length (CA), stem diameter (DC), shoot fresh weight (PSA). There was a significant difference at 0.1% by the F test between the substrates evaluated for all traits. Considering the number of leaves (NL), substrates Plantimax[®], humus and compost resulted in higher values (4.36, 3, 94 and 3, respectively). For RL there was no significant difference between the substrates analyzed. The substrate Plantimax promoted the highest shoot length and stem diameter with values of 10, 3 and 3.15 cm respectively. Considering the fresh weight and dry weight of roots and shoots, significant differences were observed between treatments, with superiority of substrate Plantimax[®], which provided further development for these features. Importantly, a suitable substrate must have a proper balance of essential nutrients for plants and be resistant to diseases and weeds. In this study it was observed the emergence of weeds in all substrates, except for the Plantimax[®]. It was inferred from the results obtained that the best production of tomato seedlings occurred at the commercial substrate Plantimax[®]. The improved yield might also be explained because in this pH the substrate border is suitable for absorption of nutrients. Also their ability to retain water was superior to other substrates. Supported by CNPq, UFSJ and UFVJM.



3238 - Agronomy

fahd rasul

IMPACT OF NATURAL PLANT GROWTH REGULATORS ON THE GROWTH, YIELD AND QUALITY OF SUNFLOWER(*HELIANTHUS ANNUUS* L.)

Rasul,F; Bilal,A; Khan,HZ; Cheema,SA; Ahmed,A; Khaliq,T; Saleem,MF; Rehman,H;

Department of agronomy, University of agriculture faisalabad 38040;

Moringa and Brassica are known for their allelopathic and growth promoting effect. A field study to investigate the response of sunflower (*Helianthus annuus* L.) to foliar application of moringa and brassica leaf water extracts was conducted at the Agronomic Research Area, University of Agriculture Faisalabad, during spring, 2011. Experiment was laid out in complete randomized design with thirteen treatments that were replicated thrice. Foliar sprays of moringa (2%) and brassica (2%) water extracts were applied alone and in combination at 30, 60 and 90 days after sowing (DAS). All the treatments increased the yield of sunflower as compared to control. Highest sunflower yield (3242 kg ha⁻¹) was recorded in plots treated with three sprays of moringa and brassica water extracts mixture (T12) which was 22% more as compared to control and it was followed by plots treated with two sprays of moringa and brassica water extracts mixture (T11). One spray of moringa and brassica water extracts combination also significantly affected the sunflower yield over the control (T0), but it was less effective as compared to treatment (T12) in which three foliar sprays of moringa and brassica water extracts were applied. Three sprays of moringa and brassica (T12) water extracts combination significantly affected the plant height (198.11 cm), stem diameter (2.35 cm), head diameter (23.02 cm), number of achenes per head (1302), achenes weight (65.17 g), achenes yield as well as biological yield (14700 kg ha⁻¹) of sunflower as compared to their sole application. Three sprays of water also affected almost all the yield parameters as compared to control but remained less effective as compared to treatments (T12), in which three foliar sprays of moringa and brassica water extracts mixture were applied.



3304 - Agronomy

Fernando David Sánchez Mora

PRODUCTIVITY AND SANITY OF CACAO (*Theobroma cacao* L.) GENOTYPES IN THE CENTRAL ECUADORIAN COAST

Sánchez-Mora, SMFD; Garces-Fiallos, Garcés, F.R.; Vera-Chang, Vera, Ch.J.; Ramos-Remache, Ramos, R.R.; Medina-Jara, Medina, S.M.;

Unidad de Investigación Científica y Tecnológica-UICYT, Universidad Técnica Estatal de Quevedo-UTEQ, Ecuador;

The objective was to identify and select cocoa outstanding genotypes with desirable characteristics regarding to sanity and production in order to incorporate them into a breeding program of the Cocoa type National. Methodology Evaluated the sanity and productive of 58 clones of cacao (*Theobroma cacao* L.) at the Experimental 'La Represa', UTEQ, located at coordinates 79°30'23" east longitude and 01°00'35" latitude South, located in the upper basin Guayas River (77 msnm), and this area is classified as tropical rainforest (bh-T), with an average temperature of 24.5°C and average annual rainfall of 2,178 mm. The research phase lasted 12 months. Using descriptors such as number of healthy pods, diseased pods, productive potential, percentage of diseased pods, number of broom witch, pod and seed rates and performance. The values recorded were for tree 7 years old. Multivariate analysis and descriptive statistics was utilized for analysis statistical. To observe the variation of genotypes, is performed a multivariate analysis, obtaining the correlation between variables, and also developed a cluster analysis and principal components. Using Cluster analysis were obtained three groups, where Group 2 had the highest similarity matrix, formed by eight genotypes with an excellent characteristics of sanity and productive, represented 13.79% of the materials in the study. The 100% total variance was partitioned in 8 principal components (PC). The first PC explains 40% of the total variation where the grouped variables have more contribution are the number of healthy pods (-0.97), pod production potential (-0.88), performance kg ha⁻¹ per year (-0.86), the second principal component explained 33% of the total variance and the variable of greatest contribution was the number of diseased pods (0.82). By $\bar{x} \pm 1sd$ was determined that the material L15-H43 reported the percentage of diseased pods with 17.07% of incidence, the genotype L42-H80 stood out for its lowest number of witches' broom (2.90 brooms per tree) and the L20-H48 genotype had the highest production of dry cocoa 1478.07 kg ha⁻¹ per year. The genotypes identified in this work are part of a breeding program of the Cocoa type National. It continues to conduct will sanity assessments and productivity in order to verify more information on their behavior. Besides, genotypes tolerant to disease are will undertake artificial inoculations.



2911 - Agronomy

Flávio Martins Santana

EVALUATION OF FUNGICIDE TREATMENT FOR FUSARIUM HEAD BLIGHT SUPPRESSION IN SPRING WHEAT

Santana,FMS; Cargnin,AD;

Embrapa Trigo;

Fusarium Head Blight (FHB) is one of the most important wheat diseases around the world. The disease is caused by *Fusarium graminearum*. In 2011, two experiments were carried out at Embrapa Trigo, in Passo Fundo-RS. Those experiments were part of a multi-state coordinated field study. The study aims to evaluate the FHB control by fungicide application on a susceptible spring wheat cultivar. Two experiments were carried out in field conditions. The first one was sowed in June 17th with soybean as previous crop, and the second one in July 6th, with corn as previous crop. BRS 208 was used as the wheat cultivar. Both experiments were conducted with four replicates with 12 square meter each plot. There were two fungicides pulverization: First, when 25% to 50% of the plants were at the flowering stage, and the second one, at 7 to 10 days after. There were 9 treatments with different fungicides plus 1 check control without fungicide. The fungicides used were triazols alone or mixed with strobilurins. A hundred spikes were collected from each plot at the wheat soft-dough stage. It was evaluated the disease Incidence (I), Severity (S) and the Fusarium Index (FI). The harvested grains from six central lines were weighed in order to estimate the Hectolitre Weight (HW) and also the Grain Yield (GY). All data were statistically analysed and the Duncan test was applied using the Genes software. There were differences between experiments and among treatments at 5% of probability. At the second experiment, a high level of soil borne wheat mosaic virus (SBWMV) had occurred, which probably affected severely the grain yield results, in spite of the lower FHB incidence and severity in comparison to the first one. In the first experiment, for the HW analysis, there was no statistic difference verified among fungicide treatments and the check treatment. The incidence ranged from 26% (check) to 16% (Tebuconazol). The yield ranged from 2569 kg (check) to 3053 kg (epoxiconazol + strobilurin). There were also statistic difference between the check control and the others for S and FI. In the second experiment there were no differences verified for S and HW. There were statistic difference for the I (12% to 5%), FI (0.2 to 0.0), and GY (2780 kg to 3286 kg). However in this case the lower yield was not from the check control, probably because the SBWMV. In general, all fungicides reduced the FHB, and consequently giving a higher grain yield in comparison to the check control.



2913 - Agronomy

Flávio Martins Santana

INHERITANCE OF RESISTANCE TO NET BLOTCH (DRECHSLERA TERES) IN A BARLEY RANDOM INBRED POPULATION.

Santana,FMS; Minella,EM; Cargnin,AC; Clebsch,CCC; Kovaleski,MK;

Embrapa Trigo;

Net blotch is one of the most important diseases of barley in Brazil. The pathogen *Drechslera teres* is the causing agent. The disease is better controlled by the adoption of integrated pest management systems, by using crop rotation, resistant varieties and fungicide application. In 2011, at Embrapa Trigo, 103 random F8 inbred barley lines derived from a resistant x susceptible cross and the parents were evaluated for net blotch resistance in a greenhouse trial using four replicates with 3 plants each. The 105 genotypes population were inoculated with a local single isolate of *D. teres*. Plants were inoculated at 30 days after sowing, and scored 10 days later with a scale ranging from 1 (resistant) to 10 (very susceptible). Between the extremes, intermediate notes differ basically by the extension of the net lesions, and range from MR (moderately resistant) to S (susceptible). Genotype mean score ranged from 1 (resistant) to 7.5 (susceptible). Dunnett analysis divided the population in two major groups according to the reaction in the parental genotypes: 23 individuals scoring 1 to 3 (resistant) and 79 scoring 5 to 7.5 (susceptible). The roughly 1 resistant to 3 susceptible ratio suggests a two gene model controlling resistance in this population. The population is under evaluation in a growth chamber for resistance to net blotch at seedling stages.



2912 - Agronomy

Flávio Martins Santana

SURVEY OF FUNGI IN CROP RESIDUES ON SOILS UNDER DIFFERENT MANAGERMENTS.

Santana,FMS; Cargnin,AD; Dalmago,GAD; Clebsch,CCC; Kovaleski,MK;

Embrapa Trigo;

Necrotrophic fungi, which are pathogenic to plants, are able to survive on crop residues that are left over the soil surface after a crop season in the no tillage production system in Brazil. For some of them, crop rotation is crucial to reduce the primary inoculum of a disease by reducing the fungi survival. Because of that, it is suitable and useful to quantify the amount of pathogenic fungi that might survive on the soil residues over season's crop. The goal of the present work was to verify which pathogenic fungi were present on the soil stubble and quantify them. In the summer of 2009 at Embrapa Trigo, was started a long-term experiment with different crops system rotation. The treatments were carried out in four blocks replicate with the following crops rotation: 1) soybean/wheat/soybean; 2) soybean/oat/corn/wheat; 3) corn/wheat/soybean/oat; 4) soybean/rye/corn-brachiaria/wheat; 5) corn-brachiaria/wheat/soybean/turnip; and 6) soybean/rye/corn/wheat. In the late spring of 2011, samples of stubbles were collected from each plot and were taken to the plant pathology laboratory in order to isolate the fungi in PDA medium plates. The most important fungi pathogens, considering wheat and soybean as the main crops, and more frequently isolated were: *Bipolaris sorokiniana*, *Fusarium graminearum*, *Drechslera tritici-repentis*, and *Macrophomina phaseolina*. *B. sorokiniana* was most found at the treatments 4 and 6 where wheat was the last crop and rye the previous cereal crop. *F. graminearum* and *M. phaseolina* were most found at treatment 3, where oat was the last crop, and wheat the previous one. *D. tritici-repentis* was most found at treatment 1, which is wheat growing every winter. A statistic difference was detected among the treatments. *M. phaseolina* ranged from zero (treatments 2 and 6) to 20,5 colonies (treatment 3) in average, which correspond to 34% of the soybean stubble with viable inoculum of *M. phaseolina*. *B. sorokiniana* ranged from 1 (treatment 3) to 16 colonies (treatment 4), which correspond to 26,6% of inoculum in rye plus wheat stubbles. *F. graminearum* ranged from 1,5 (treatment 2) to 16 (treatment 3), which correspond to 26,6% of colonies from soybean plus oat. There was no statistic difference among treatments for *D. tritici-repentis*. In conclusion, the data indicate that crop system rotation affects the fungi population on the soil surface, which consequently might affect the level disease severity of the following crops in the system production.



3193 - Agronomy

Gabrieli Scariot

GENETIC UNIFORMITY OF MORPHOLOGICAL CHARACTERISTICS AND CYTOGENETIC ANALYSIS OF BRAZILIAN WHEAT CULTIVARS

Scariot,G; Brammer,SP; Scheeren,PL; Castro,RL;

Embrapa Trigo;

Cultivar characterization is essential for protection and registration of plant varieties, benefiting the breeder, the seed producers and the farmers in general. The objectives of this study were to evaluate wheat cultivars, as for some morphological important characteristics in describing a cultivar and confirming genetic stability by pollen viability analysis. Plants were collected from cultivars BRS 327, BRS 329, BRS 331, BRS Guamirim and BRS Parrudo, from genetic seed multiplication plots at the Embrapa Trigo experimental field (Passo Fundo, RS), in the winter of 2011. The description of the cultivars was done according to the standards for the National Register of Plant Varieties (MAPA, 2010). The following characteristics were described: number of spikelets per spike (nEsp), number of grains per spike (nGrE), spike length (cE) and spike density (dE). For the glume, the following measurements were taken: glume length (cGl), glume width (IGl), length of the glume beak (cdGl), and the shape of the glume shoulder (foGl). In relation to the grain, grain width (IGl) and grain length (cGl) were measured and classified as cited by the descriptors. For the cytogenetic analysis, 2500 pollen grains per genotype were analyzed. The technique used was of Squash, using 1% acetic carmine dye. Evaluation results showed that for the morphological characteristics of nEsp, nGrE, cGl and fGr the coefficient of variation was low (less than 10%) or medium (between 10% and 20%), allowing the differentiation of cultivars with good accuracy. This did not occur with other characteristics, like cdGl, foGl, cGr, dE, and cE IGl, where the coefficient of variation was greater than 20%, indicating that these characteristics are less reliable to differentiate cultivars. As for the pollen viability, it was found that the percentage of viable pollen grains was 96% for BRS Guamirim, 97% for BRS 329, BRS 331 and BRS Parrudo, and 98% for BRS 327, indicating high genetic stability. Therefore, it would be useful to review the morphological characteristics of wheat used as descriptors and include studies of genetic stability and uniformity in VCU (Value for Cultivation and Use) assessments, allowing a better characterization of the genotypes at the time of protection and registration of cultivars. MAPA - Ministério da Agricultura Pecuária e Abastecimento.



3218 - Agronomy

Genei Antonio Dalmago

HIDRIC STATUS IN MAIZE PLANTS AS A FUNCTION OF NO TILLAGE SOIL MANAGEMENT

Dalmago,GA; Faganello,A; Denardin,JE; Fochesatto,E; Santi,A;

EMBRAPA - EMBRAPA TRIGO;

In the last years, the frequency of the crop failure as result of short periods of water stress has increased. It is hypothesized that a compacted soil layer, at 7 to 12 cm depth and nutrients concentration are limiting the root growth. A study was carried out to evaluate the water potential on corn plants grown under no-tillage system with a compacted soil layer. Two experiments were designed for this study. The first experiment was located at the experimental area of the Cooperativa Cotricampo, in the 2011/2012 crop season. The experimental design was a split plot, with a four replication. In the main plots consisted of soil management treatments such as: chiseling, 12 months previously chiseling and no chiseling. The subplots consisted of use of seeder equipped with narrow knives at 10 and 15 cm depths and seeder equipped with offset double disks at 7 cm of soil depth. In the second experiment the main plot was gypsum placement such as: surface, buried and no gypsum. The subplots consisted of use of seeder equipped with narrow knives at 10 and 15 cm depths and seeder equipped with offset double disks at 7 cm of soil depth. Water potential and plant leaf temperature were measured with a Scholander pressure chamber and an infrared thermometer, respectively. Through the experiment period, water potential was bellow -1.5 MPa in almost all treatments. Thus, indicating that the plants were all the time under water deficit. In any experiments it was not detected a significant interaction between water potential and temperature. However, significant treatment differences were detected in a single measurement date, in both experiments. At this date, leaf water potential gave an indicative that the treatments with seeder equipped with knife at 15 cm depth provided better water availability to plants in comparison to other treatments. On the other hand, the leaf temperature indicated the opposite, which meant that, it is likely that, plant water content was resulted from specific weather conditions rather than from soil. The results obtained are not enough to make conclusions yet.



3191 - Agronomy

Gilberto Omar Tomm

Eradication of blackleg disease of canola in Brazil ? a success story

Tomm,GO; Kutcher,HR; Easton,A;

Embrapa Trigo;

Canola (*Brassica napus* L.) research and commercial production started in Brazil in the mid-1970's. Lack of technology adapted to Brazilian conditions hindered the expansion of canola production. From 1980 to 1997 the cropped area averaged 11,400 ha per year with a mean yield of 906 kg/ha. In 2000, blackleg, incited by the fungus *Leptosphaeria maculans* (Desmaz.) Ces. & De Not. (asexual state *Phoma lingam* (Tode:Fr.) Desmaz.), was discovered in southern Brazil. The disease caused partial and even total destruction of some canola fields, which made production insecure and it was suggested that the canola cropping area would sharply decline. In April and May, 2002, canola was sown into 4-replicate, RCBD experiments at five locations under natural inoculum to evaluate 18 *B. napus* genotypes from diverse origins. Disease incidence and severity were evaluated after transversely cutting the lower portion of each stem of 50 plants taken at random from each plot. Two canola hybrids, Hyola 43 and Hyola 60, were identified with adequate agronomic characteristics, and complete resistance to the pathogenicity group of *L. maculans* present in Brazil and Paraguay. Timely efforts for registration of these hybrids [Pest Risk Analysis-PRA (a 289 pages document)], and importation of seed from Australia allowed commercial production of resistant hybrids over thousands of hectares, just one year after studies began. Following registration of these hybrids, field experiments identified optimum seeding dates and other beneficial agronomic practices, which were followed by intensive training of farmers and technical assistants led by researchers. Canola production has continued as a result of further introductions of new, blackleg resistant (Hyola) hybrids, technical assistance to farmers and the guaranteed purchase of canola at a price equivalent to soybeans. The joint efforts of researchers, oil extraction companies, breeding companies and suppliers of other inputs resulted in an average of 32,300 hectares of Brazilian production per year, with yields increasing to an average of 1,656 kg/ha between 2002-2007. The cropping area has continued to increase steadily, reaching 59,100 ha in 2011. The worldwide availability of knowledge and genetic material for canola production, when combined with the efforts of professionals and companies with the appropriate technologies and attitudes overcame the challenges of canola production in countries in which canola R & D is still scarce.



3219 - Agronomy

Gilberto Rocca da Cunha

THE IMPACTS OF CLIMATE VARIABILITY/CHANGE ON WHEAT CROP IN BRAZIL: IS THE WORST YET TO COME?

Cunha,GR; Santi,A; Fernandes,JMC; Pasinato,A; Dalmago,GA; Pires,JLF;

Empresa Brasileira de Pesquisa Agropecuária, Centro Nacional de Pesquisa de Trigo (Embrapa Trigo);

Wheat, be it due sensitivity to extreme climate fluctuations or to its importance in the global food system, is one of the most studied crops in the world. In spite of the countless reports on regionalization, agricultural zoning, climatic risk analysis, bioclimatic requirements and weather influence on pests, yield and grain quality, there is a paucity of information on the the likely effects of a changing climate on wheat production. The current climate-associated limitations and its variability for cultivating wheat in Brazil are well known and have been systematically overcome by means of technological innovation. What is the future probably like? Is the worst yet to come? What is the pathway of technological innovation on wheat in Brazil for scenarios A1, B1, A2 and B2 from IPCC for climate change research and assessment? To answer such questions is the main objective of this work. Climatic data from PRECIS model provided by the National Institute for Space Research (INPE), in a regular grid of 0.5° x 0.5°, covering the whole of Brazilian territory, from the baseline period of 1961-1990, to starting years of each decade (2010, 2020, 2030, 2040, 2050, 2060 and 2070) were used all the way to the top line period of 2071-2100. Additionally, for current climate evaluation, a series of historical data was employed from 1991-2010. A wheat growth and development model (CSM-CERES Cropsim Wheat/DSSAT) and an epidemiological model were used for estimating yield and Fusarium Head Blight incidence, respectively, across scenarios and current climate variability. Model outputs were integrated to GIS tools to produce risk maps. The results presented and discussed in this study, e.g. the outlook of higher FHB risks and more frequently negative impacts on wheat yield caused by El Niño phenomenon in Southern Brazil, are a contribution of the "Future Agricultural Sceneries for Grains Project" (in Portuguese Projeto Cenários Agrícolas Futuros para Culturas de Grãos - SCAF Grãos).



3334 - Agronomy

Giovani Theisen

KNIFE-ROLLER: A METHOD FOR LESS SOIL-DISTURBANCE IN GROUND LEVELING AT LOWLANDS PADDIES

Theisen,G; Bonow,JFL; Fipke,MV; Silva,JJC; Verneti-Junior,FJ;

Embrapa Clima Temperado;

The rice harvest in lowlands occurs predominantly in flooded - or highly wet soils and the machines traffic causes deep tracks on soil and compaction. A ground leveling is a requisite to use crop rotation after the rice harvest in lowlands, and this task should be done in the autumn or in the spring prior the sowing. These operations require big tractors with a great soil disturbance and associated costs. One alternative to adjust the soil leveling after the rice harvest is the use of the knife-roller, equipment that corrects the ground imperfections originated by the machines traffic at harvest. A field experiment was carried out in lowlands at Embrapa Clima Temperado, Capão do Leão county, RS, Brazil, to evaluate the soybean performance under three systems of soil leveling (one pass of knife-roller; two-cross knife-roller; and knife roller plus harrowing) applied in autumn after the rice harvest. In the spring, half of the area was shallow harrowed. The experiment was conducted in a split-plot design with 4 replications, and were evaluated the soybean stand, grain yield and uniformity. There were no differences in soybean yield and stand between all leveling systems, but the spring harrowing increases the variability of these parameters. The results permit to conclude that in wet or well-watered paddies the knife-roller should be used to leveling the soil after the rice harvest, and in this case the equipment properly replaces the plowing-and-harrowing on lowland soil management.



3192 - Agronomy

Giovani Theisen

SUGRACANE PRODUCTION IN LOWLANDS PLANTED OVER RIDGES MADE WITH A RICE'S LEVEE-PLOW

Theisen,G; Fipke,MV; Reis,A; Bonow,JFL; Silva,SDA;

Embrapa Clima Temperado;

Almost all demanded ethanol in Rio Grande do Sul (RS), Brazil is supplied from others states, with a local production that meets only 3% of consumption. The crescent demand has motivated to increase the ethanol production in RS, to reduce this dependence and to aggregate more opportunities for diversification in the primary sector. The sugarcane areas in RS is located in the highlands, however the new agro-climatic zoning determined for this culture has identified some areas suitable for cultivation in lowlands. These areas, with bad drainage and occupied with irrigated rice and beef cattle production, can be cultivated with sugarcane if properly managed. The sugarcane has a low tolerance for very high wet soil conditions, and requires some steps to prevent this stress condition over the crop. One of the techniques in that sense is planting over beds, that consist of structures resulting from the preparation and adjustment of the soil, forming parallel levees or ridges on the ground, on which are sown or planted the crops. This allows the cultivation of dry-crops in a lowland soil, and allowing to the surface irrigation. For preparation of the ridges in lowlands is used specialized machinery, used in grain crops in countries of North America and Europe. The raised beds for planting sugarcane can be constructed alternatively with a levee-plow, a machine used in irrigated rice fields. In an area previously leveled, plowed and graded, the levee-plow was used for making the levees (0.4m height and 1.7m apart); the furrow for planting sugarcane on the levees was done with a narrow trencher (0.15m width and 0.2m deep); and the furrow between ridges, to drainage, was done with a large trencher, whose effect also contributes to the covering the sugarcane with soil in planting. Using only this adapted equipment from rice production, an experiment (RCB, 4 reps.) was carried out in Embrapa Clima Temperado, at Capão do Leão, RS, Brazil, to evaluate the performance of 30 genotypes of sugarcane, including clones and varieties with medium to early cycles. The results indicate that the use of trenchers and rice's levee-plow can be used in the sugarcane implementation in the lowlands, and the system of ridges was appropriate in order to make the drainage of area in the rainy season. Among the 30 cultivars evaluated, there was obtained an average yield of 59 t ha⁻¹, with cultivars better adapted reaching above 80 t ha⁻¹ in the first season of cultivation.



3252 - Agronomy

Guilherme Borba Menezes

Desiccation timing of vetch and its effects on maize crop.

Borba-Menezes,G; Régis-Ferreira,P; Correia,S; Menagati,G; Barreto-Maass,M; Soares-Guterres,B;

UFRGS;

The objective of the experiment was to determine the most appropriate time for drying the vetch (*Vicia sativa*) to get better synchrony between N release of its residues and the need for the corn plant in succession. The experiment was conducted in Eldorado do Sul-RS, Brazil, in the growing season of 2010/2011. Three treatment were tested: vetch desiccation in the day of corn sowing and 20 days after corn sowing and a treatment without vetch. The experimental design was randomized blocks, with four replications. Vetch was sown on May 17, 2010. On the sowing day of corn, August 19, the dry matter yield of vetch was 3,9 y ha⁻¹. Corn hybrid used was the Pioneer 30F53 Hx P RR with Herculex Bt technology an resistance to the herbicide glyphosate. Plant 10.0 pl m⁻², with row spacing of 0,5 m. It was applied the rate of 100 kg ha⁻¹ of N at the V6 stage, according to the scale of Ritchie et al. (1993). With the delay of 20 days in the vetch desiccation time, it was obtained a yield of 9.6 t ha⁻¹, which was 16 and 21% higher compared to treatments in which vetch was desiccated on the sowing day of corn and on the check without vetch. In relation to the control without vetch, the delay of the vetch desiccation in 20 days after corn sowing resulted in a gain of 1.2 t ha⁻¹ for grain yield and an extra revenue of \$ 280.00 per hectare in the corn crop.



3286 - Agronomy

Hossein Soleimanzadeh

Effect of rapid canopy development on seed yield of safflower in the north of Iran

Soleimanzadeh,H;

Department of Agriculture and Plant Breeding, Pars Abad Moghan Branch, Islamic Azad University, Pars Abad Moghan, Iran;

Rapid canopy development in crop increases interception of solar radiation and can be resulted in increases crop yield. Therefore, this study was conducted to investigate the relationship between canopy development and crop yield in safflower as well as traits that affect canopy development. The study included 8 safflower genotypes (Arak 2811, DS-1, Fariv, Jila, Koseh, PI, Zarghan 279 and Varamin 295). Laboratorial tests and field experiment carried out at Islamic Azad University, Pars Abad Moghan Branch in 2010 - 2011. The results showed that the correlation of seed vigor with rapid canopy development and grain yield was not significant when there were optimum plant density in field. Rapid canopy development had significant effect on seed yield. Cultivars with faster canopy development produced more seed yield. Leaf area index and crop dry matter (at beginning of exponential growth phase), relative leaf area development rate (during the exponential phase), the average of individual leaf area and leaf area ratio was introduced as effective traits in rapid canopy development in safflower. Keywords: Canopy development; Grain yield; Safflower



3288 - Agronomy

Hossein Soleimanzadeh

Effects of Azotobacter and nitrogen chemical fertilizer on yield and yield components of wheat (*Triticum aestivum* L.)

Soleimanzadeh,H;

Department of Agriculture and Plant Breeding, Pars Abad Moghan Branch, Islamic Azad University, Pars Abad Moghan, Iran;

The effect of seed inoculation by Azotobacter and different levels of nitrogen fertilizer on growth and yield of wheat (Pishtaz cultivar) was studied in experiment farm of Islamic Azad University, Pars Abad Moghan Branch during 2010 growing season. The experiment treatments were arranged in factorial based on a complete randomized block design with three replications. Four nitrogen fertilizer levels of 25, 50, 75 and 100% N recommended with two levels of Azotobacter: with and without Azotobacter (control) were assigned in a factorial combination. Results showed that plant height, grains number per ear and biological yield were significantly higher in inoculated plants than in non-inoculated plants. Plant height, ear length, grains number per ear, biological yield and grain yield were increased with increasing N level above 75% N recommended in non-inoculated plants, whereas no significant difference was observed between 50 and 100% N recommended. The positive effect of Azotobacter inoculation was decreased with increasing N levels. According to the results of this experiment, application of Azotobacter in present of 50% N recommended had an appropriate performance and could increase grain yield to an acceptable level, so it could be considered as a suitable substitute for chemical nitrogen fertilizer in organic agricultural systems. Key words: Azotobacter, Grain yield, Nitrogen fertilizer, Wheat.



2852 - Agronomy

Hussein Fawzy Hussein Abouziena

EFFICIENCY OF PLANT POPULATION AND REDUCED HERBICIDES RATE ON MAIZE PRODUCTIVITY AND ASSOCIATED WEEDS

El-Metwally, I;

National Research Center;

Two field experiments were conducted during the summer season of 2010 and 2011 at the Experimental Farm at Kfar El-Khawazim, Talkha district, Dakahlia Governorate, Egypt to study the performance of maize plants and associated weeds to four plant population (20000, 25000, 30000 and 35000 plants/fed) and eight weed management treatments (Acetochlor at 75% of recommended rate, Acetochlor at 750 cm³/fed (recommended rate), Fluroxypyr at 75% of recommended rate, Fluroxypyr at 200 cm³/fed (recommended rate), Bentazon at 75% of recommended rate, Bentazon at 750 cm³/fed (recommended rate), two hoeing and un-weeded check). The results showed that narrowing the spacing between maize plants from 30 cm to 17 cm caused a significant reduction (21%) in the total weed dry weight. Reduced herbicide rate caused insignificant differences on maize weeds if compared to the recommended herbicide rate. Maize weeds could be controlled with 75% of the recommended Acetochlor herbicide rate. Fluroxypyr at 200 cm³/fed produced the lowest broadleaved weeds dry weight under maize sowing at 30000 plant/fed. While, the lowest dry weight of grass resulted from hoeing twice with sowing maize at 35000 plants/fed. Planting maize at 35000 plants/fed gave the lowest total dry weight of weeds when Acetochlor herbicide at 563 cm³/fed was applied. The greatest grain yield resulted from sowing maize at 30000 plants/fed (7.14 plants m⁻²). Uncontrolling weeds caused a significant decrement in the grain yield by 29.7% compared to hoeing treatment. Acetochlor at 750 cm³/fed, hand hoeing produced the greatest grain yield. The two superior treatments significantly increased the grain yield/fed than the unweeded check by 42.9 and 42.3%, respectively. The results also indicated that no significant differences were recorded between Acetochlor at the full rate of 750 cm³/fed, two hand hoeing and Acetochlor at 75% of recommended rate on maize grain yield. Protein and oil percent in corn grains were decreased by 8.0 and 9.2% due to the weed interference. It could be concluded that sowing maize at 30000 plants/fed (7.14 plants m⁻²), and controlling weeds mechanically by hoeing or chemically using Acetochlor herbicide at the recommended rate produce the greatest grain yield.

Key words: maize, plant population, herbicide rate, weeds, grain, interaction



2599 - Agronomy

ISAAC R. FANDIKA

EFFECTS OF IRRIGATION ON TUBER DEVELOPMENT AND TUBER YIELD OF OCA CULTIVARS (OXALIS TUBEROSA MOL.)

Fandika,IR;

Institute of Natural Resources, Massey University;

There is little information on oca (*Oxalis tuberosa* Mol.) in modern production systems, despite its economic potential. This project investigated oca tuber yield and tuber formation under irrigation and rain-fed conditions in New Zealand. A split-plot experiment with rainfall and irrigation as the main treatments and cultivars as the sub-treatments was established on the Pasture and Crop Research Unit, Massey University in October 2009 until June, 2010. There were four replicates, plant population was 3.8 plants m², receiving 60N+26P+70K+30s kg ha⁻¹ at planting, followed by 100 kgN ha⁻¹, 21 days later. Irrigation was based on replenishing 25 mm of 30 mm soil's moisture deficit scheduled using soil water balance technique. Gaseous exchange, tuber formation and yield parameters were measured and subjected to ANOVA using the PROC GLM procedure in SAS. Crop water use in rain-fed treatments was 75% of irrigation treatments. Photosynthetic water use efficiency increased with irrigation, whilst leaf vapour pressure deficit increased with water stress (p 0.5). Water stress reduced photosynthetic water use efficiency, tuber growth, total tuber yield and marketable tuber yield.



2843 - Agronomy

JB Ochanda Ogola

RADIATION INTERCEPTION BY A CASSAVA (*Manihot esculenta*) CROP IN A DRY ENVIRONMENT

Ogola, JBO; Mathews, C;

University of Venda;

Cassava (*Manihot esculenta*) is one of the most productive tropical crops on marginal lands. However, in the high latitude areas low temperatures during winter may lead to loss of leaves and hence a reduction in the proportion of intercepted radiation. This may permit the introduction of a winter legume as an intercrop thus increasing the overall productivity of the cassava-based cropping systems. This study aimed at assessing radiation interception by four cassava genotypes (Lal, Local-Mzinti, I-89/00715 and Mzinti) during the winter months at Thohoyandou, South Africa. A field experiment was conducted in 2010/2011, under rainfed conditions, using a randomized complete block design replicated three times. The proportion of intercepted radiation (IR) was determined between 22 and 42 weeks after planting (WAP) by measuring photosynthetically active radiation above and below the crop canopy on clear, cloudless days using a sunfleck ceptometer. Genotype did not affect the proportion of IR between 22 and 42 WAP. The proportion of IR ranged from 96% (23 WAP) to 42% (39 WAP) but there was a general decline in the proportion of IR between 26 and 40 WAP. This period coincided with the winter months (June - August). The proportion of IR was less than 60% between 34 and 42 WAP (about two months). Therefore the productivity of cassava-based cropping systems in this dry environment may be improved through incorporation of an early maturing winter legume as an intercrop growth conditions during both years of experiments ($R^2=75\%$, p)



3264 - Agronomy

Jônatas Galvan

EMERGENCY OF THE LOLIUM MULTIFLORUM BY SOWING DEPTH, STRAW COVER AND SOIL COMPACTION

Galvan,JÔNATAS; Rizzardi,MAUROANTÔNIO; Galvan,MÁRCIO;

Universidade de Passo Fundo;

Ryegrass (*Lolium multiflorum* Lam.), family Poaceae, occurring widely in southern Brazil, especially in Rio Grande do Sul, where it is used as livestock feed, and as agricultural ground cover, during the winter. Ryegrass plants flowering and bear fruit in abundance in late spring and after physiological maturity seed abscission occurs, which, if not harvested they fall and remain dormant until late summer, when germination begins. The objective of this study was to evaluate the effects of soil compaction, straw cover, and sowing depth on emergency of ryegrass. The experiment was performed in greenhouse with an experimental design of randomized blocks. The treatments were: eight sowing depth (0, 1, 2, 3, 4, 5, 7.5 and 10 cm), three levels of corn straw cover (0, 5 and 10 t.ha⁻¹) and three levels of soil relative bulk density (Dsr) (0.75; 0.89; 0.99). The Dsr was determined by dividing soil bulk density by the maximum density (Proctor Test). The seeds were sown in plastic cylinder of 100 mm diameter, the soil was pressed until the desired compaction. The emergence evaluation occurred 60 days after the experiment was implanted. There was interaction between sowing depth and soil compaction and sowing depth and straw cover. Generally, two and three centimeters of depth favored the plants emergence, however, do not differ statistically when at one centimeter depth in soil with Dsr 0.75, and zero and one centimeter in soil with Drs 0.99. Considering the corn straw cover, two and three centimeters promoted greater emergency, but there is no difference from one to four centimeters in cover of 5 t.ha⁻¹, and one centimeter with 10 t.ha⁻¹ of cover. The adverse conditions for germination were depths exceeding five centimeters, regardless the amount of cover or soil compaction. Thus it is noted that the main factor involved in the ryegrass emergence is sowing depth.



3266 - Agronomy

Jônatas Galvan

VIABILITY OF RYEGRASS SEEDS GLYPHOSATE SENSITIVE AND RESISTANT

Galvan,J; Rizzardi,MA;

Universidade de Passo Fundo;

Ryegrass (*Lolium multiflorum* Lam) is an annual grass adapted to low temperatures temperate climate, unable to resist the summer heat of tropical climates, and developing only during the winter and spring. Ryegrass plants flowering and bear fruit in abundance in late spring and after physiological maturity seed abscission occurs, which, if not harvested they fall and remain dormant until late summer, when germination begins. This phenomenon, natural seeding, is very useful for the cattle ranchers, but for farmers this can lead to control difficulties due to the occurrence of plants in different development stages, since germination occurs incrementally. This phenomenon is even more serious due to the fact that the glyphosate resistance of this species, the main agricultural herbicide, is widespread throughout the state of Rio Grande do Sul. The objective of this study was to evaluate the ryegrass viability over time, in order to generate information for the management of the seed bank of this species. An experiment was conducted with 100 ryegrass seeds, glyphosate sensitive and resistance, previously tested in dose response curve, with sterile soil were placed in fabric permeable bags and wrapped in plastic with mesh size less than the diameter of the seed, and sowed at 5 cm depth. Samples of four replicates per treatment were collected every three months when it was evaluated the number of seeds still present, which were submitted to germination test in BOD, and the seeds that did not germinate after 14 days submitted to tetrazolium test. The results indicated that for one year, approximately 50% of the seeds were no longer found in the soil. It was also observed that the percentage of the seeds collected that germinate in BOD or proved to be viable in tetrazolium reduced to only 25% after a year, most remarkable fact in the seeds from glyphosate resistant plants. It is concluded that the seeds present high primary dormancy, but low secondary dormancy, especially observed in seeds glyphosate resistant.



2693 - Agronomy

Jude.J.O Odhiambo

EFFECT OF GREEN MANURE LEGUME ROTATION WITH MAIZE ON SELECTED SOIL CHEMICAL PROPERTIES

Odhiambo,JJO;

University of Venda;

Green manure legumes (GML) in rotation with cereal crop such as maize has the potential to improve soil fertility. A two-year field study was carried out on a deep, clay soil at Thohoyandou, Limpopo province, South Africa to determine the effect of green manure in rotation with maize on selected soil chemical properties (pH, P, organic C and total N). The rotation system (GML-maize-GML-Maize) consisted of five (5) GML species viz. sunhemp (*Crotalaria juncea*), mucuna (*Mucuna pruriens*), lablab (*Lablab purpureus*), cowpea (*Vigna unguiculata*) and butterfly pea (*Clitoria ternatea*) and two (2) fallow control plots, followed by maize for two seasons (2007/8 and 2008/9). Maize planted on the fallow control plots either received N (fallow control +N) or no N application (fallow control -N). The plots measured 4 m x 5 m and the treatments were arranged in a randomized complete block design replicated three times. At the end of the two seasons, soil pH, available P, organic C, and total N were determined. There were no significant differences in soil pH among the treatments. The pH ranged from 6.02 (sunhemp) to 6.24 (lablab). Soil available P in fallow control -N (2.12 mg kg⁻¹) and cowpea (2.00 mg kg⁻¹) were significantly higher than in butterfly pea plots (1.46 mg kg⁻¹) but not different from all other treatments. Organic C level in sunhemp rotation plot (2.20%) was significantly higher than in the fallow control -N rotation plot (1.88%) but was not different from all other treatments. Total N in sunhemp rotation plots (0.07%) was significantly higher than in all other treatments. Fallow control +N had the lowest total N (0.05%). Lack of differences between the GML and the fallow control treatments and the inconsistencies in differences between the treatments in the soil chemical properties measured possibly suggest that a longer term rotation may be necessary in order to observe any significant differences in the measured soil chemical properties between the GML and fallow control treatments in these highly weathered soils of semi-arid region of Limpopo province, South Africa.



3149 - Agronomy

Lília Sichmann Heiffig del Aguila

SPACE ARRANGEMENTS AND CONSORTIUM IN THE INITIAL DEVELOPMENT OF JATROPHA CULTURE

Heiffig-Aguila,LS; Gallo,PB; Saavedra-Aguila,J;

Embrapa Clima Temperado;

The study aimed to investigate and evaluate the *Jatropha curcas* crop management, especially spatial arrangements for maximum agricultural productivity. In greenhouse conditions were produced *Jatropha* seedlings in plastic bags of 1.7 L with a commercial substrate Rendmax Citrus. For the emergence and maintenance of the seedlings, irrigation, fertilizer application and other cultural practices and phytosanitary control, were carried out as needed. When the seedlings were 60 days of emergence were transplanted rows in the field by hand and fertilized in accordance with the recommendation. In Mococa-SP, the experiment under field conditions was conducted in a randomized block design with split plot arrangement and five replications, consisting of three levels of spatial arrangement factor - row spacing x plant spacing (plots) and two levels of intercrop factor (subplots), resulting in six treatments: T1 = 4.0m x 3.0m, without intercropping deployment, T2 = 4.0m x 3.0m, with intercropping implementation, T3 = 3.0m x 3.0m, without intercropping deployment, T4 = 3.0m x 3.0m, with intercropping implementation; T5 = 3.0m x 2.0m, without intercropping deployment, T6 = 3.0m x 2.0m, with intercropping implementation. Since the time of transplant (13/04/2010) was not as suitable due to a low rainfall, plants were irrigated. After the dry season, especially July and August, a good distribution of rainfall favored the development of the culture of *Jatropha*. The traits evaluated were phenological stages, leaf area index, plant height, agricultural productivity and efficient use of land. Consortium, as treatment with *crotalaria*, were not statistically significant differences for the LAI until 3 months post-transplantation and a small difference to the average height of plants at the 2nd month. The efficient use of land values were greater than 1.0 for all treatments consortium, while the yield of *Jatropha* was null. It was concluded that considering mainly the sustainability factor, the consortium of *Jatropha*, in the early stages of development, with intercrops is quite feasible, to confirm for a more efficient use of land and allow the generation of income for the property.



2854 - Agronomy

Magda Laiara Bezerra de Lima

INITIAL GROWTH OF JATROPHA CURCAS L. AS A FUNCTION OF SOURCES AND DOSES OF ORGANIC FERTILIZERS

Lima,MLB; Ruppenthal,V; Schulz,DG; Fradoloso,JF; Fey,R; Zoz,T; Lana,MC;

Universidade Federal do Ceará;

In order to determine the best dose and source of organic fertilizer on initial growth of *Jatropha curcas* L., an experiment was performed in the city of Marechal Cândido Rondon - Paraná. The experimental design was a randomized block design in 5 x 4 factorial scheme of each organic fertilizer sources (poultry litter, cattle manure, fish manure and urban waste composting) consisting of five doses of each source (50, 100, 200 and 400 L.m⁻³ and a control without fertilizer addition), with four replicates of one pot per treatment, measurements were performed at 30, 60, 90 and 120 days after transplanting (DAT) to the pots. Morphometric measurements of seedlings consisted of plant increase and increase stem diameter. Data were tabulated and subjected to analysis of variance by the F test (p 0.05) with adjustments for regression equations and polynomial response surface using the statistical program Genes. Subsequently, we performed the calculation of maximum efficiency for each measured variable. The increase in physic nut seedling height from 30 to 120 DAT in pots showed a quadratic adjustment in plants that received cattle manure and urban waste compost with a maximum increase estimated at 30 DAT. The estimated point of maximum technical efficiency for fertilizer dose was 254 L.m⁻³ with fish manure. There was linear increase with soil plus manure or composting, whereas with the addition of poultry manure there was a linear decline not responding positively to fertilization doses and DAT, possibly resulting from the toxic effects. Seedlings conducted on a substrate formed by soil plus fish manure, composting or cattle manure showed the highest values for increase of stem diameter. The estimated maximum point for fish manure dose was 165 L.m⁻³ while there was a linear increase on stem diameter with the use of cattle manure and composting. The maximum increase in stem diameter was reached at approximately 71 DAT for all fertilizers tested. The best initial growth of seedlings *J. curcas* was obtained by fertilization with veal manure, fish and urban waste compost, with doses of maximum efficiency between 200 and 400 L.m⁻³. The use of poultry litter resulted in lower values for the morphometric variables analyzed. To the best initial development of *Jatropha curcas* L. recommended application of veal manure, fish and urban waste compost at doses between 200 and 400 L.dm⁻³ and poultry litter at doses below 200 of L.m⁻³.



3202 - Agronomy

Magda Laiara Bezerra de Lima

SEEDLINGS PRODUCTION OF YELLOW MOMBIN (*SPONDIAS MOMBIN* L.) GROWN ON SUBSTRATES OF AGROFORESTRY RESIDUES

Lima,MLB; Lima,AA; Carvalho,CAC; Lima,LA; Beber,PM; Paiva,AV;

Universidade Federal do Ceará;

The aim of this study was to evaluate the biomass production of Caja (*Spondias mombin* L.) seedlings grown on different agroforestry residues substrates available in the Amazon regions. Each substrate was prepared by using, 2/3 of the lime treated soil according to soil analysis, and 1/3 of each organic residue (peanut hull, sawdust and seed *Euterpe oleracea*), soil without the addition of any organic residue was used as control. Substrates were kept in polyethylene bags in greenhouse at the Federal University of Acre. The selection of *Spondias mombin* L. seedlings was made according of vigorous of the seedlings and absence of pests / diseases, all of them must be with at least four metaphylls. Irrigation was performed daily until the removal of the seedlings. Each seedling was divided into shoots and roots, and kept in oven on 60° C for 5 days, until a constant weight was achieved for each plant material. Dry shoots and roots were weighing on an analytical balance, and variance analysis and Tukey test was made by using Sisvar 5.0 statistical analysis software. Experiment was complete randomized. Averages of dry matter for the shoots of, control, bark peanuts, sawdust, and açai seed were found to be 0.771 g, 2.000 g, 0.779 g and 2939 g respectively; while for roots we found 5.283 g, 10.433 g, 4.118 g and 18.402 g respectively. We can conclude that using *Euterpe oleracea* in soil; can produce high biomass for both shoots and roots, as indicated from the dry weight of *Spondias mombin* L.



3296 - Agronomy
Marcio Zilio

MORPHO-PHYSIOLOGICAL TRAITS OF SOYBEAN CULTIVAR NS4823-RR UNDER WATER DEFICIT IN GREENHOUSE ENVIRONMENT

Zilio,M; Souza,CA; Correa,C; Stefen,DLV; Ataide,RCN; Sponchiado,JC; Coelho,CMM;

Universidade do Estado de Santa Catarina;

The aim of this work was evaluate morphological and physiological traits of soybean cultivar NS4823-RR under water restriction during reproductive stages. A greenhouse pot experiment was carried out, in a completely randomized design with three replications; consisted of 6x6x2 factorial, with 6 phenologic stages (R1-R6) under water stress, 6 consecutive evaluation dates (0, 2, 4, 6, 8, 10 days after water stress) and 2 irrigation levels (30% and 80% of field capacity of soil - FC). The control treatments were well-watered soybean plants at to 80% FC during all experiment time. The plant height, leaf area, leaves number and nodes by plant, leaf relative water content (LRWC), root/shoot dry mater and chlorophyll content were evaluated. Data were submitted to variance analysis using F-test, averages were compared by Tukey test (P) or regression analysis was fitted. Plant height growth rate (cm.day⁻¹;) was higher in all plant stages without water restriction than water restriction plants, which R3 stage had the great difference (7.8 cm.day⁻¹;) . Water restriction plants presented reduction in growth of R1 to R3 stages and in R4, R5 and R6 stages wasn't growth. The leaves number per plant under water restriction from R4 to R6 stages were not affected. The nodes number showed higher increase in all plant stages without water restriction than water restriction plants, which the great difference was observed in R4 stage (2 nodes). Water restriction plants showed lesser leaf area than plants without water restriction. The lowest leaf area were observed under water stress at R3 stage (34.7 cm²) and the smaller reduction at R5 stage (6.4 cm²). The LRWC in water restriction plants from R1 to R3 stages didn't present influence of day number with water restriction. But a linear reduction of LRWC was observed from R4 to R6 stages, however R5 stage was more water restriction sensitive (21.2%). Water restriction plants from R1 to R4 stages had smaller chlorophyll content than plant without water restriction, but R4 stage plants had highest reduction (only 9.6 SPAD unit). The root/shoot ratio was higher in water restriction plants (0.7) than in plants well-watered (0.45). Overall, the R3, R4 and R5 stages were more water stress sensitive to evaluated traits.



3340 - Agronomy
Marcio Zilio

YIELD COMPONENTS OF SOYBEAN CULTIVAR NS4823-RR UNDER WATER STRESS IN GREENHOUSE ENVIRONMENT

Zilio,M; Souza,CA; Werner,F; Sponchiado,JC; Tormem,ME; Zanesco,PR;

Universidade do Estado de Santa Catarina;

The aim of this work was evaluate the yield components of soybean cultivar NS4823-RR under water stress during reproductive phase. The work was performed in greenhouse, in a completely randomized design with three replications. The treatments were arranged in a 7x2 factorial, which 7 phenologic stages (R1-R7) were submitted to water restriction with 2 irrigation's levels (30% and 80% of field capacity of soil - FC). The control treatments were well-watered soybean plants at to 80% FC during all experiment time. The soybean cultivar NS4823-RR (roundup ready; a super-early and undetermined growth habit) was used. In each stage plants were submitted to water restriction for 10 days. The number of pod per plant (NPP), number of grains per plant (NGP), weight of grains per plant (WGP) and weight of 100 grains (W100) were the yield components evaluated. Data were submitted to variance analysis using F-test, averages were compared by Tukey and Dunnett tests (P) and a simple correlation analysis was done. Water restriction didn't affect W100 compared to control, except when water restriction was imposed in R6 stage (11.6 g *versus* 28.3, 26.2, 21.2, 19.5, 19.3 and 19.1 g). When water restriction was imposed in R3, R4, R5 e R6 stages there was reduction in NPP compared to control, which R3 stage showed the lowest NPP (38.3). The NGP from R1 to R6 stages with water restriction was lower than control, which R4 stage was more water restriction sensitive (66). The R1 to R6 stages with water restriction showed lower WGP than control, which R6 stage showed the lowest value (9.6 g). The NGP and NPP presented negative correlation with W100 and positive correlation with WGP. Such characteristics explain the fact of plants in R3 and R4 stages with water restriction compensated the lower NPP and NGP through W100 increased. Water restriction plants in R6 stage didn't present such compensation because lack water happened in time of photoassimilated accumulation in grains, which led yield more light grains. R7 stage was less affected by water restriction, because it's the beginning of physiological development. In that stage, the reduction potential of yield components with water restriction it was lower, since NPP, NGP and W100 were defined in earlier stages. Therefore, R6 stage of cultivar NS4823-RR plants was more water restriction sensitive.



3302 - Agronomy

Marcos Lima Campos do Vale

VARIATIONS ON PHOSPHORUS ADSORPTION CAPACITY AS A FUNCTION OF WATERLOGGING

Vale,MLC; Sousa,RO; Silva,JB; Sehn,CF;

Eliseu Maciel Agronomy College, Pelotas Federal University;

The biological reduction of iron oxides during a waterlogging period, followed by its reoxidation during a drying period, leads to an increasing on the reactivity of the soil iron oxides fraction, and consequently to an increasing on its phosphorus adsorption capacity (Alva et al., 1980). One way to evaluate this phenomenon is the use of adsorption isotherms which describe quantitatively the solute adsorptions to surfaces of solids, under temperature and pressure constant conditions, showing the amount of adsorbate sorbed as a function of an equilibrium concentration (Bohn et al., 1985). Among the most used models for describe the elements adsorption, the Langmuir have been received special attention because it enables to estimate of quantitative and qualitative parameters, which express the soil maximum adsorption of phosphate and a constant related to the adsorption energy, respectively (Sposito, 1989; Soares et al., 2006). In this sense, the aim of this study was to evaluate the changes on phosphorus maximum adsorption capacity as affected by the soil waterlogging period. The experiment was conducted in the greenhouse. The treatments comprised three soil classes, two Albaqualfs and one Argiaquolls, with different phosphorus maximum adsorption capacities - PMAC (high, medium and low), which were conducted dried or waterlogged, in a 2x3 factorial structure. Experimental units were composed by samples of 2 Kg of dried soil, conditioned in plastic vessels. After six months of waterlogging, the vessels were drained. PMAC measurements were performed according to Braga (1980), for all experimental units at two periods: immediately and six months after the drainage. An increasing on PMAC was observed for waterlogged soils immediately after the drainage, compared to PMAC observed for dried soils due to reoxidation process of reduced iron oxides which increase the phosphorus adsorption. Six months after drainage, no PMAC differences were observed between waterlogged and dried soils, for all soil classes.



3372 - Agronomy

Marcos Ventura Faria

INFLUENCE OF EXHAUSTED SUBSTRATE OF PLEUROTUS SP. ON MELOIDOGYNE JAVANICA

Faria,MV; Ferreira,SGM; Dallemole-Giaretta,R; Faria,CMDR; Botelho,RV;

Unicentro;

Nematodes of the genus *Meloidogyne* are responsible for significant losses in productivity of various crops. The control using depleted substrates has been studied as an alternative to chemical control. The objective of this study was to evaluate the effect of substrate depleted of *Pleurotus* sp. the control of *Meloidogyne javanica*. The experiment was conducted in the greenhouse of the Department of Agronomy UNICENTRO. In pots of 1 kg, containing the substrate soil and sand (2:1, v: v), previously sterilized separately was added quantities of 0, 5, 10, 15 or 20 g / kg soil substrate *Pleurotus* spp and drained of an aqueous suspension containing 4000 eggs of *M. javanica*. Fifteen days later each pot was transplanted a change of tomato with 21 days of age. The experiment was conducted in completely randomized design with eight replicates per treatment. No amount of extract depleted of *Pleurotus* sp pre-established in this study reduced the number of nematode galls. For the number of eggs, only the doses of 10 g / kg of soil treatment differed from the control means by Dunnett's test.



3254 - Agronomy

María Rosa Simón

INFLUENCE OF SEPTORIA LEAF BLOTCH ON WHEAT YIELD AND PROTEIN ACCUMULATION UNDER N APPLICATIONS ON GRAINS IN DIFFERENT POSITIONS IN THE SPIKE

Simón,MR; Liaudat,JP; Fleitas,AC; Castro,AC; Schalamuk,SJ;

Facultad de Ciencias Agrarias y Forestales;

Septoria Leaf Blotch (SLB) caused by the ascomycete fungus *Mycosphaerella graminicola* causes reductions in yield and quality in wheat (*Triticum aestivum* L.). SLB is a necrotrophic pathogen that reduces photosynthesis rates by affecting leaf area index and reducing dry matter in the grain which could increase Grain Protein Concentration (GPC). It is known that grain position in the spike may affect not only weight but also GPC and other nutrients. Distal and Basal grains are smaller than medium grains and therefore, they might differ in GPC. On the other hand, Nitrogen (N) fertilization is required for achieving high yields and improving quality in wheat but may enhance the development of SLB, depending on the environment, cultivar and genotype-environment interaction. The aim of this work was to investigate how fungicides and N fertilization affect yield, and GPC in grains from different position within the spike. A field experiment was conducted in a split-split plot design at Estación Experimental Julio Hirschhorn, Facultad de Ciencias Agrarias y Forestales, La Plata, Argentina. Fungicide treatments were the main plot (1-without fungicides; 2- Folicur fungicide (Triazol, 500cm³/ha); 3-Nativo fungicide (Strobilurin + Triazol, 600cm³/ha); N fertilization rates were the subplots (0, 70 and 140 kg N/ha) and cultivars were the sub-sub-plot (Buck Guapo, Klein Escorpion and Baguette 10). Severity caused by the disease, yield and GPC in distal, medium and basal grains were evaluated. Data were analyzed by ANOVA for split-split plot designs. Disease severity was negatively correlated with N rates and fungicide applications. Nativo fungicide containing strobilurins, caused the highest disease control compared with Folicur. Cultivars Buck Guapo and Klein Escorpion showed the highest values of severity. Yield reductions were 23% in treatments without fungicides compared with the controls with fungicides. Number of spikes/m² and grains/spike increases significantly with 70 kg N/ha but major rates caused decreases, whereas yield increased with all N rates. Fungicide applications caused a decrease in GPC due to an increase in yield. Within the spike, grains from distal and basal positions showed the highest levels of GPC comparing with medium grains. No interaction between N rates, grain position within the spike and fungicide applications were evident



3097 - Agronomy

Marines Batalha Moreno

NUTRIENT CONTENT IN LEAVES OF STRAWBERRY PLANTS TREATED WITH UV-C RADIATION DURING STRAWBERRY CROP

Moreno,MB; Crizel,GR; Leite,TB; Cantillano,RFF; Rombaldi,CV;

Universidade Federal de Pelotas;

The use of UV-C radiation in post-harvest has developed excellent results, as the rotting prevention and activation of cellular defense mechanisms. However, few studies have proposed the use of UV-C in fruit and plants pre-harvest and there is not much information on literature about how plants would react when exposed to those stressing agents. Therefore, this study aimed to assess the nutrient content in leaves of strawberry plants treated with ultraviolet (UV-C) during cultivation. Strawberry plants, cv. Aromas were treated as follow: the first treatment (T1) - using UV-C lamps ("Phillips" ® 30W) and incidence of 39 $\mu\text{W}/\text{S}^2$, with applications every three days for 10 minutes at dusk; the second treatment (T2) - plants without applying UV-C. By the time the 24th application was completed, the leaves collection started, being selected only the 4th leaf without petiole of plans for T1 and T2 of both cultivars, the samples were collected randomly in six plants of each treatment. These leaves were dehydrated in the microwave for a period of 15 minutes, the leaves were crushed and the material went to perform the N, P, K, Mg and Ca analysis. Experimental design followed a model entirely randomized, with three biological and two analical repetitions. From the results obtained it was possible to compare the nutrients levels withinthe plant leaves of this study with the levels considered suitable by the literature. It can be seen that there are nutrient deficiency, and other nutrients in excess in the leave, in both T1 and T2 by comparing to literature. The averages among treatments were compared by Tukey test (P 0.5). Potassium levels (T1: 2,24a and T2: 2,06b), calcium (T1: 1,74b and T2: 2,38a) and nitrogen (T1: 2,26a and T2: 2,34a) were the nutrients within the requirements by literature in both treatments, but the levels of potassium and calcium differed between the treatments, and calcium levels were lower in T1 and higher nitrogen for T1. The nutrient phosphorus levels (T1: 0,66a and T2: 0,69a) were considered high, magnesium presented low levels (T1: 0,38a and T2: 0,36a), which does not affect the plant tolerance to diseases and pests, except viruses. Thus, it is concluded that the application of UV-C in pre-harvest might be raising the potassium content and reducing the calcium content in plants of strawberry.



3255 - Agronomy

Marines Batalha Moreno

TOTAL CHLOROPHYLLS CONTENT IN LEAVES OF STRAWBERRY PLANTS TREATED WITH UV-C RADIATION

Moreno,MB; Crizel,GR; Leite,TB; Cantillano,RFF; Rombaldi,CV;

Universidade Federal de Pelotas;

The high consumption of strawberries [*Fragaria x ananassa* Duch] has providing an increase in its cultivation. For this reason, new technologies to increase productivity has emerged in recent years. This technologies are able to improve the quality of the fruits that are very perishable and susceptible to diseases. Among these researches for new technologies, there is the use of stress techniques, such as (UV) ultraviolet light. This light that, upon reaching a vegetable, physiologically active it, inducing this way its defense mechanism and stimulate a greater production of compounds of the secondary metabolism. In order to obtain information about this technology, it's intended to evaluate the total content of chlorophyll in leaves of strawberry that has been treated with UV-C radiation during its cultivation and the others that haven't untreated. The way as the Strawberries, CV. Aromas has been treated is described following: T1 - indicates the application of UV-C lamps (Phillips® 30W) and incidence of 39 μ WS2, with applications every three days for 10 minutes; T2 - indicates the plants without UV-C application. The analysis of the content of chlorophyll were performed every 4 radiation applications. This analysis were measured using a Soil Plant Analysis Development chlorophyll meter (SPAD-502, Minolta, Japan). With this was measuring two leaves per plant in each experimental unit, totaling 96 sheets per treatment. The average level of total chlorophyll for the T1 was 43.16, not different from T2 with a average value equal 43.15. This result suggest the use of moderate doses of UV-C for the strawberries' cultivation, without to affect the photosynthetic capacity of the plants. Therefore, one of the factors from the photosynthetic efficiency of plants and from the growth and adaptability to different environments is the chlorophyll, constantly being synthesized and destroyed (by photo-oxidation) in the light presence. This pigment is essential in the conservation of luminous radiation into chemical energy and, consequently in its growth and adaptability to different policies. This result allows to conclude the use of UV-C radiation in pre harvest does not affect the total chlorophylls and it can be evaluated with higher incidences of radiation if order to use this technique as a good way to induce the plant's resistance during cultivation.



2820 - Agronomy

Masanori Inagaki

EFFECTS OF STONE MULCH ON WATER USE AND GRAIN YIELD IN WHEAT GROWN UNDER SOIL WATER DEFICIT STRESS

Inagaki,MN;

International Center for Agricultural Research in the Dry Areas;

With global warming, the main wheat-producing area of northern Syria may well experience an increasing severity and frequency of drought. The development of water-saving technologies will likely become more important for stabilizing wheat yields. Stone mulching is an empirical strategy that has ancient origins for increasing yield and mitigating drought in dryland agricultural regions worldwide where stony or gravelly soils are fairly common. This study has two aims, (1) to examine the effects of a stone mulch on water use under controlled conditions, and (2) to determine to what extent stone-mulch treatments can increase grain yield in field conditions. Fifty seeds of durum wheat variety 'Cham 1' were planted in each plastic tray containing 9 kg dry weight of the field-soil mix and placed in a greenhouse. After seedling establishment, stone-mulch treatments were imposed consisting of three levels of soil coverage: no stones (control), half-covered and fully-covered with fist-sized stones with three replications. Trays were irrigated periodically to maintain average soil moisture levels within 25-35% (gg^{-1}) from germination to booting stage. Soil moistures were then allowed to fall to 12.5-15% until maturity. Transpiration was estimated as the difference between the water loss by trays with plants (evapotranspiration) and trays without plants (evaporation). Under the stone-mulch treatments, evapotranspiration decreased slightly whereas evaporation from the soil surface decreased strongly. Meanwhile, transpiration increased by 14% and 24% in the half-covered and fully-covered stone mulches, respectively. Seeds of 'Cham 1' were sown in 24 m² field plots and grown under rain-fed conditions in the two cropping seasons 2010 and 2011 in which total water receipts of irrigation and rainfall were 287 mm and 321mm, respectively. Stone-mulch treatments imposed consisted of three different levels of soil coverage with four replications. A comparison of grain yields between stone mulch treatments for the two cropping seasons showed that grain yield was greatly different between seasons but was also significantly increased by stone mulches in both seasons, with average increases of 12 and 24% in the half- and fully-covered treatments, respectively. In conclusion, stone mulches can significantly depress evaporative loss from the soil surface and this saved water is then available to be used by a cereal crop with consequent increases in biomass and grain yield.



3091 - Agronomy

Md. Amzad Hossain

CURCUMIN AND MINERAL CONTENTS OF TURMERIC (*CURCUMA LONGA* L.) AT DIFFERENT GROWTH STAGES IN OKINAWA, JAPAN

Hossain,MA; Akamine,H; Ichiro,N; Tamaki,M;

University of the Ryukyus;

Turmeric (*Curcuma longa* L.), a spice and herbal plant, is generally planted in March-April and harvested from September to January in tropics and subtropics in South-East Asian countries. Four turmeric lines (Ryuduai gold, Aki ukon, Ryuidai-11 and Ryudai-44) were evaluated in 2005-2006, 2006-2007, 2009-2010 and 2010-2011 on dark-red soil (pH 6.0) in Okinawa to determine proper harvest time for high quality yield. Yield, curcumin, mineral, N and C of turmeric were evaluated at 3-5 tiller stage (September), peak shoot and rhizome developing stage (October), shoot drying and rhizome maturing stage (November-December) and dry shoot and mature rhizome stage (January). Turmeric yield was very low until November, and increased by 117% from October to January, 62% from November to January and 13% from December to January. Curcumin, bis-demethoxy curcumin, demethoxy curcumin, mineral and N content of turmeric differed with the growth stages. Curcumin percentage (%) in turmeric-rhizome was 5-20% higher in October-December than in September and January, but total curcumin per plant was higher in December and January than in November or earlier. Potassium (K), Ca, Mg and P were major minerals, and Na, Al, Fe, S, Si and Mn were minor minerals in turmeric. Sodium, K, Ca, Mg and Fe content of turmeric was very high in September, and decreased drastically from October and remained almost constant from November to January. Phosphorous and N content was higher with longer growth period of turmeric. Considering yield, curcumin content (%), total curcumin per plant and mineral content (%), turmeric should be harvested from shoot drying stage (November-December) for higher yield with high curcumin content.



3235 - Agronomy

Murilo Miguel Durli

INFLUENCE OF THE NITROGEN ON THE YIELD AND QUALITY OF THE WHEAT GRAIN

Pereira,T; MANTOVANI,A; DRUM,G; DURLI,MM; MATHIAS,V;

UNOESC;

The objective of this study was to evaluate the influence of doses and timing of nitrogen application on the yield and quality of the wheat grains. The experiment was carried out in the season 2010/11, in Campos Novos, SC, using the BRS 220. The experimental design was in randomized blocks with three repetitions, with the following treatments: T1 - without nitrogen application (N), T2 - 33.75 kg N ha⁻¹ at tillering and 0 kg ha⁻¹ at booting, T3 - 67.5 kg N ha⁻¹ at tillering and 0 kg N ha⁻¹ at booting, T4 - 135 kg N ha⁻¹ at tillering and 0 kg N ha⁻¹ at booting, T5 - 67.5 kg ha⁻¹ N at tillering and 67.5 kg N ha⁻¹ at booting, T6 - 33.75 kg N ha⁻¹ at tillering and 33.75 kg N ha⁻¹ at booting, having the urea as a source of N. After harvesting, the following determinations were performed: hectolitre weight, yield (kg ha⁻¹) and total protein content (%). The results were submitted to the variance analysis and comparison of means by Tukey test (5%). The hectolitre weight ranged from 76.5 (T2) to 77.3 (T3), however no significant difference between treatments was presented. The treatments were characterized as type 2 wheat, according to Annex IV of IN 38, of 11.30.2010, of the Ministry of Agriculture, Supply and Livestock (MAPA). The yield and protein were superior to all treatments with N application, when compared to the T1 (without nitrogen). The T1 has obtained an average yield of 3143 kg ha⁻¹ and total protein content of 11%. T4, T5 and T6 were those with higher productivity and higher levels of total protein (3917, 3962 and 3988 kg ha⁻¹ and 14, 15 and 14% respectively). The low rainfall at the stage of planting to tillering (August-September) may have impaired the absorption of the nitrogen in the initial stage of the crop development, thus compromising the hectolitre weight and productivity, because not all the nitrogen coverage offered in was absorbed by the plant. From the results we can conclude: a) the hectolitre weight did not vary in function of the dose and season of the nitrogen application b) any amount of nitrogen than the zero promoted increases in productivity and protein content of the wheat grains, c) the dose of 33.75 kg N ha⁻¹ at booting + 33.75 kg N ha⁻¹ at tillering (T5) was found to be the highest level of total protein and increased productivity for BRS 220.



3317 - Agronomy

Murilo Miguel Durli

PRODUCTIVITY AND QUALITY OF BEAN GRAINS (PHASEOLUS VULGARIS L.) IN FUNCTION OF DOSE AND TIME OF NITROGEN APPLICATION

Bones,LF; Coelho,CMM; Pereira,T; Durli,MM; Mantovani,A;

UNOESC;

The nitrogen fertilization in beans is a common practice in western Santa Catarina, with the use of high doses of nitrogen, and no work of reference to determine the effect of this practice on productivity. Considering this situation, this study aimed to evaluate the influence of dose and timing of nitrogen application on the yield components and quality of beans (*Phaseolus vulgaris* L.). The experiment was conducted in the city of Campos Novos - SC, in 2011/2012 season, with the use of Perola cultivar, using 14 seeds per meter, 0.45 m spacing between lines and under tillage system. The experimental design was a randomized block with four replications. The treatments were: T1 - 0 kg ha⁻¹, T2 - 45 kg ha⁻¹ in V4, T3 - 45 kg ha⁻¹ in V8, T4 - 45 kg ha⁻¹ in R5, T5 - 90 kg ha⁻¹ in V4, T6 - 90 kg ha⁻¹ in V8 and T7 - 90 kg ha⁻¹ in R5. The yield (kg ha⁻¹), number of pods/plants, number of seeds/pods, number of nodes/plants and total protein content (%) were determined. The results were subjected to analysis of variance by Tukey test at 5% probability. The productivity results showed significant differences among treatments. With the use of 90 kg ha⁻¹ in R5, we obtained a 2245 kg ha⁻¹ production, differing significantly from the 45 kg ha⁻¹ dose in V4 and from the control (0 kg ha⁻¹), with 1828 and 1819 kg ha⁻¹, respectively. Increasing levels of N in common bean increase productivity regardless the stage of implementation. The number of pods per plant was influenced by the application of 90 kg ha⁻¹ in R5, with 15.6 pods per plant, while the number of nodes per plant in V4 was 14.1 nodes compared to control, which obtained 11.3 pods/plant and 11.7 nodes/pod. However, the number of seeds per pod and total protein content did not change as a function of N rates and application times. It is possible to conclude that the nitrogen topdressing fertilization affects the seeds productivity as a function of the change in the number of nodes and pods per plant.



3267 - Agronomy

Nathália Leal de Carvalho

COMPARATIVE OF FUNGICIDES FOR SEED TREATMENT OF WHEAT

Carvalho-Nathalia,NLC; Camera-Juliane,JNC; Ranzi-Camila,CR; Bonini-Cleiton,CLB; Guths-Guilherme,GG;

UNIVERSIDADE DE PASSO FUNDO;

The seed quality is a key factor in agriculture, having a direct impact on production, seed treatment is a good ally in the control of plant diseases. Aiming compare the efficacy of different fungicides, an experiment was conducted at the Laboratory of Plant Pathology/ Mycology at University of Passo Fundo. The treatments were: iprodione dose of 1.5 mL.kg⁻¹, carbendazim 1.5 mL.kg⁻¹, carboxin+thiram dose of 2.5 mL.kg⁻¹, carbendazim +thiram dose of 2 mL.kg⁻¹, triadimenol dose of 2.5 mL.kg⁻¹ of seed, and the control only water was applied. The cultivar BRS 327 were sown in wooden boxes containing soil and vermiculite. For sanity analysis the seeds were placed on BDA culture media and incubated for seven days, after the evaluation proceeded. Were estimated: emergence, rate of seedlings emergence, mean height of plants and their parts (root, shoot, epicotyl), asymptomatic transmission and treatments efficiency was estimated by ABBTT's formula. The experimental design was randomized blocks with seven treatments and four replicates, the data were compared by ANOVA and compared by Tukey test at 5% probability. For the complex of fungi present in the seed the fungicides that stood out were carbendazim + thiram, iprodione, and triadimenol. The rate of emergence is interfered by the treatment. All treatments were effective for reducing asymptomatic transmission. The transmission did not differ between treatments.



3270 - Agronomy

Nathália Leal de Carvalho

PATHOGENICITY OF THREE RACES OF CERCOSPORA SOJINA IN SOY

Camera-Juliane,JNC; Carvalho-Nathalia,NLC; Deuner-Carolina,CCD;

UNIVERSIDADE DE PASSO FUNDO;

The frog-eye leaf spot, caused by the fungus *Cercospora sojina*, causes severe damage in soy. The study was conducted at the Laboratory of Plant Pathology at University of Passo Fundo, aiming to confirm the pathogenicity of three races of *Cercospora sojina* (race 23, 24 and 25) in BRS Bragg and BMX Magna cultivars. A monosporic isolate was made and was inoculated in Petri dishes containing culture media of tomato extract. The dishes remained in a growth chamber at 25 °C for 30 days and 12 hours photoperiod, until obtaining abundant sporulation. From these colonies was prepared a suspension at a concentration of 40×10^3 conidia.mL⁻¹ to inoculate plants with three fully expanded leaves, that were kept in a moist chamber for 48 hours at 25 °C and 12 hours photoperiod. Fifteen days after inoculation proceeded the isolation of 100 discs from last fully expanded trifoliate leaves, being sterilized and placed in petri dishes on V8 media and incubated at 25°C for 25 days and 12 hours photoperiod. End of this time, slides were prepared with pathogen structures and measured 400 conidia. The races of *C. sojina* had elongated, fusiform, multicellular and hyaline shape, and the colonies circular shape and dark color. The length and width of conidia varied from 30 to 110 mm x 7 to 10 mm and the number of septa varied from 1 to 11. Through the measurements and calculation of septa was possible to confirm the pathogenicity of *C. sojina*, through morphological characterization of the fungus.



3269 - Agronomy

Nathália Leal de Carvalho

VIRULENCE OF CERCOSPORA SOJINA ISOLATES IN SOY

Camera-Juliane,JNL; Carvalho-Nathália,NLC; Deuner-Carolina,CCD;

UNIVERSIDADE DE PASSO FUNDO;

The frog-eye leaf spot, caused by *Cercospora sojina*, has caused epidemics in soy, due to its breeding program initiated for resistance to diseases in Brazil. The experiment was conducted at the Plant Pathology Laboratory and growth chamber at UPF. The objective of this study was to determine the virulence of three races of *C. sojina* (race 23, 24 and 25) in two soybean cultivars: Bragg and BMX Magna. The isolates were provided by Embrapa Soja, it was the isolation and peaked Monosporic to petri dishes containing culture medium tomato paste. The Petry dishes remained in a growth chamber at 25°C for 30 days and 12 hours photoperiod, until obtaining abundant sporulation. From these colonies was prepared a suspension at a concentration of 40×10^3 conidia.mL⁻¹ to inoculate plants with three fully expanded leaves. The plants were kept in a moist chamber for 48 hours at 25°C and 12 hours photoperiod. Fifteen days after inoculation the incidence was evaluated, number and diameter of lesions per leaflet of the last fully expanded trifoliate leaves. The symptoms appeared as small spots of red-brown color, which coalescence with time. When inoculated on BMX Magna, races 24 and 25 were more virulent with higher severity, number and diameter of lesions, when compared with the race 23. There was no difference between races on BRS Bragg, it was also observed that the younger leaves are more susceptible to disease.



2861 - Agronomy

Patrícia Coelho de Souza Leão

AGRONOMY ENGINEER

Leão,PCS; Lima,MAC; Silva,SF; Trindade,DCG;

Embrapa Semiárido;

The objective of this study was to evaluate the influence of leaf removal and topping on the yield, biomass and quality of grapes 'Syrah' in the São Francisco Valley. The experiment was established in 2010 in a commercial vineyard of 'Syrah' in Casa Nova-BA (9°16'S; 40° 52'W; 413.5 m), during three production cycles. The treatments consisted of combinations of leaf removal and topping, as follows: control (treatment performed by the winery); leaf removal and no topping; leaf removal and two toppings when berries groat-sized, bunches begin to hang (phase 1) and when berries beginning to touch (phase 2); leaf removal and one topping in phase 2; leaf removal and one topping in phase 1; no leaf removal and two toppings in phases 1 and 2; no leaf removal and one topping in phase 2 and no leaf removal and one topping in phase 1. The experimental design was randomized blocks with four replications and 10 plants per plot. Higher yields in the first two cycles of production, but also a greater number of bunches in the 2nd and 3rd cycles were observed in plants submitted to leaf removal and one topping in phase 1. There was a higher production of fresh mass of branches in the leaf removal and no topping treatment, which showed the best results for production of fresh leaves in the first cycle of production. However in the 2nd and 3rd cycles, there was no influence of leaf removal and topping on the production of fresh mass of branches and higher fresh and dry weight of leaves were obtained in treatments with two toppings or one topping in phase 2. The mean of Ravaz index were 3.0, 3.5, and 2.3, respectively, on the 1st, 2nd and 3rd production cycles. The sugars and organic acids content in the berries were not affected by treatments. The brightness of skin was higher with no leaf removal in three cycles, but did not differ from control in the 2nd and 3rd cycles. Still, with no leaf removal, under the conditions of the 1st cycle, the attribute a^* was more negative, indicating a higher proportion of green pigments, even though the more visible pigments were anthocyanins. However, the response was not maintained and showed more negative values in 2nd cycle, in treatments with leaf removal alone or combined with topping. The highest values of b^* , representing the presence of yellow pigments were observed when one used topping only in phase 2. It is possible that leaf removal in the conditions of the first cycle, had promoted greater degradation of yellow pigments.



2862 - Agronomy

Patrícia Coelho de Souza Leão

EFFECTS OF LEAF REMOVAL AND TOPPING ON YIELD AND QUALITY OF GRAPE 'SYRAH' IN THE SÃO FRANCISCO VALLEY, NORTHEAST BRAZIL.

Leão,PCS; Lima,MAC; Silva,SF; Trindade,DCG;

Embrapa Semiárido;

The objective of this study was to evaluate the influence of leaf removal and topping on the yield, biomass and quality of grapes cultivar Syrah in the São Francisco Valley. The experiment was established in 2010 in a commercial vineyard in Casa Nova-BA (9°16'S; 40° 52'W; 413.5 m), during three production cycles. The treatments consisted of combinations of leaf removal and topping, as follows: control (treatment performed by the winery); leaf removal and no topping; leaf removal and two toppings when berries groat-sized, bunches begin to hang (phase 1) and when berries beginning to touch (phase 2); leaf removal and one topping in phase 2; leaf removal and one topping in phase 1; no leaf removal and two toppings in phases 1 and 2; no leaf removal and one topping in phase 2 and no leaf removal and one topping in phase 1. The experimental design was randomized blocks with four replications and 10 plants per plot. Higher yields in the first two cycles of production, but also a greater number of bunches in the 2nd and 3rd cycles were observed in plants submitted to leaf removal and one topping in phase 1. There was a higher production of fresh mass of branches in the leaf removal and no topping treatment, which showed the best results for production of fresh leaves in the first cycle of production. However in the 2nd and 3rd cycles, there was no influence of leaf removal and topping on the production of fresh mass of branches and higher fresh and dry weight of leaves were obtained in treatments with two toppings or one topping in phase 2. The mean of Ravaz index were 3.0, 3.5, and 2.3, respectively, on the 1st, 2nd and 3rd production cycles. The sugars and organic acids content in the berries were not affected by treatments. The brightness of skin was higher with no leaf removal in three cycles, but did not differ from control in the 2nd and 3rd cycles. Still, with no leaf removal, under the conditions of the 1st cycle, the attribute a^* was more negative, indicating a higher proportion of green pigments, even though the more visible pigments were anthocyanins. However, the response was not maintained and showed more negative values in 2nd cycle, in treatments with leaf removal alone or combined with topping. The highest values of b^* , representing the presence of yellow pigments were observed when one used topping only in phase 2. It is possible that leaf removal in the conditions of the first cycle, had promoted greater degradation of yellow pigments.



2863 - Agronomy

Patrícia Coelho de Souza Leão

IMPROVEMENT OF COLOR OF CRIMSON SEEDLESS GRAPE BY PLANT REGULATORS IN THE SÃO FRANCISCO VALLEY, NORTHEAST BRAZIL.

Leão,PCS; Lima,MAC; Santos,FC; Trindade,DCG;

Embrapa Semiárido;

This study aimed to improve the color of grape cv. Crimson Seedless in the São Francisco Valley, through the application of plant growth regulators. The experiment was conducted during two growing seasons in the years 2010 and 2011 in a commercial vineyard, in Petrolina, PE, Brazil. The treatments were represented by the control, ethephon (1 mL.L^{-1}) and abscisic acid (ABA) applied to a single concentration of 400 mg L^{-1} , in 2010, and two concentrations (400 and 600 mg.L^{-1}) in 2011. In both cases, concentrations were tested in three different ways: a) single application of 15 days before estimated harvesting (DBH); b) in two applications of half of the dose, first one 90 days after pruning (DAP) or during the berry softening and the second at 15 DBH, and c) in a single application at 90 DAP. The variables evaluated were: yield per plant, total number of bunches and color class as the percentage of uniform red berries, where 1 = 0-25%, 2 = 26-60%, 3 = 61-90% and 4 = 91-100%, bunch weight, berry size, skin color, measured by the attributes Luminosity (L), a^* and b^* ; color index for red grapes, pulp firmness, elasticity of skin, soluble solids, sugars soluble content, titratable acidity, total extractable polyphenols, yellow flavonoids, anthocyanins and antioxidant activity. The experimental design was randomized blocks with four replications. There was no influence of ABA and ethephon application on yield, bunch weight and number of bunches. The number of bunches in classes 1 and 4, in 2010, and 1, 3 and 4, in 2011, differed significantly between treatments. In the 2010 season, the number of bunches in class 4 was higher in treatments with two applications of 200 mg L^{-1} of ABA and one application of 400 mg.L^{-1} of ABA at 90 DAP. In 2011 season, the application of ethephon resulted in a higher number of bunches in class 4, but did not differ from other treatments with ABA. The anthocyanins responded positively to ABA treatments in both growing seasons. In 2010, the content was higher at 400 mg.L^{-1} of ABA applied at 15 DAC. In 2011 the better response was observed when it was applied 600 mg.L^{-1} of ABA at 90 DBH, however not differed from treatments with ethephon and two applications of 300 mg.L^{-1} of ABA. Furthermore, ABA increased soluble solids and total extractable polyphenols at 2010 season.



2816 - Agronomy

Rafael da Silva Messias

EFFICIENCY OF FOLIAR APPLICATION OF A NATURAL BIOSTIMULANT IN MAIZE CROP

Messias,RS; Galli,V; Silveira,CAP; Silva,SDA; Rickes,E; Rombaldi,CV;

Embrapa Clima Temperado;

The present study aimed to evaluate the effect of foliar application of formulations based on shale water (SW), the constituent water of shale pyrobituminous rock, on vegetative growth, yield and accumulation of soluble sugar and starch in maize grains. The experiment was carried out in Pelotas, Rio Grande do Sul, Brazil using the maize hybrid (Zea mays) Pioneer 30F53. Block design was randomized with five replicates and five treatments: C (without foliar application); DW-M (Micronutrients diluted in distilled water); SW-M (Micronutrients diluted in SW); SW-1 (SW dose 1); SW-2 (SW dose 2). Formulations were applied twice during the vegetative growth period and once during the reproductive phase with the use of a pressurised sprayer (CO₂). At physiological maturity, cobs and aboveground plants were harvested, dried at 65 °C and weighed in order to evaluate fresh weight (FW) and dry weight (DW) of plants and yield of maize grains. The starch and the total soluble sugar (TSS) content of maize grains were quantified by the method with anthrone (Hodge and Hofreiter, 1962). The foliar spraying of SW-2 resulted in an average of 16.75 tons/ha of FW and 7.48 tons/ha of yield, while control showed an average of 12.90 and 6.39 tons/ha, respectively. This increase of 30% in the FW with a corresponding increase of 12% in DW could be of interest if the crop main goal is the production of silage, either for animal feed or for the production of biofuel. On the other hand, the application of SW-1 did not increase weight and yield, indicating a dose dependent effect. The enrichment of SW with micronutrients (SW-M) also showed yield improvement in relation to control, but had no positive effect on DW or FW. SW-1 and SW-2 treatments accumulated the highest contents of starch; however, only SW-2 treatment showed high starch/TSS ratio, whereas SW-1 treatment showed great amounts of TSS, which could have a negative effect, since these grains may stay more susceptible to insects during storage. Furthermore, it seems that SW contribution in starch accumulation was higher than micronutrient supplementation, since the starch content was equal or even higher on SW-1 treatment, without micronutrients enrichment, than SW-M. This study showed that the foliar application of SW stimulated vegetative growth and yield of maize grains and also increased starch and sugar content in grains, representing an improvement of quality.



2890 - Agronomy

Renick Peries

Subsoil manuring: Innovative approach to addressing subsoil problems targeting higher water use efficiency in Southern Australia

Peries,RR; Singh,JS; Sale,P;

Department of Primary Industries;

Dense and impervious subsoils can be a major impediment to achieving potential water use efficiency (WUE) from cereal and canola crops grown in high rainfall Southern Australia. The placement of large volumes of organic matter within and above the heavy clay layers of the soil in a single deep ripping operation, referred to as subsoil manuring (SM), in over 12 to 36 months led to improvements in soil bulk density (25%) and a corresponding increase in soil macro porosity. This resulted in nearly a 37% increase in plant available water (PAW) capacity that contributed to yield increases of between 27% and 96% across different soil types and rainfall regimes. The temporal change in soil physical properties with SM, of the otherwise hostile subsoil, led to capture and storage of summer rainfall (with a near doubling of the summer fallow efficiency) and made it available to crops during grain filling in the following spring when below average rainfall conditions existed. A participatory action research (PAR) approach is being used in the validation of the technology across a range of soil types and seasons with an economic analysis conducted in parallel. The development and use of the first commercial SM machine in the region is seen as a great success story in the adoption of a technology that has the potential to double the crop yield in the region and revolutionise the farming system. The research, development and extension continuum in the adoption of this technology within the 'best practice' guidelines of the grains industry are highlighted.



3179 - Agronomy

Reza Deihimfard

**DEPARTMENT OF AGROECOLOGICAL, ENVIRONMENTAL SCIENCES RESEARCH
INSTITUTE, SHAHID BEHESHTI UNIVERSITY**

Deihimfard, REZA; Nassiri, MEHDI; Koocheki, ALIREZA;

Shahid Beheshti University;

To evaluate the scope for enhancing productivity of sugarbeet (*Beta vulgaris* L.), a modified version of SUCROS (SUCROSBEET) model was calibrated and validated for the diverse sugarbeet-growing environments of Khorasan province in the northeast of Iran. The validated model was used to estimate potential, water and nitrogen-limited yields and yield gaps of sugarbeet for 6 locations across the province. Some Questionnaires were then sent to the location extension agents to obtain information on the main sugarbeet producing fields in each district. The model well simulated yield of sugarbeet under all production situations (with RMSE of 9.03 Mg ha⁻¹). Simulation results of the SUCROSBEET model showed that the lowest and highest potential yield were obtained in Sabzevar (100 Mg ha⁻¹) and Neishaboor (137 Mg ha⁻¹), respectively. Despite the fact that most farms had been irrigated up to 20 times over seasons, there were still yield gaps of an average 42 Mg ha⁻¹ due to water shortage. To reach the potential yield in the studied areas, more than 2000 mm water as irrigation are required in Sabzevar and TorbatJam and 1400 to 1500 mm in Ghoochan and Neishaboor, respectively. On average, to fill nitrogen-limited yield gap, 440 to 530 kg ha⁻¹ of nitrogen for sugarbeet uptake are also needed. However, the farmers in various locations have been able to apply only 50% of the sugarbeet nitrogen demands during the past decade. This yield gap in sugarbeet, which reflects the actual yield gap in the irrigated environment, is essentially due to non-adoption of improved crop management practices and could be reduced if proper interventions are made.



3282 - Agronomy
Saeid Soufizadeh

Maize (*Zea mays* L.) performance under competition with C4 weed species

Soufizadeh, Saeid; AghaAlikhani, Majid; Bannayan, Mohammad; Zand, Eskandar;
Hoogenboom, Gerrit; M. Manschadi, Ahmad;

Department of Agroecology, Environmental Sciences Research Institute,
Shahid Beheshti University, Tehran, Iran;

Determination of the best amount of nitrogen (N) fertilizer application in maize that results in high grain yield under weed competition is of great importance. In order to study the effect of weed competition on maize performance and identifying whether or not N application rate affects by weed species, an experiment was conducted in 2008 at the Research Field of Tarbiat Modares University. The experiment was established as a randomized complete block design with factorial arrangement of treatments and three replications. First factor was N fertilizer at the three following rates: 138, 184 and 230 kg N ha⁻¹. Second factor consisted of two weed species; i.e. redroot pigweed (*Amaranthus retroflexus* L.) and proso-millet (*Panicum miliaceum* L.). Third factor was planting each weed species at low and high densities. Yield and yield components of maize was assessed at final harvest. Results indicated that weed competition significantly reduced maize grain yield compared to 230 kg N ha⁻¹ control treatment. The highest grain yield (1077 g m⁻²) was achieved in treatment 230 kg N ha⁻¹ while the lowest yields belonged to high densities of redroot pigweed and proso-millet fertilized with 184 and 230 kg N ha⁻¹, respectively (643 and 565 g m⁻²). Increasing millet density resulted in significant loss of maize grain yield only. Maize grain yields in competition with low densities of proso-millet and pigweed were 800 and 795 g m⁻², respectively which reduced to 693 g m⁻² when weed densities increased. Difference in N application rate did not cause significant differences in yield components of maize under weed competition. However, high densities of proso-millet and redroot pigweed resulted in significant reductions of the number of rows per ear and the number of grains per row, respectively. Overall, results indicated that in fields where a nitrophile species is the dominant weed species, increasing N application rate beyond the optimum rate not only does not increase maize grain yield but also reduces its yield and causes pollution of environment.



3165 - Agronomy

Satori NAKAMURA

MORPHOLOGICAL CHANGES IN ROOTS OF PISUM SATIVUM L. INOCULATED WITH PREINCUBATED RHIZOBIA WITH NARINGENIN

Satori-Nakamura,SN; Atsushi-Matsumura,AM; Hiroyuki-Daimon,HD;

Graduate School of Life and Environmental Sciences, Osaka Prefecture University;

Root nodule formation followed by N₂-fixation in a legume-rhizobia symbiosis is often inhibited by various environmental factors. In field pea (*Pisum sativum*) grown in temperate region of western Japan, low temperature under late seeding condition should be considered as a limiting factor for early growth. Of inhibition mechanisms, decreasing flavonoid compounds released from legume roots for nod gene activation might be of importance. A preincubation of rhizobia with flavonoid (priming) has previously been reported in some legumes, but the effect on nodulation varied with plant species. This work is focused on whether preincubation of rhizobia with naringenin affects nodulation and root development of *P. sativum*. Seeds of pea cv. Usui, leading variety in Japan, were surface sterilized and sown in a plant box containing 0.8% agar medium. Six-day-old seedlings were transplanted into a plastic box containing Broughton & Dilworth liquid medium supplemented with KNO₃ at 10 mg N/L, and incubated in a growth chamber (22°C, 14 h light). Seedlings were inoculated with *Rhizobium leguminosarum* bv. *viciae*. For preparation of *R. leguminosarum* primed with naringenin, 10 ml of a bacterial suspension from 3-day-old subculture were aseptically added to 50 ml of sterile 10 mg/L naringenin solutions and incubated at 30°C for 48 h without shaking. The suspensions were filtered with 0.45 µm pore size paper, centrifuged, and then used as inoculants. Root nodules were found at 7 days after inoculation (dai) in both priming treatment (PT) and the control. At 14 dai, nodule numbers in PT were higher than those in the control. However, acetylene-reducing activity (ARA) and fresh weights of root nodules per plant were not significantly different between PT and the control. At 28 dai, nodule numbers, fresh weight and ARA per plant in PT were higher than those in the control. On the other hand, ARA per a root nodule was lower than that in the control. Plants inoculated with primed rhizobia showed alternative root structure such as loss of the second order lateral roots and the continuous nodule formation along the root axis. These results suggest that priming treatment of rhizobia with naringenin before inoculation might induce earlier formation of root nodules due to inhibiting lateral root differentiation, indicating that root system development of pea plants occurs with a trade-off between the nodulation and lateral branching under unsuitable environmental conditions.



3407 - Agronomy

Seyed MohammadReza

EVALUATION OF DROUGHT TOLERANCE INDICES AND THEIR RELATIONSHIP WITH GRAIN YIELD OF WHEAT GENOTYPES

Ehteshami, SEYEDMOHAMMADREZA; Ebrahimzadeh, MOHAMMADREZA;

The University of Guilan;

Abstract Drought stress is one of the most important problems for crop production in arid and semiarid areas. Breeding and release of high yielding and drought tolerant varieties along with advance agronomic practices is effective way to manage drought and water deficit in agriculture. In order to this study, an experiment was designed in the form of split plot within randomize complete block with three replication. SSI (Stress Susceptibility Index), (MP) Mean Productivity), TOL (Tolerance), GMP (Geometric Mean Productivity) and STI (Stress Tolerance Index) indices were used to evaluate susceptibility and tolerance of the genotypes. The results of this study showed Genotypes number 5 and 19 had higher grain yield in non-water and water stress condition. According to STI, GMP and MP, genotype number 5(Alvd //Aldan/las*2/3/ Gaspard-1) and (BABAX/LR22//BABAX) had the highest water stress tolerant and yield in studied conditions. Also, results of correlation of drought tolerant indices showed STI, GMP, and MP as the best indices for yield predicting. KEY WORDS: Wheat, Drought, Drought tolerance, index.



3087 - Agronomy

TAIANE PETTENON BANDEIRA

AGRONOMIC TRAITS OF THE HYBRID CANOLA HYOLA 61 UNDER DIFFERENT PLANT ARRANGEMENTS

Bandeira,TP; Chavarria,G;

Universidade de Passo Fundo;

Canola *Brassica napus* (L.) is a plant specie of great interest to producers and researchers. It can be used in grain production systems during the cold season. Due to canola grains high oil content it is used for biodiesel production. It is also used for human food, as one of the most healthy oils. The main canola crop problems are uneven maturation and natural pods dehiscence, resulting in heavy crop losses. One way to minimize losses, is to use an appropriate plant arrangement when the crop is seeded. Thus, the objective of this study was to evaluate the expression of canola agronomic traits, and their effects on final yield, assigning different plant arrangements. The field experiment was carried out at the experimental field of Faculty of Agronomy and Veterinary Medicine, University of Passo Fundo, Passo Fundo-RS, during the 2011 growing season. The experimental design was a randomized blocks with split plots using in the plots row spacing (17, 34, 51 and 68 cm) and in the subplots plant densities (15, 30, 45 and 60 plants/m²) with four replications. The assessed traits were: the number of primary branches (NPB), secondary (NSB), tertiary (NTB) and quaternary (NQB), the number of pods on primary (NSPB1), secondary (NSB), tertiary (NST) and quaternary (NSF), the number of pods per plant (NSP), the number of grains per plant (NGP) and the final yield (kg/ha). Data were subjected to analysis of variance and the when significant to regression model. The variables number of pods in the secondary branch ($p = 0.0004$), number of pods in the tertiary ($p = 0.000$), number of secondary branches ($p = 0.000$), number of tertiary branches ($p = 0.000$), number of pods per plant ($p = 0.000$), and number of grains per plant ($p = 0.000$) showed significant difference in the density trait and yield ($p = 0.0025$) for row spacings. The linear regression model was predominant negative for the analysed traits. Significant traits regarding plant density were for 15 plants/m², and row spacing factor. Thest yield was obtained with 17cm row spacing and 45 plants/m² density.



3086 - Agronomy

TAIANE PETTENON BANDEIRA

EFFECT OF CANOLA SPATIAL PLANT ARRANGEMENTS ON THE LEAF AREA INDEX AND PRODUCTIVITY

Bandeira,TP; Chavarria,G;

Universidade de Passo Fundo;

Appropriate plant spatial arrangement in canola is extremely important because it can be a way of management for better light, water and nutrient utilization, and crop yield increase. The objective of this study was to appraise, in a non-destructive method, the leaf area index (LAI) of canola hybrid Hyola 61, under different plant arrangements (line spacing and seeding rates) relating them to yield. The experiment was conducted in the experimental field of the Faculty of Agronomy and Veterinary Medicine, University of Passo Fundo, Passo Fundo-RS. The experimental design was a randomized blocks with split plots, distributing in the subplot row spacings (17, 34, 51 and 68 cm) and in the plots plant densities (15, 30, 45 and 60 plants/m²). The work was repeated in two consecutive growing season (2010 and 2011), based on samples randomly collected from four plants in each subplot and estimating the LAI, starting at plant flowering. The analyzed traits were total leaf area (TLA)/cm², leaf area unit (LAU/cm²), number of leaves per plant (NLP), leaf area index (LAI) and yield (kg/ha). Variables TLA and LAU and yield were significantly influenced by variations in the row spacing, in 2010. In 2011, only the trait NLP and yield were significantly influenced by the different spacing. There were differences in plant density variations, TLA, NLP and in LAI, and LAI for the two years of evaluation. The most appropriate adjustment to achieve high LAI was 17 cm row sapacing with 60 plants/m² density. The highest yield was obtained when canola plants were grown in 17cm row spacing.



3237 - Agronomy

Tiago Teixeira

MORPHI-AGRONOMIC CHARACTERIZATION OF SYNTHETIC WHEATS ACCESSIONS (TRITICUM DURUM X AEGILOPS TAUSCHII)

Teixeira,T; Toniazzo,C; Brammer,SP; Cargnin,A;

Embrapa- Trigo;

The synthetic wheat is a cross between a tetraploid species *Triticum durum* and another diploid *Aegilops tauschi*, and the hybrids have the artificial resynthesis of hexaploid genome from the duplication of chromosomes with colchicine. This germplasm may be a source of agronomically important genes to the genetic improvement of wheat such as resistance to pests and diseases. For this it is necessary to investigate a genetic uniformity and select genotypes that are similar to wheat grown for later use in genetic improvement. The objective of this work was to evaluate synthetic wheats accessions as the morpho-agronomic characters that resembled the wheat cultivars. Were analyzed one hundred accessions in the experimental field of Embrapa Trigo (Passo Fundo, RS) in 2011, from the International Center for Maize and Wheat Improvement (CIMMYT). The accesses are kept, multiplied and evaluated by the Active Germplasm Bank of Embrapa Wheat. The agronomic characteristics evaluated were: vegetative habit, waxy sheath, stem and spike, both transformed into a scale of 1 to 5 days, emergence to silking cycle, emergence to flowering cycle, both measured in number of days and grain yield in grams. The experiment was conducted in the design of Families with intercalated checks, where de access were considered the families (one repetition) and the checks the commercial cultivars of *T. aestivum*, Wheat BR 23, Trigo BR 18-Terena, IAS 54, Jacui (with 6 repetitions). Each plot was comprised of a single line of 1m in length. The information was subjected to analysis of variance and selection index of Pesek & Baker (1969). The analysis of variance showed that there is significant variation among accessions for all morphological characteristics, indicating that there are genotypes with potential for inclusion in breeding programs. Selection index allowed selecting the top ten accessions with the greatest potential for breeding programs: CASS02B00006S, CASS02B00011S, CASW00GH00067S, CIGM.93.302, CIGM.93.403, CIGM88.1239-3B, CIGM92.1666, CIGM92.1696, CIGM92.1698 and CIGM93.225. These genotypes have potential for genetic gain of up to 126.13% on average for production gain. Of these, access CIGM92.1696 presented the best genetic gain index. The selected accessions may be included in breeding programs aimed at genetic resistance to biotic and abiotic stresses in new wheat cultivars.



3172 - Agronomy

weijian zhang

GROWTH RESPONSE OF WINTER WHEAT (TRITICUM AESTIVUM L.) TO WARMING WITH DIFFERENT DIURNAL TEMPERATURE RANGES UNDER FIELD CONDITIONS IN EAST CHINA

Zhang,WJ;

Chinese Academy of Agricultural Sciences;

A better understanding of actual crop responses to warming under different diurnal temperature ranges (DTR) will benefit assessment of the impact of climate change impacts on food production. A three-year experiment with a Free Air Temperature Increase (FATI) facility was conducted to investigate winter wheat response to warming with different DTR (AW: all-day warming; DW: daytime warming; NW: nighttime warming) at Nanjing, China. An increase in temperature by 1.5°C significantly shortened the length of the pre-anthesis phase by 12.7, 8.3 and 10.7 d in the AW, DW and NW plots, respectively, whereas the length of the post-anthesis phase was prolonged by about 2.0 d. Warming enhanced the above-ground biomass slightly and increased grain yield significantly by 17.0, 21.3 and 22.9% in the AW, DW and NW plots, respectively. Nitrogen concentrations increased in the vegetative tissues but were decreased in the grain with warming. Warming tended to decrease the leaf photosynthesis rate, but significantly increased the green leaf area, seed setting rate and harvest index. No significant impacts of DTR changes on winter wheat growth were found. Our results demonstrate that anticipated warming in East China may enhance winter wheat productivity but will decrease grain quality.



3318 - Agronomy

Ximena Carolina Lizana Campos

EXPANSINS EXPRESSION IN WHEAT GRAINS AFFECTED BY HIGH TEMPERATURE

Lizana,XC; Calderini,DF;

Universidad Austral de Chile;

The length of the grains is the dimension earlier defined during grain development. This trait has been found closely associated with grain weight and similar to expansins expression (cell wall proteins responsible for the elongation of the tissues). There is no information about how the expression of these genes is affected by environmental stresses such as high temperature. The aim of this study was to evaluate the effect of different temperatures on the expression of expansins (TaExpA 6, 4 and 8), in two wheat varieties contrasting in grain weight and temperature sensitivity. A field experiment was conducted at the Experimental Station of the Universidad Austral de Chile (39° 38' S) evaluating the response of 2 wheat varieties (Pandora INIA and Huayun INIA) to 3 thermal regimes: control (T0 at environment temperature) and two treatments (T1 and T2) over the control. Heating treatments were assessed at 3 phenophases: Boot-anthesis, beginning (3 to 15 days dda, BGF) and middle (20 to 32 DAA, MGF) of grain filling. The weight of carpels of flowers was measured at anthesis. During the grain filling, fresh and dry weight of grains and grain dimensions (length, wide and height) were measured. The endosperm cell number was counted 20 DAA. Grain weigh (position 2 in the spikelet) of Pandora (66 mg) was higher than Huayún (55 mg). Final grain weight was significantly associated with carpels weight in both varieties ($r^2 = 0.51$, P)



2827 - Agronomy

Yasuhiro Tsujimoto

CAN AFRICAN SOILS SUPPLY A CRITICAL NEED OF SILICA FOR SUSTAINABLY INCREASING RICE YIELDS?

Tsujimoto,YT; Muranaka,SM; Saito,KS; Asai,HS;

Japan International Research Center for Agricultural Sciences;

Rice is a specific silica-accumulator, by which rice plants enhance resistance against biotic and abiotic stresses. Booming demand of rice in sub-saharan Africa (SSA) requires rapid increases in rice production, and hence more Si supply from soils, irrigation water, or external inputs. Since many parts of the SSA soils are highly weathered and desilicated, there is expected risk that soil Si cannot support enough demand of rice production increasing in the SSA. However, Si has received far less study than the other major nutrients. This study evaluated current Si nutrient status of rice plants in relation to Si-supplying capacity of soils under different fertilizer and irrigation management practices in the region. Plant and soil samples were collected at maturity from 113 rice fields in Benin, Ghana, Guinea, Kenya, Madagascar, Mozambique, and Nigeria, the major rice-growing countries of the SSA. The sample fields consisted of 29 % irrigated, 61 % rainfed, and 9 % upland conditions. Mineral fertilizer was used at 60% of the fields in a range of 10-191 kg N ha⁻¹ with various but non-Si-containing forms. The grain yields were between 0.7 and 9.9 t ha⁻¹ with average values of 2.8 t ha⁻¹ and 3.7 t ha⁻¹ for the non-fertilized and fertilized fields, respectively. Si concentration of straw ranged 1.9-7.5 %, of which 81 % was below the critical deficiency level at 5% (Dobermann and Fairhurst 2000). Amounts of water-soluble Si after anaerobic incubation of soils at 40 °C for 1 week were highly correlated with the straw Si concentration by fitting Mitscherlich relationship ($r^2=0.64$) among fields with no fertilizer or no drought stress irrespective of the countries. Deficient water supply under rainfed and upland conditions significantly lowered the straw Si concentration. Although the effect of fertilizer input was not statistically significant, straw Si concentration was lower than the above correlation curve where receiving more than 100 kg N ha⁻¹. The result revealed that low Si concentration of rice plants was widespread due to the limited supplying capacity of soils in the SSA. In improving rice production in the region, further studies should include Si management, particularly in cases of high-yielding practice with mineral fertilizer inputs, and where supply of Si is not expected from irrigation water. The extraction method used in this study can be a useful index to assess Si-supplying capacity of soils for wide range of agro-environments in the SSA.



3090 - Agronomy

Yoshihiro Hirooka

Evaluation of the effects of cultivars and nutritional environments on dynamics of leaf area index of rice by using plant canopy analyzer

Hirooka,Y; Homma,K; Shiraiwa,T; Kuwada,M;

Graduate School of Agriculture, Kyoto University;

Leaf area index (LAI) is an important indicator for understanding many aspects of crop development, growth and management. The nondestructive measurements by plant canopy analyzer are expected to evaluate the LAI dynamics. This study aimed to establish the evaluation method for LAI dynamics in rice by using plant canopy analyzer, LI-COR LAI-2000, and analyzed the effects of cultivars and nutritional environments on the dynamics. Field experiments were conducted in Kyoto in 2010 and 2011 under five nutritional environments (Standard fertilizer, Low fertilizer, 1-year non-fertilized, 8-year non-fertilized and 51-year non-fertilized). We used six diverse rice cultivars (Nipponbare, Beniasahi, Kasalath, Bei Khe, Takanari and B6144F-MR-6-0-0), which included indica and japonica, or improved and traditional. LAI and DIFN (Diffuse non-interceptance) of each cultivar in each environment were measured by LAI-2000 once or twice a week (LAI-2000 measurements). LAI was also measured destructively at three weeks interval (destructively measurements). Several growth curves were applied on LAI-2000 measurements (LAI and DIFN) to obtain the parameters such as relative growth rate, maximum growth rate, maximum LAI, and so on. The effects of cultivars and environments on the parameters were tested by using analysis of variance. The growth curves were well corresponded with the LAI-2000 measurements, suggesting that the obtained parameters substantially shows the features in LAI dynamics. The parameters were significantly different among cultivars and environments. Some of the parameters for which interaction of cultivars and environments was not significant are thought to be suitable for genotypic evaluation. These results suggest that the method which parameterizes LAI dynamics with plant canopy analyzer numerically show the characteristic of the cultivars and the environments. Thus, it is thought that the method is quite useful to improve simulation models to predict growth and yield of rice. We are now analyzing the parameters in relation to plant nutritional conditions.



3134 - Agronomy

Zhang Zhengbin

WHEAT EVOLUTION UNDER CLIMATE CHANGE WARMING

Zhang,ZHENGBIN;

Center for agriculture resource research, Institute of genetics and development biology, Chinese Academy Sciences;

Wheat originated about before 10000 years in southwest of Asia, wheat evolution first affected by climate change and secondly controlled by human. There are many evidences show that global average temperature rose about 1.5, and CO₂ content of air rose about 40% in recent 200 years. Meanwhile, in China, average temperature rose about 0.48, 0.5 in recent 100 years, climate change warming markedly in the north of China, especially in the winter season, that resulted in winter wheat plant area was enlarged in China, winter wheat plant areas were moved to the north and replaced lots of spring wheat in some cold areas. Meanwhile, there are many problems were showed out in wheat production and breeding, many modern winter wheat varieties has some spring wheat traits and without good cold resistances, so they grow quickly before winter and in spring season and easily get cold stress in winter and spring season. So the aim and direction of wheat breeding should be adjusted for suiting to climate change warming in China. The agronomic and physiological traits of 30-60 kinds of wheat evolution materials were investigated in Yangling of Shaangxi province and Shijiazhuang of Hebei province in 1996, 1997 and 2011 by us, the results show that as follow, the mature day changed early as wheat evolution from diploid (AA, BB) & rarr; tetraploid (AABB) & rarr; hexaploid (AABBDD)& rarr; landraces& rarr; modern cultivars, and most of modern wheat varieties matured early 15-22 days than that of many kinds ancient wheat species in Chain. Compared with ancient species, the modern cultivars have big leaves and ear, more and large seed, high harvest index and high yield, but short plant height. There are many physiology traits changed in wheat evolution, the size of leaf stomata increased, but stomata frequency decreased, that resulted in transpiring rate and photosynthetic rate was decreased, but the leaf water use efficiency increased, because the transpiring rate decreased more than photosynthetic rated. Some genes evolution related with climate change will be studied in future. Key Words: wheat; evolution; climate change; warming

* This work was supported by National Basic Research Program of China (2010CB951501)**Correspond author: zzb@sjziam.ac.cn



Poster Session

**Biomedical, Health-Beneficial and
Nutritionally Enhanced Plants**



3390 - Biomedical, Health-Beneficial and Nutritionally Enhanced Plants

Ana Paula Ferrari

COMPARATIVE STUDY OF PETIVERIA ALLIACEA L. AND PHYLLANTHUS NIRURI L. IN RELATION TO THEIR ANTIOXIDANT POTENTIAL

Ferrari,AP; Silva,MGF; Bosse,MA; Haminiuk,CWI; Marchese,JA; Cabral,ISR; Carpesa,ST;

Department of Chemical, Federal University of Technology - Paraná (UTFPR), Pato Branco/PR, Brazil.;

In search of alternative sources of natural antioxidants, this study aimed to analyze the antioxidant activity of *Petiveria alliacea* L. and *Phyllanthus niruri* L., popularly known as guiné and quebra-pedra, respectively, using the methods of scavenging free radicals •DPPH (2,2-diphenyl-1-picrihidrazil) and ABTS. The antioxidant activity of ethanolic and dichloromethane extracts of plants were compared to that of commercial antioxidant BHT (butylated hydroxy toluene), BHA (butylated hydroxy-anisole) and α -tocopherol. The values obtained for the sequestering of free radical DPPH•, with IC₅₀ were 21.881 mg/mL and 2.524 mg/mL for the ethanol extracts of *P. alliacea* and *P. niruri*, respectively. To the extract with dichloromethane, the results were 17.011 mg/ml and 17, 868 mg/ml for *P. alliacea* and *P. niruri*, respectively. For BHT, BHA and α -tocopherol, the values were of 0.115 mg/mL, 0.072 mg/mL and 0.061 mg/mL, respectively, using ethanol as solvent. To analyze ABTS, the results found were 42.902 and 219.382 μ mol of trolox/g of sample in ethanol extracts of *P. alliacea* and *P. niruri*, respectively. As for the dichloromethane extracts, the same plants gave values of 33.710 and 155.04 μ mol of trolox/g sample, respectively. The synthetic antioxidant BHT, BHA and α -tocopherol had concentrations of 4262.0, 4816.7 and 5270.0 μ mol of trolox/g of sample, respectively. Thus, the sequestration of free-radical antioxidants used in the food industry was higher than the extracts tested. However, these species are not discarded as to its possible use as natural antioxidants.



3392 - Biomedical, Health-Beneficial and Nutritionally Enhanced Plants

Ana Paula Ferrari

COMPARATIVE STUDY OF THE ANTIOXIDANT POTENTIAL OF TWO WEEDS

Ferrari,AP; Silva,MGF; Bosse,MA; Haminiuk,CWI; Marchese,JA; Cabral,ISR; Carpes,ST;

Department of Chemical, Federal University of Technology - Paraná (UTFPR), Pato Branco/PR, Brazil;

The picão-preto (*Bidens pilosa* L.) and fedegoso (*Senna occidentalis* L.) besides being considered weeds, are widely used in popular culture in the treatment of various diseases such as malaria. Thus, taking advantage of the popularity of these plants and their ease of propagation, we sought through this study, other uses for this plant. Thus, this study aimed to analyze the antioxidant activity of the same, using the method of sequestering free radical DPPH• (2,2-diphenyl-1-picrihidrazil) with ethanol and dichloromethane extracts, and antioxidant activity *B*-carotene/linoleic acid system from ethanol extract. We found significant activities of sequestering for the free radical DPPH•, with IC₅₀ (concentration of antioxidant needed to reduce by 50% the initial concentration of DPPH•) of 2.916 mg/mL for ethanol extract and 20.581 mg/mL for the extract in dichloromethane to *B. pilosa*, demonstrating that the extraction with ethanol showed higher antioxidant activity. To *S. occidentalis* analysis showed the same result of 6.814 mg/mL for the ethanolic extract, and 16.682 mg/mL in dichloromethane extract, showing again that the extraction in ethanol showed best results. To analyze by the system *B*-carotene/linoleic acid noted that the ethanol extract of *B. pilosa* showed greater activity than the ethanolic extract of *S. occidentalis*, which agrees with the results obtained by analysis of scavenger DPPH•, which are of 95.696% and 94.384% respectively. The results obtained in this study, we observed that *Bidens pilosa* had a higher antioxidant than *Senna occidentalis* for the ethanol extracts, which may be an alternative source of compounds with antioxidant effects.



3394 - Biomedical, Health-Beneficial and Nutritionally Enhanced Plants

Ana Paula Ferrari

COMPARATIVE STUDY OF THREE METHODS IN RELATION TO THEIR ANTIOXIDANT POTENTIAL OF QUASSIA AMARA L.

Ferrari,AP; Silva,MGF; Bosse,MA; Haminiuk,CWI; Marchese,JA; Cabral,ISR; Carpes,ST;

Department of Chemical, Federal University of Technology - Paraná (UTFPR), Pato Branco/PR, Brazil;

The pau-amargo (*Quassia amara* L.) is considered a good source of compounds with antioxidant activity. This study aimed to determine the antioxidant activity of ethanolic and dichloromethane extracts through three methods for sequestering free radicals. Assessment of antioxidant activity was evaluated by sequestration of free radical DPPH• and ABTS, and the system *B*-caroteno/linoleic acid. The antioxidant activity of extracts was compared to commercial antioxidant BHT, BHA and *B*-tocopherol. We found high activities of sequestering for the free radical DPPH•, with IC₅₀ (concentration of antioxidant needed to reduce by 50% the initial concentration of DPPH•) of 0.088 mg/mL for ethanol extract and 9.728 mg/mL for the extract with dichloromethane. For BHT, BHA and *B*-tocopherol, the values were 0.115 mg/mL, 0.072 mg/mL and 0.061 mg/mL, respectively, analyzed using ethanol as solvent. As for the sequestering of free radical ABTS, the ethanol extract showed 618.913 µmol of trolox/g sample, and 38.612 µmol of trolox/g sample in the extract with dichloromethane. For the synthetic antioxidant BHT, BHA and *B*-tocopherol, the results were 4262.0, 4816.7 and 5270.0 µmol of trolox/g sample, respectively. For the analysis of antioxidant activity by *B*-caroten/linoleic acid system, the result obtained with the ethanol extract was 96.654% of antioxidant activity, being 63.21, 68.18 and 70.46% of antioxidant activity for synthetic antioxidants. The activities of the antioxidants used in food industry were higher than with extracts. However, one can observe that it presents a high activity in the sequestering of free radicals, behaving as an excellent natural antioxidant.



3383 - Biomedical, Health-Beneficial and Nutritionally Enhanced Plants

Juliana de Souza Dode

**Herbs and spices, *Rosmarinus officinalis*, *Pimpinella anisum* L.,
Origanum vulgare and *Artemisia dracunculus* L. with potentially health-beneficial
phenolic content**

Dode, J; Chim, JF; Gandra, EA; Zambiasi, RC; Jacques, AC; Chaves, FC;

UFPEl;

Herbs and spices are aromatic ingredients that potentiate food flavor. In addition to their organoleptic role, these plants possess great health beneficial potential. Volatile and non-volatile compounds identified in herbs and spices have proved to be strong antioxidants. Commonly used food condiments, *Rosmarinus officinalis*, *Pimpinella anisum* L., *Origanum vulgare* and *Artemisia dracunculus* L. were evaluated for their total phenolic composition using the Folin-Ciocalteu method and results were expressed in gallic acid equivalents (mg GAE 100 g⁻¹ fresh weight, fw). *O. vulgare* had the highest phenolic content with 2279.4 mg GAE 100 g⁻¹ fw, followed by *R. officinalis* 1337.6 mg GAE 100 g⁻¹ fw, *A. dracunculus* 554.8 mg GAE 100 g⁻¹ fw, and *P. anisum* 164.3 mg GAE 100 g⁻¹ fw. This data supports the antioxidant potential suggested for these herbs and spices, of which worth mentioning carvacrol in *O. vulgare*, and carnosol, rosmanol, rosmaridiphenol and rosmariquinone in *R. officinalis*.



2818 - Biomedical, Health-Beneficial and Nutritionally Enhanced Plants

Rafael da Silva Messias

BIOFORTIFICATION OF MAIZE GRAINS WITH FOLIAR APPLICATION OF A NATURAL BIOSTIMULANT

Messias,RS; Galli,V; Ávila,LO; Silva,SDA; Schirmer,MA; Rombaldi,CV;

Embrapa Clima Temperado;

The objective of this study was to evaluate the effect of the application of shale water (SW), the constituent water of shale pyrobituminous rock, on the antioxidant activity and accumulation of carotenoids and phenolic compounds in maize grains. Experiments were performed using maize hybrid (*Zea mays*) Pioneer 30F53 grown on field at Pelotas, Rio Grande do Sul, Brazil. Block design was randomized with five replicates and three treatments: C (without foliar application); SW-1 (SW dose 1); SW-2 (SW dose 2). Formulations were applied twice during the vegetative growth period and once during the reproductive phase with the use of a pressurised sprayer (CO₂). Cobs were collected to evaluate secondary metabolism. Antioxidant activity was quantified by the methods from Brand-Williams et al (1995) and Arnao et al (2001); phenolic compounds by the method from Adom and Liu (2002), and total carotenoids content by the method adapted from Rodriguez-Amaya and Kimura (2004). The expression of genes coding to enzymes from carotenoid pathway, such as phytoene synthase (*psy1*), carotenoid ϵ -hydroxylase (*cyp97c*) and *B*-carotene hydroxylase (*hyd3*), was verified by RT-qPCR. The foliar application of SW increased the levels of total phenolic compounds in maize grains, compared to the other treatments, due to the increase in bound phenolic content. This result was observed when both doses of SW was applied, indicating no dose dependent effect. However, total antioxidant activity was significantly higher in grains from the SW-2 treatment, due to the higher activity of liposoluble fraction, probably related to the increase in total carotenoids also observed in this treatment. This increase in carotenoid content was directly related to the upregulation of *psy1*, *hyd3* and *cyp97c* genes, whose transcript accumulation correlated significantly with total carotenoids determined among treatments. There was also a *hyd3/cyp97c* ratio of 3.8 folds and 4.5 folds in SW-1 and SW-2, respectively, indicating a greater allocation to the carotenoids metabolic pathway branch associated to the synthesis of *B*-carotene, *B*-cryptoxanthin and zeaxanthin. Antioxidant activity as well as phenolic compounds and carotenoid content were significantly stimulated by the application of SW. There was also a close relationship between transcript accumulation and carotenoid content, indicating that transcription and physiological response occurs simultaneously.



Poster Session

Crop Breeding & Genetics



3265 - Crop Breeding & Genetics

Ahn Sang-Nag

MAPPING QTLs FOR MESOCOTYL ELONGATION IN WEEDY RICE

Lee, HYUNSOOK; Kang, JUWON;

Chungnam National University;

Direct seeding is becoming popular in Korea because it requires a lower labor cost relative to the transplanting method. The mesocotyl is an embryonic structure between the scutellar node and coleoptilar node and is directly related to rice seedling emergence, since it elongates during germination to push the shoot tip above the soil. A large variation in mesocotyl elongation exists among rice accessions. Mesocotyl elongation in rice is controlled by several genetic factors and is also affected by environmental factors. In this study, we mapped QTL for mesocotyl elongation using F7 lines from a cross between the cultivated rice, Ilpumbyeo and a weedy rice, PBR. This weedy rice showed long mesocotyl than the elite japonica cultivars. After a repeated phenotyping of 86 lines for mesocotyl length, a subset of 30 lines selected from the two extreme phenotypic tails was used for the bulked segregant analysis. Phenotypic data showed transgressive segregation, with several lines having even longer mesocotyls than the PBR. Two QTL were identified on chromosomes 1 and 3. These two QTL were confirmed using 87 F7 lines. Two QTL, qMel-1 and qMel-3 on chromosomes 1 and 3 accounted for 21.4% and 13.0% of the phenotypic variance, respectively. The PBR allele was associated with an increase in mesocotyl elongation at both loci. It is noteworthy that two QTL for mesocotyl elongation were colocalized with the QTL for mesocotyl length reported in the previous QTL reports. These QTLs can be introgressed into cultivar background using marker assisted backcrossing in an effort to enhance the level of mesocotyl elongation.



3469 - Crop Breeding & Genetics

Akihiko Kamoshita

JAPANESE UPLAND RICE BREEDING AND YIELD FORMATION FRAMEWORK FOR IMPROVEMENT OF DROUGHT RESISTANCE IN RICE

Kamoshita,A;

University of Tokyo;

The objectives of this presentation are firstly to summarize national upland breeding efforts in Japan between 1929 and 2006, and secondly to present a framework of crop physiological yield formation framework in which disciplinary roles of molecular biologists, physiologists, agronomists and breeders are inferred. Literature reviews on Japanese upland rice breeding and other relevant drought resistance studies analyzed by yield formation framework. Institutional plant breeding has contributed to the increase in yields of rainfed upland rice in Japan from 1.9 t ha⁻¹ in 1929 to 2.8 t ha⁻¹ in 2006. Varieties with shorter growth duration and with deeper root system were developed. Various knowledge in improving drought resistance, such as raised bed screening system, has been produced, which may be used for crop improvement in drought-prone regions in Asia, Latin America and Africa. Fast advancement of molecular biology have developed two new breeding approaches, transgenic approach and DNA marker assisted selection approach. Any genetic improvement for drought resistance, if meaningful in the target field environments, needs to be identified in the yield formation framework. The proposed yield formation framework divides numerous secondary putative drought resistance traits into (1) escape mechanism (such as heading date), (2) plant type (such as plant height and tiller numbers), (3) avoidance mechanism (such as deep root system, root penetration, stomata regulation), (4) tolerance mechanism (such as osmotic adjustment, membrane stability, proline, glycine betaine, aquaporin, antioxidant, LEA protein), (5) index (such as leaf rolling score, canopy temperature, leaf water potential, carbon isotope discrimination). Interrelationship of these group traits are put in the direction of easiness of phenotyping and upstream/downstream of genetic regulation. In case of rice, escape mechanism and plant type have large influence on yield components, and modification and manipulation of these trait groups in response to water deficit would be highlighted as important researchable agenda. Conclusions: Japanese research associated with improvement of rice drought resistance was highlighted. New yield formation framework incorporating various putative drought resistance traits was presented considering easiness of phenotyping and genetic regulation to facilitate effective multi-disciplinary research collaboration.



2834 - Crop Breeding & Genetics

Alfredo do Nascimento Junior

BRS SATURNO: TRITICALE CULTIVAR

Nascimento-Jr, ANJ; Sôe-Silva, MSS; Caierão, EC; Luiz-Scheeren, PLS;

Embrapa;

In Brazil, 69,350 hectares of triticale were recorded in the year of 2009, corresponding to the smallest planted area over the last nine years. In that year, the national average yield of triticale grain was 2,157 kg ha⁻¹. Currently, triticale is grown in the states of Rio Grande do Sul, Santa Catarina, Paraná, Mato Grosso do Sul, São Paulo, and Minas Gerais. The largest areas were harvested in Paraná and São Paulo, and together, account for 86% of the national triticale production. In the south of Brazil, the occurrence of Fusarium head blight (FHB) is one of the most yield-limiting factors for triticale and other winter cereals. The search for less susceptible genotypes is constant in breeding programs. Cultivar BRS Saturno resulted from the cross between PFT 512/CEP 28 - Guará, conducted by Embrapa Trigo, in 1995. Between 2002 and 2004, seeds of that line were multiplied and purified. From 2003 to 2010, the genotype was tested in the Value for Cultivation and Use of Triticale (VCUTCL) trials at various locations in southern Brazil, where it stood out for its grain yield, hectoliter weight and less susceptibility to FHB. The line was assessed in trials of Distinctness, Uniformity and Stability (DUS) in 2003, 2004 and 2005 by Embrapa Trigo, in Passo Fundo. Triticale cultivar BRS Saturno is resistant to powdery mildew (*Blumeria graminis*), tolerant to blight, resistant to leaf rust (*Puccinia tritica*), and moderately resistant to leaf spots (*Bipolaris sorokiniana*, *Drechslera* spp. and *Stagonospora nodorum*) and to the Soilborne wheat mosaic virus (SBWMV), moderately susceptible to pre-harvest sprouting, to the Barley yellow dwarf virus (BYDV) and bacterial leaf streak (*Xanthomonas translucens* and *Pseudomonas* spp.), and susceptible to blast (*Pyricularia oryzae*) and Fusarium head blight (*Fusarium graminearum*), with a lower susceptibility level to fusarium than any other Brazilian triticale cultivars. BRS Saturno is hexaploid, has a medium cycle (70 - 85 days from emergence to heading and 135 - 150 days to maturity), and plant height of 117 cm (in Passo Fundo). This is the second Brazilian triticale cultivar totally developed in Brazil. The lower susceptibility to FHB, excellent grain quality, higher hectoliter weight and its considerable yield adaptability are good parameters to indicate this cultivar in the cereal production systems. BRS Saturno grains can be used in human and animal nutrition and its flour can be used for the production of cookies and pasta.



2851 - Crop Breeding & Genetics

Alice Casassola

SELECTING PARENTAL WHEAT LINES BY DNA MARKERS AIMING TO INCREASE THE GENETIC DIVERSITY AND THE LEVEL OF RESISTANCE TO LEAF RUST IN BRAZILIAN GERMPLASM

Casassola,AC; Brammer,SP; Chaves,MS; Caierão,E; Wietholer,P;

University of Passo Fundo;

The success in obtaining new cultivars more productive and with enhanced levels of resistance to diseases depends directly on the accurate choice of parental genotypes. The phenotypic similarity of the cultivated materials, because of the selection pressure, hampers the selection of genotypes genetically distant, which would result in enhanced variance within the progenies. The selection of genetically distinct parental genotypes showing similar phenotype can be assisted by using microsatellite molecular markers of non-expressed regions. The objective of this study was to characterize phenotypically and determine the genetic distance among wheat genotypes, to assist in the selection of parental to induced crosses. Six wheat lines (PF 030132, IWT 04019, PF 9027, PF 040488, PF 950351 and PF 979002), previously characterized to leaf rust resistance at adult plant stage, were grown in a growth chamber until the heading stage, and then transferred to a greenhouse. For the phenotypic characterization traits such as plant height, cycle and characteristics of grains (color, hardness, weight and diameter) were assessed and the data were analyzed by the Euclidean distance. The genetic distance was estimated using 97 microsatellite molecular markers and the data were analyzed by Nei72 coefficient. The results obtained by phenotyping generated a data matrix with an average distance of 2.15, where the largest distance observed was between PF 030132 and IWT 04019 (5.08) and the lower distance was between PF 040488 and PF 950351 (1.49). However, considering the data matrix of the 42 polymorphic loci, the average distance was 0.26 and the largest distance observed was between PF 950351 and IWT 04019 (0.59) and the lower among PF 040488 and PF 030132 (0.16). This study showed that microsatellite molecular markers of non-expressed regions can help the selection of genetically diverse genotypes despite their phenotypic similarity. These findings indicate that is possible to obtain enhanced levels of variability within the progeny and that wheat lines used in this study can be used as parental for future crosses, since they have genetic diversity and agronomic traits suitable to the standards required by the Embrapa Wheat Breeding Program.



2901 - Crop Breeding & Genetics

Ana Lúcia Variani Bonato

GENETIC DIVERSITY EVALUATION OF TRITICUM TAUSCHII ACCESSES USING MICROSATELLITES MARKERS

Bonato,ALV; Brammer,SP; Almeida,AB; Cordeiro,MCR;

Embrapa Trigo;

Related species of crop plants are important for breeding programs as source of genetic variability. *Triticum tauschii* Coss. Schmal. ($2n = 14$) is the D genome donor of cultivated hexaploid wheat, *Triticum aestivum* L. ($2n = 42$, AABBDD) and is source of several disease resistance genes, including resistance to leaf rust. This disease is caused by the fungal agent *Puccinia tritici* which limits the wheat production in Brazil. The knowledge of genetic similarity in different wheat accesses is important for a more precise and efficient use of these genetic resources. The objective of this work was to evaluate the genetic diversity of *T. tauschii* accesses from Embrapa Trigo seed collection using microsatellites markers. The accesses which came from Manitoba, Canada, were divided into two groups. The first, with 38 accesses RL (Leaf Rust Laboratory), was molecularly characterized at Embrapa Trigo and, the second, with 40 accesses NE (Input Number), was phytopathological and cytologically evaluated previously at Embrapa Trigo, and molecularly characterized at Embrapa Cerrados. Seeds from the *T. tauschii* genotypes were disinfected and germinated in filter paper. Early emergent leaves were used to extract genomic DNA for PCR reaction with 20 and 28 pairs of specific *T. tauschii* microsatellite primers at Embrapa Trigo and Embrapa Cerrados, respectively. After 2% agarose gel electrophoresis process, the amplified alleles were analyzed and generated a binary matrix which was utilized by NTSYS 2.0 program to calculate the genetic similarity. The results ranged from 0.17 to 0.92 and from 0.12 to 1.0 among accesses from the first and second group respectively. Genetic relationship within groups indicating a high level of genetic diversity and may be used as an additional support in crosses planning for transference of useful genes from diploid to hexaploid level in wheat breeding.



3109 - Crop Breeding & Genetics

ANGÉLICA REOLON DA COSTA

GENETIC DIVERGENCE AMONG GLOBE ARTICHOKE CLONES

Reolon-Costa,A; Grando,MF; Cravero,VP; Morlin,B;

Universidade de Passo Fundo;

The globe artichoke (*Cynara cardunculus* vr. *scolymus* (L.) Fiori) genetic breeding aims to answer the demands of the consumer market. The evaluation of large number of character simultaneously is a necessary step in order to screen plants to be used as parents in crossing schemes. The objective of this work was to evaluate the genetic diversity of globe artichoke clones by multivariate analysis and select plants presenting suitability for in natura consumption. Thirty-nine clones, belonging to six commercial varieties, were established in experimental field at University of Passo Fundo (Brazil) in 2010 and evaluated in commercial stage for 17 quantitative characters, using UPOV (2001) descriptors. The data were submitted to multivariate analysis in which the Euclidean distance, the relative contribution of different characters towards genetic divergence, using UPGMA method, and a dendrogram were obtained. The techniques of multivariate analysis demonstrated the existence of genetic divergence among clones. The traits with greatest relative contribution for genetic divergence were: the yield (42, 47%), the outer bract length (33, 05%), the number of secondary heads (6, 27%), period of implantation harvested (6, 11%) and the length of primary head (5, 00%) accounting for 91, 19 % of the variability observed the population of clones. The greatest diverging clones were the number 2 and 38, belonging to variety Improved Green Globe, with a Euclidean distance (D_2) = 99, 55 and the most similar clones were the number 15 and 24 belonging to varieties Romanesco and Green Globe ($D_2=21,21$). Cluster analysis revealed five groups. The groups II and III aggregated clones with characteristics desirable for in natura consumption. Group II presented higher values of diameter of primary head, length and diameter of secondary heads. While group III was composed of clones with higher outer bract width, fresh mass of the primary head, diameter of the bottom and higher period of implantation harvested. The clones included in these two groups may be used as parents in genetic breeding programs or for in vitro cloning.



3110 - Crop Breeding & Genetics

ANGÉLICA REOLON DA COSTA

GERMINATION POTENTIAL OF HALF-SIB PROGENIES OF GLOBE ARTICHOKE

Reolon-Costa,A; Grando,MF; Cravero,VP; Didoné,S; Satori,G; Barbosa,D;

Universidade de Passo Fundo;

The tendency of the globe artichoke (*Cynara cardunculus* vr. *scolymus* (L.) Fiori) genetic breeding is to develop cultivar propagated by seeds. So plants with good seed production and with high germination rate are required. This work aimed to evaluate seed germination rate of globe artichoke from 12 progenies selected for in natura consumption. The study was conducted at Universidade de Passo Fundo-Passo Fundo-RS, Brazil. Eleven selected plants, from C0 recurrent selection cycle, were cross pollinated by insects (*Apis mellifera*) in greenhouse in order to obtain segregating progenies. The germination test was conducted in scrolls germitest, moistened, without further addition of water with three lives/scrolls. The scrolls germitest where placed in 20°C constant temperature chamber, with photoperiod of 12 hours. A completely randomized design, with four replications was used. Each replication was composed by 50 seeds of each progeny, totalizing 200 seeds by treatment. The evaluation was performed twenty-one days after sowing and assessments were performed according to the criteria established by Rules for seed analysis (Brazil, 1992). The data were submitted to analysis of variance and the averages were compared by Tukey's test (5%error probability). There was variation of germination rate among the progenies evaluated. The highest percentage of germination was obtained from seeds of progeny number 4 (88%) which did not differ statistically from the progeny 1 (82%). These results are important since germination rate is low in the original cultivars, which compromises the plant stand in the establishment of culture. The lower seed germination rate were observed in progeny 9 (18%) and progeny 3 (0%). These progenies may be excluded from the next cycle recurrent phenotypic selection C1. Among progenies evaluated it was possible select half-sib progenies with good germination potential.



3231 - Crop Breeding & Genetics

Ariano Martins de Magalhães Júnior

CONTRIBUTION OF MORPHO-PHYSIOLOGICAL DESCRIPTORS ON DETERMINATION OF GENETIC DISSIMILARITY IN RICE GENOTYPES

Streck,EA; Magalhães-Jr,AM; Fagundes,PRR; Franco,DF; Severo,ACM; Fonseca,GM; Aguiar,GA; Lopes,JL; Oliveira,FA;

Embrapa Clima Temperado/UFPel;

The classification of genotypes through multivariate analysis has provided effective contributions in breeding of many cultures, because it provides parameters for the identification of parents to enable higher heterotic effect in the progeny and greater ability to recover superior recombinants in segregating generations. This study aims to evaluate the genetic dissimilarity of a group of 37 rice genotypes with likely potential use in plant breeding, which were field evaluated for ten morpho-physiological characters: plant height; length the panicle; cycle; foliar pubescence; panicle weight, length, width and thickness of grains, and length and thickness of the stem. The experiment was conducted in the agricultural year 2011/2012 at the Lowland Experimental Station of Temperate Climate Center (Embrapa) in Capão do Leão/RS/ Brazil, delineated in plots with 6 rows of 5 m and spaced 17.5 cm, with established plant density of 100 kg ha⁻¹ of viable seeds. The analysis was processed through the computational applicative in genetics and statistics GENES. To obtain the importance of characters, multivariate analyzes were used by the generalized distances Mahalanobis cluster. Based on these results, it was found that for the character which has the largest contribution was the foliar pubescence 85.27%, which was given five different ratings before its intensity in the rice plants (1- absent, 2-weak, 3-medium, 4-strong and 5-very strong pubescence). Alpha The dendrogram was obtained by Multivariate Analysis to measure dissimilarity using the UPGMA method. It was built in a graph which provides the information of genetic distances among the present group of genotypes tested. The genetic distance is proportionally related to the significance of clustering characters obtained in the previous evaluation. Thus, a distance of 75% could be identified among the three distinct groups of genotypes. Depending on the results obtained, it can be concluded that it was possible to discriminate the genotypes assessed using multivariate analysis towards the descriptors of rice, showing possible sources contributing to genetic improvement of this crop.



3415 - Crop Breeding & Genetics

Arun ambatipudi

BREEDING COTTON GENOTYPES FOR THE NEEDS OF ORGANIC SITUATION IN DEVELOPING COUNTRIES

Patil,SS; Roner,TINA; Baruah,RAJEEV; Ambatipudi,ARUN; Messmer,MONICA; Forster,DIONYS;

University of agricultural sciences, Dharwad;

The era of GM cotton has increased productivity of cotton but it has adversely affected the genetic diversity of cotton. Organic cotton provides a vital source of refugea and serve the cause of sustainability of resistance to bollworm (when farmers are refusing to raise refugea). Breeding potential varieties for organic situation can enhance productivity of organic cotton and make farmers self reliant for seed needs and restore the seed chain of non GM varieties which is a major threat to promotion of organic cotton. Presently the varieties developed for conventional farming situation are being cultivated in organic farming. The study was aimed at understanding the need to develop genotypes exclusively for different situations of organic cotton. Objective: 1. Comparison of cotton genotypes in conventional and organic situation. 2. Evaluation of variability among early generation lines and stabilized lines and comparison of hybrids and varietal options for organic situation. Evaluation of Breeding material was taken up in locations of Karnataka ,Madhya Pradesh and Orissa states of India. the performance of genotypes differed in organic situation as compared to conventional situation depending upon the inherent differences in tolerance to biotic stresses and some differences in ability to observe organics forms and nutrients. The option of varieties ensures self sufficiency of seed needs. Some potential hybrids can become an option provided approaches like training for back yard seed production and community seed production is given. Compact varieties with synchronous maturity revealed high productivity in receding moisture situation and suit high density planting. Evaluation of breeding materials under organic condition helps in developing genotypes most suited for organic situation. Farmers participatory approach helps in understanding the intricate needs of small farmers, ensures self sufficiency for seed needs.



3416 - Crop Breeding & Genetics
Arun ambatipudi

DEVELOPMENT OF HETEROTIC GROUPS BASED ON THE PERFORMANCE OF CROSSES

Rajeev,S; Patil,SS; Ranganath,HM; Swathi,P; Pranesh,KJ; Pooja,VGOANKAR;

University of Agricultural Sciences, Dahrwad;

Performance of hybrids and the magnitude of heterosis depend up on the genetic diversity existing between the parents. To maximize heterosis it is necessary to develop groups of genetically diverse parents. Such diverse parents can be utilized in development of heterotic populations .Grouping of genetically diverse genotypes can be done based on phenotypic measure of distance (D2 analysis) and molecular markers are relatively less reliable than that of groups formed based on actual performance of hybrids. Development of heterotic groups based on combining ability and hybrid performance. Comparing the approaches of determining diversity among cotton genotypes. The principle of predicted double cross performance were adopted in determining pairs of lines and a pairs of testers of a genetically diverse heterotic box. The set of hybrids involving the line as a common parent gives an idea about the combining ability pattern of the concerned line. The higher or lower performance of the hybrids is itself taken as reflection of genetic distance existing between the parents. Based on seed cotton yield, crosses were arranged in decreasing order. Two most potential heterotic boxes were identified based on the predicted double cross performance. The comparison of diversity analysis done based on phenotypic diversity and molecular diversity was done and correlation was determined between performance and diversity values. The reasons for complementation of parents leading to heterosis were ascertained. Crosses were selected based on productivity without compromising fibre quality traits. Choice of diverse parents based on productivity is more useful than just based on phenotypic and molecular diversity. Based on the performance of crosses it is possible to identify set of diverse groups of parents serving as base material for further exploitation through schemes of population improvement for combining ability.



3310 - Crop Breeding & Genetics

Carlos Roberto Riede

FOURTY YEARS OF WHEAT BREEDING ACTIVITIES AT IAPAR, BRAZIL

Riede,CR; Campos,LAC; Scholz,MBS; Okuyama,LA; Garbuglio,DD;

Agricultural Research Institute of Paraná - IAPAR;

The wheat breeding program was the first to start activities when IAPAR was created in 1972. The major goal during the last 40 years were to develop suitable new cultivars, adapted to the meridional region of Brazil, which includes the states of Paraná (PR), São Paulo (SP), Mato Grosso do Sul (MS) and Santa Catarina (SC). Thirty three new cultivars were developed and released for cultivation. Besides Brazil, some of them have been cultivated in Paraguay and Bolivia due to similar environments. The main objectives were to breed for: a) Increasing grain yield; b) high industrial and nutritional qualities; c) major disease resistance; d) environmental stresses; and good agronomic adaptative traits. Used breeding methodologies were: a) germplasm introduction either from Cimmyt or other national institutions; b) crossing block exploitation for artificial hybridizations, mainly single or three way crosses; c) selection procedures as modified bulk method; d) grain yield evaluation in preliminary yield trials; e) Multi-location VCU trials of advanced lines; f) DHE trial of elite lines; g) Laboratory grain selection and gluten strength evaluation; h) screening for pre-harvest sprouting reaction. The VCU trials network is a partnership among IAPAR, Embrapa Soybean Center and Meridional Seed Producers Foundation, all located in Londrina-PR-Brazil. The more important from the 33 released cultivars were: a) IAPAR 1-Mitacoré (1980); b) IAPAR 6-Tapejara (1982); c) IAPAR 17-Caeté (1986); d) IAPAR 29-Cacatú (1988); e) IAPAR 53 (1992); f) IAPAR 78 (1996); g) IPR 85 (1999); h) IPR 110 (2003); i) IPR 118 (2004); j) IPR 130 (2008); k) IPR 144 (2009), and l) IPR Catuara TM (2011). Some of these cultivars were sown in large areas of the wheat crop in Brazil. New cultivars are innovations which can be subjected to property rights including registration at the RNC - National Cultivar Registration Office and protection at the SNPC - National Cultivar Protection Service, allowing the official seed multiplication and collection of royalties to better support the breeding activities. This research has received grant support from the State of Paraná Government, Brazilian Council for Scientific Development - CNPq and Meridional Foundation for Support to Agricultural Research.



3308 - Crop Breeding & Genetics

Chang Hyu Bae

CHARACTERISTICS OF EARLY HEADING RICE (ORYZA SATIVA L.) LINES DERIVED FROM GAMMA-RAY IRRADIATION

Ryu, JAIHYUNK; So, HYUNSU; Lyu, JAEIL; Bae, CHANGHYU;

Sunchon National University;

This study was carried out to evaluate genetic variation of early-heading rice (*Oryza sativa* L. cv. Dongjin 1) lines derived from gamma-ray (60Co, 300 Gy) irradiation. The average heading date of the 5 early-heading lines in M7 and M8 generation was faster than that of untreated control as 11 (line -2), 10 (line -5), 6 (-1 line), 5 (-3) and 4 days (line -4), respectively. The culm length and ear length of the selected lines was shorter than that of control. Grain quality of the selected lines was not different compared with control. According to RAPD and ISSR analyses, polymorphic rate of the early-heading lines was higher than that of control. The result indicates that the gamma-ray promote variation at DNA level. When genetic variations of Ehd1 region were evaluated by nucleotide analysis, nucleotide length of the Ehd1 region was 935 bp (control, line -2 and -4) and 936 bp (line -1, -3 and -5). In addition, seven sites of nucleotide transposition and insertion were detected in the Ehd1 region of the selected lines. Sequence similarity matrix (SSM) of the region ranged from 0.991 to 1.000 with an average of 0.995. Relationship of gene expression among Ehd1, Ehd2 and Ehd3 of the selected lines was detected by RT-PCR.



3405 - Crop Breeding & Genetics

Shreekant S Patil

'GENETIC CORRELATION' A REFINED LEVEL OF DETERMINING ASSOCIATION OF QUANTITATIVE CHARACTERS IN COTTON

Ranganath, HM; Patil, SS; Rajeev, S; Manjula, SM;

University of agricultural sciences, Dharwad;

In sexually reproducing crops, only a part of the genotypic value namely breeding value is transferred to the progeny. Hence determining the components of phenotypic value up to the level of breeding values becomes important. Correlated response of a character to selection practiced for another quantitative character also depends upon the strength of genetic correlation existing between them. It is necessary to establish relations and estimate co variances that are required in determining genetic correlation. In this study the data generated on half sibs and full sibs is utilized by using NC designs. Determining Genetic correlations and comparing these values with Genotypic and Phenotypic correlations. From a set of 48 intra hirsutum crosses (8 Lines X 6 Testers) co-variance of half sibs and fullsibs was utilized to determine genetic correlations among quantitative characters and compared with phenotypic and genotypic correlations. At the level of breeding value (r_A), seed cotton yield exhibited highest positive genetic correlation with number of bolls per plant (0.75) followed by monopodia per plant (0.65), boll weight (0.54). As compared to this seed cotton yield showed negative genetic correlation with lint index (-0.39), ginning outturn (-0.24), seed index (-0.23). There was a clear differences in magnitude and direction of association among quantitative characters when measured at the level of breeding value (r_A) as compared to genotypic and phenotypic correlation. This clearly suggests that the inferences on relationships among characters and predicted correlated response can be wrong if phenotypic and genotypic correlations are used. The strength of genetic correlation among quantitative traits differed considerably from phenotypic and genotypic correlations. Determining phenotypic and genotypic correlations loses significance once this approach of determining genetic correlation is widely used in different crops.



3244 - Crop Breeding & Genetics

Daijiro KANEKO

Expanding photosynthetic RSEM_crop models with NDVI comparison between MODIS and SPOT for yields in continental regions

Kaneko,D; Kumakura,T;

President of Remote Sensing Environmental Monitor, Inc.;

The recent concern about food scarcity and farmland acquisition motivates the expansion of the present system named Remote Sensing Environmental Monitor (RSEM) for crop yield monitoring. The authors have developed a photosynthesis model for rice production to address such issues. The system includes a photosynthetic sterility yield model using meteorological re-analysis data and precise land use and cover (LULC) classification of crop field in Asian countries. The validation concept is based on the fact that the carbon hydrate in grains has the same chemical formula as cellulose in grain vegetation. This paper describes the extension of the concept of RSEM-rice model in Asia to winter wheat and maize yields in other continents. The approach of the effective LAI in RSEM crop models incorporate MODIS NDVI in addition to 1km resolution of SPOT VEGETATION. The NDVI difference between MODIS and SPOT is considerable, depending on land cover types of grain plants or vegetations such as forests and grassland. The conversion of the NDVI difference originates from two reasons, i.e., spectrum band width and sensor sensitivity response functions of MODIS Spectrometer and SPOT VEGETATION. PSN and net PSN using moderate resolutions of MODIS NDVI are computed by NDVI values on paddy fields. The comparison intends to clarify the difference between the MODIS PSN, which is calibrated by FLUXNET, and present NDVI by the carbon partitioning validation (CPV) method proposed by authors. The present basic conception of photosynthesis model using multi-satellite and meteorological data in continental scales is expanding to three crops, which are winter wheat at two modeling sites at Katanning and Wagga Wagga in Australia, secondly maize at Lincoln, Illinois and Clinton in Iowa, U.S.A, and the last soybean at Cuiaba in Rondonia and Tres Langoas sites in Mato Grosso do Sul, Brazil.



3397 - Crop Breeding & Genetics

Danielle Cunha Cardoso

LARGE-SCALE EXPRESSION OF GENES INVOLVED IN JASMONATES BIOSYNTHESIS IN COFFEE PLANTS INFESTED WITH LEAF MINER

Cardoso,DC; Martinati,JC; Giachetto,PF; Guerreiro-Filho,O; Vidal,RO;
Carazzolle,MF; Maluf,MP;

Agronomy Institute of Campinas;

Jasmonic acid (JA) is a plant hormone that activates the expression of defense genes whose biosynthesis is catalyzed by a group of enzymes collectively known octadecanoid pathways. The aim of this study was to identify the transcriptional changes of genes related to octadecanoid pathway in order to support the studies of the mechanisms that lead to resistance/susceptibility in coffee plants infested by the leaf miner. leaves samples were collected from two coffee genotypes; resistant and susceptible to leaf miner (*Leucoptera coffeella*) in three different times of infestation: time zero (T0 - before infestation), time 1 (T1 - oviposition) and time 2 (T2 - hatching eggs) and the RNA samples were extracted. A total of 22.500 EST sequences from the Coffee Genome Database were selected for the 12 X 135K array synthesis, each one represented by 6 different oligos. Differential expression was established by comparisons of gene fold change values, and those with values ± 2 were considered differentially expressed. 57 gene sequences related to biosynthesis of plant hormones were identified. We identified 13 genes specifically related to alpha-linolenic acid metabolism which is the substrate central to defense-related metabolites, which oxygenation is the initial step of the JA pathway. Of these 13 genes, those encoding the enoyl-CoA hydratase, and phospholipase A2 maintained four times more expressed in T0. Susceptible plants increased the levels of these transcripts only in later stages. Differential expression (fold change between 8 and 17) of two sequences coding for jasmonate O-methyltransferase and lipoxygenase also were observed in the resistant plants in T0, and on susceptible plants when these expression was not differential at any stage of infestation. In these plants was observed overexpression of the sequences encoding the enzyme 12-reductase oxophytodienoate in T1 and T2 (fold change between 4 and 5). For all other genes encoding enzymes of the pathway was not observed differential expression. These results indicate that alpha-linolenic acid levels is low, particularly on susceptible plants, since in these plants lipases levels of transcripts did not show differential expression at any stage of infestation. Possibly, JA pathway was not the main defense mechanism activated in genotypes studied, although it was more rapidly activated in resistant plants.



2905 - Crop Breeding & Genetics

Danyela de Cássia da Silva Oliveira

GENETIC SIMILARITY IN OAT (AVENA SATIVA L.) USING THE REMAP TECHNIQUE

Oliveira,DCS; Silveira,SFS; Luz,VK; Pacheco,LW; Wolter,DD; Viana,T; Silva,RM; Maia,LC; Oliveira,AC;

Federal University of Pelotas;

Transposable elements are mobile fractions of genomes that can quickly accumulate mutations and increase the genetic variability. REMAP markers amplify genomic regions between retrotransposons and microsatellite regions with high power to detect polymorphisms. The detection of genetic variability in oat is essential for proper choice of adopted parents in crossing blocks. The aim was to analyze the genetic variability in oat cultivars validating the use of the REMAP technique. The experiment was conducted in the Plant Genomics and Breeding Center, Federal University of Pelotas. We analyzed twelve oat cultivars: Albasul, Afrodite, Barbarasul, Brisasul, Carlasul, Chiarasul, Dilmasul, IAC 7, UFRGS 19, UPF 15, Taura and URS 21. Extraction of DNA was performed on leaves through the method modified CTAB 2%. After, amplifications were performed by polymerase chain reaction, using five combinations of primers, four of them made with primers designed on the LTR region of the retrotransposon Fatima of wheat and primers ISSR (Inter single sequence repeat) - (GCA)_n (A), (GCA)_n (T) and (GCA)_n (A). The fifth combination consisted of a primer designed on the transposable element PONG of rice, combined with a primer ISSR - (GA)_n (C). The REMAP technique proved to be efficient detecting a total of 154 polymorphic fragments. The groups formed by UPGMA method, corresponding values were supported by the analysis of the cophenetic correlation coefficient of 0.90, indicating satisfactory agreement between the data matrix and grouping. Taking as the point to cut the average similarity between genotypes, the cluster analysis allowed the formation of six groups. Group I was formed for Barbarasul, Brisasul, Carlasul, Chiarasul, Dilmasul and IAC 7, where only Carlasul and Chiarasul did not differ. Group II was composed by the cultivars URS 21 and Afrodite. Genotypes UFRG 19, UPF 15, Albasul and URS Taura, remained isolated forming groups III, IV, V and VI respectively. The cultivar URS Taura showed the greatest genetic diversity of other cultivars. The REMAP technique is effective for detecting genetic similarity in oat genotypes. Aiming at increasing the number of different complementary alleles, crosses between genotypes from different groups would be preferred.



3401 - Crop Breeding & Genetics

Dr. Keshava Murthy B C

DEVELOPMENT OF HIGH GRAIN PROTEIN AND LYSINE RICH GENOTYPES IN RICE

Bangalorechannappa, Dr Keshava Murthy;

GPB, UAS, Bangalore;

Total grain protein in rice is an important nutritional parameter and development of quality rice with enhanced nutrition is very essential for eradication of malnutrition in the developing world. Habitually, plant breeding in rice is more focused towards the development of high yielding and stress tolerant varieties. Large amount of rice recombinant inbred lines population of F9 generation were developed and analyzed for agronomic and quality traits. Wide range of variability for the traits were observed for total grain protein variation was observed in the range of 4.10 to 18.75 percent with an average of 12.07 percent. Two genotypes were identified for having high lysine of 4.3 percent. Naturally rice and oats are rich in lysine content than any other cereals and on average lysine content varies from 3.5-4.0 percent in rice varieties. Two DNA pools contrasting for high and low protein content were analyzed to identify markers through bulk segregants analysis. Among the 300 polymorphic SSR primers screened, 8 primers co segregated with the two bulks and parents, BPT-5204 and HP-14. Among these, one SSR on chromosome 3 was found to be co-segregating with individuals of the bulk and was associated with high protein content in grains. Essential amino acid, lysine, is very low in cereals where rice and oats are have moderately high concentration varying from 3.5-4.0 percent. HPLC analysis showed variation of about 2-8 % in the high protein inbred lines. Earlier research studies have proven potential use GM to improve grain nutritional quality. However, none of the transgenic approaches have so far been successful in commercializing the varieties. Breeding for nutritional enhancement is rather highly difficult compared to traits. Grain yield and protein content may be improved simultaneously up to one stage, beyond which an increase in protein results in a decrease in grain yield. Many factors like, Weather, cultural practices, fertilizer application, water management, and weed control also affect levels of protein. Hence hybridization followed by selection in a huge recombinant inbred line population was carried out with the aim selecting high yielding varieties with enhanced nutrient contents. Several promising inbreds/introgression lines with preferred plant type and enhanced nutrition have been and Identification of minor and major QTLs affecting total grain protein and essential amino acids is under progress.



3323 - Crop Breeding & Genetics

Edjane Gonçalves de Freitas

A MIXED-MODEL APPROACH FOR SELECTION OF SUPERIOR SUGARCANE VARIETIES USING PEDIGREE INFORMATION

Freitas,EG; Pastina,MM; Garcia,AAF;

Department of Genetics, "Luiz de Queiroz" College of Agriculture, University of São Paulo, Piracicaba, São Paulo, Brazil;

The major aim in evaluating varieties is to predict their future performances. Analysis of yield data in different environments is a classic routine in quantitative genetics. Selection of varieties for yield is usually based on information from a series of field trials known as multi-environment trials (METs), but in many cases the information of pedigree is ignored. While pedigree information has been used extensively in animal breeding, its adoption on a routine basis in plant breeding has been less extensively. Benefits in using pedigree information can be two-fold. Firstly, the performance estimate of varieties are more accurate through the use of information from relatives. In addition, breeding values can be estimated for each variety helping to quantify the potential of each variety as a parent in the breeding program. Sugarcane breeding programs evaluate mainly yield (tonnes of cane per hectare - TCH) in METs to select new varieties (clones or genotypes). In Brazil, yield is measured through three years after field implantation. In this work, we propose an approach to analyze sugarcane yield data combined across trials and harvests incorporating pedigree information (relationship matrix). Mixed model was used to analyze TCH data and different variance-covariance structures were tested with and without pedigree information. We evaluated 53 varieties in 16 trials using complete randomized block designs with three to six replications and two to five harvest years. To select the most suitable variance-covariance structures we considered the Akaike Information Criterion (AIC). The best selected structure was the uniform for both trials and harvests. We also found that there are deviations in the rank of individuals between the models tested. These results show that incorporating the relationship information may help in the selection of future commercial varieties and in the choice of parents for new crosses.



3154 - Crop Breeding & Genetics

Eduardo Beche

HYBRID BREEDING IN BRAZILIAN SPRING WHEAT: HETEROSIS FOR YIELD AND ITS COMPONENTS

Beche,E; Capelin,MA; Munaro,LB; Silva,CL; Pagliosa,ES; Benin,G;

Graduated Program in Agronomy of Universidade Tecnológica Federal do Paraná;

Efficient identification of superior hybrid combinations is a fundamental issue in wheat breeding programs (Gowda et al., 2010). Since the discovery of male sterility controlled by cytoplasmic genes (Adugna et al., 2004) or induced by chemical agents (Duvick, 1999; Gaju and Parodi, 2009) the hybrid development is glimpsed as a promise to increase the potential for grain yield and stability of crop wheat (Rajaram, 1999; Gowda et al., 2010; Chen et al., 2011). The objective this study was to estimate heterosis over mid-parent and better parent (heterobeltiosis) for grain yield and yield components in a set of diallel crosses involving 10 wheat genotypes. Parents and F1 and F2 hybrids were evaluated under field conditions in spaced plant scheme in a randomized block design with three replications. The estimated genotypic variances (σ^2_G) for parents and hybrids were significantly larger than zero for all five traits ($p > 0.01$) (Table 1). Parents and F1 hybrids showed similar σ^2_G for all traits except for plant height (PH), agreeing results reported by Gowda et al. (2010). Estimates of heritability (h^2) values were high, ranged from 0.74 to 0.99, demonstrating that the largest proportion of the phenotypic expression of traits in parents and hybrids is genetic. The mean heterosis was positive for all traits in both generations, except for the trait one hundred kernel weight (100-KW) in F2 generation (Table 01). The highest estimates of the mean heterosis was found for grain yield per plant (GYP) in the F1 (20.38%) and F2 (10.46%). The mean heterobeltiosis (heterosis better-parent) was positive value for the GYP in F1 (7.09%), that ranged among -28.73% to 40%. The maximum values of heterosis for GYP (Table 2), was obtained at BRS Guamirim x BRS 208 hybrid (F1= 51.5% and F2= 44.2%) and for this same trait, the highest heterobeltiosis was at BRS 208 x Abalone hybrid (F1 = 40% and F2 33.5%). These results suggesting the presence of genetic variability useful for selection and exploitation of commercial hybrid wheat, as also reported by several other studies (Hussain et al. 2007; Bao et al., 2009; Gowda et al., 2010).



3143 - Crop Breeding & Genetics

ELISANDRA ANDREIA URIO

Genetic stability in Brazilian wheat cultivars determined by pollen viability

Urio,EA; Brammer,SP; Cargnin,A;

UPF;

Analysis of genetic stability may allow obtaining wheat lines with better agronomic characteristics, favoring also the planing of the best parental combinations to obtain new wheat cultivars. The objective of this study was to evaluate the genetic stability by pollen viability of Brazilian wheat cultivars potentially useful for breeding programs. The genotypes used were obtained from the Active Germplasm Bank of Embrapa Trigo. Seventeen wheat cultivars released after 2000 were analyzed cytogenetically. Plants were grown in pots in a greenhouse, using soil. To evaluate pollen viability, five ears of each genotype were collected at the stage of mature pollen, fixed in Carnoy for 24 h at room temperature and stored in 70% ethanol at -20°C until the preparation of slides. The slides were prepared from the maceration of anthers from three flowers of the intermediate region of the spike, followed by staining with 1% acetic carmine. A total of 100 pollen grains optical microscope. The pollen grains were classified into two categories: viable and inviable. Pollen grains that presented normal nuclei, starch, pore and membrane, were considered viable. Empty pollen grains were assumed inviable. The size of the pollen and the presence of more than one pore was also observed. The data were subjected to analysis of variance and means Scott-Knott test at 5% significance. The results showed that all genotypes presented over 95% of viable pollen grains and only 3.8% were inviable. Less than 1% of pollen grains presented more than one pore and the pollen grain size difference reached 2.2%. Analysis of variance showed no significant differences for the viable pollen grains, inviable pollen grains and more than one pore. The size difference variable was statistically different, and when means were compared, BRS 24 proved to be different from the other cultivars. Therefore, the genotypes studied had normal pollen viability, indicating that the multiplication and seed conservation method was compared by the per slide and 500 pollen grains per plant were analyzed with an appropriate.



2856 - Crop Breeding & Genetics

Elisane Weber Tessmann

GENETIC DISTANCE AMONG WHITE OAT CULTIVARS (*AVENA SATIVA* L.) IN RESPONSE TO MANGANESE STRESS

Tessmann,EW; Nornberg,R; Luche,HS; Kavalco,SAF; Zimmer,CM; Groli,EL; Maia,LC; Costa-Oliveira,A;

Federal University of Pelotas;

Manganese (Mn^{2+}) is an essential element for plant growth, but its excess can cause damages in plants leading to decreases in yield. Genetic distance estimates can provide the identification of contrasting parents that may lead to greater heterosis in crosses. Thus, this study aimed to determine the genetic distance of white oat cultivars subjected to doses of manganese in hydroponics. The experiment was conducted at the Plant Genomics and Breeding Center (CGF), Federal University of Pelotas, Pelotas-RS. The cultivars ALBASUL, BRISASUL, FAEM CARLASUL, FAEM DILMASUL and LEONARD were used. The experimental design consisted of randomized blocks, with three replicates with ten seedlings each one. The seedlings were kept for four days in complete nutrient solution, then were subjected to treatment for four days, which was composed of 10% of the initial solution with the doses of 0,11 and 900 mg L⁻¹ of Mn^{2+} . After this, the seedlings were returned to the initial nutrient solution for four days. The characters evaluated were the initial length of the root (ILR) and shoot (ILS), the final lengths of the root (FLR) and shoot (FLS), and length of the first leaf (LFL), all in centimeters; initial dry mass of the root (IDMR) and shoot (IDMS), final dry mass of root (FDMR) and shoot (FDMS), all in grams, and number of roots (NR). The Mahalanobis distance (D^2) was used to assess the genetic dissimilarity and the matrix allowed the construction of dendrograms by UPGMA using the NTSYS software. The dendrogram based on dose 0,11 mg L⁻¹ differentiated the genotypes into two groups, the first formed by ALBASUL, and the second by the other cultivars. Furthermore, it was verified that the characteristics that most contributed to the formation of the groups were FLS (13,41%), ILS (24,99%) and LFL (21,22%). The dendrogram based on dose of 900 mg L⁻¹ formed two groups, one composed of cultivars recently released by the CGF, Brisasul, FAEM Carlasul and FAEM Dilmasul. The second group was formed by cultivar ALBASUL (released in 2003) and the cultivar Leonard, foreign and not adapted. The relative contribution to the formation of these groups, was higher from the characters FLS (17,17%), LFL (15,41%) and FDMS (18,46%). Thus, the characters of the shoot are the ones who contribute the most to differentiate the genotypes at both doses. The crossing between cultivars of different groups can be employed to obtain mapping populations to find QTLs for manganese response (Mn^{2+}) in oats.



3331 - Crop Breeding & Genetics

Felipe Bermudez Pereira

GENETIC VARIABILITY IN A F₂ SOYBEAN POPULATION FOR TRAITS ASSOCIATED WITH RESISTANCE TO STINK BUG COMPLEX

Bermudez,FP; Moller,M; Santos,MF; Rocha,F; Ferreira,M; Baldin,JP;

Escola Superior de Agricultura "Luiz de Queiroz" - ESALQ/USP;

Soybean is vulnerable to attack of pests from germination to harvest, and stink bugs are the major insect pest during the reproductive stage. By feeding directly the grains, they are responsible for reducing seed quality, germination and yield. Soybean breeding programs have not been successful in developing resistance to stink bug. Thus, this study objective was to analyze the variability of traits associated with soybean resistance to stink bugs in a F₂ population, derived from crosses between IAC-100 (resistant to stink bugs) and CD-215 (susceptible). The field experiment was conducted at the Experimental Station of Esalq/USP at Anhembi, São Paulo State, using a completely randomized design for 228 F₂ plants and the parents. Six traits were evaluated, such as grain filling period (GFP), leaf retention (LR), percentage index of pod damaged (PIPD), healthy seed weight (HSW), weight of hundred seeds (WHS) and grain yield (GY). The analysis of variance was performed for each trait by using the GLM procedure and the parameters mean, variance, asymmetry and kurtosis were estimated by the UNIVARIATE procedure, both in SAS software. Results showed that all traits presented significant differences in the F₂ population for the F test considering a 95% of probability (P).



3378 - Crop Breeding & Genetics

Fernanda Bortolini

MORPHOLOGICAL AND AGRONOMIC TRAITS OF THREE ARROWLEAF CLOVER POPULATIONS

Bortolini,F; Duarte,JG; Mittelman,A; Rosa,TC; Pires,ES;

Embrapa Temperate Agriculture;

The Arrowleaf clover (*Trifolium vesiculosum*) is a cool season annual forage specie with high percentage of hard seed and good reseeding ability. The objective of this study was to compare morphological and agronomic traits of three Arrowleaf clover populations: TV01 (selected from the cultivar Embrapa-28 'Santa Tecla'), TV02 and TV03 (derived from cv. Yuchi). The field experiment was carried out at the Lowland Experimental Station of Embrapa Temperate Agriculture, at the city of Capão do Leão, RS, Brazil. The experimental design was a randomized block design with 13 replications. Sowing was done on May 12th of 2011, using pelleted seeds with specific *Rizhobium* inoculant (SEMIA 2050 + 2051), in rows of 14 m spaced 0.20 m. The evaluations were performed on six plants per line to the following traits: plant height at 90, 120 and 130 days after seeding, plant diameter, initial vigor - visual notes from 1 (lowest) to 5 (highest); central leaflet length and width; leaf color - visual note from 1 (light green) to 5 (dark green), petiole length, number of inflorescences, fresh and dry forage yield and dry leaf yield. There were significant differences among the populations for plant height at 90 days, diameter, initial vigor, fresh and dry forage yield and dry leaf yield. The highest values were observed for the populations TV01 and TV02, which did not differ significantly, but differed from the population TV03. Dry forage yield of the populations TV02 and TV01 populations were 6432 and 6689 kg/ha, respectively, while population TV03 yielded 4682 kg/ha. The same was found for dry leaf yield, with 1838.70 and 2246.49 kg/ha to TV01 and TV02 and 1209.18 kg/ha to TV03. In relation to height, diameter and initial vigor, TV01 had 9.82 cm, 15.45 cm and 4.04, respectively. TV02 did not differed from TV01, with 9.67 cm, 15.52 cm and 4.12 and TV03 differed from the previous two with 8.30 cm, 14.23 cm and 3.16. The variables, length and width of central leaflet did not differ among populations, with 5 and 3 cm in average, respectively, as well as the average length of petiole with around 14 cm for the three populations. There were differences among populations for morphological and agronomic traits. Both populations TV01 and TV02 had better initial development as well as better forage production when compared to population TV03.



3209 - Crop Breeding & Genetics

Gabriel A. Aguiar

EVALUATION OF STRAINS OF IRRIGATED RICE AS TO THE TOXICITY OF IRON.

Almeida-Aguiar, G;

Embrapa Clima Temperado;

The Rio Grande do Sul is the largest paddy producer in the country, this activity is of great economic and social importance to the state, being grown each year around one million hectares of irrigated rice, which account for 62.2% of domestic production of this crop (IBGE, 2010). However, the average productivity of rice in the state is still low compared to that achieved on farms that adopt high technology and the productive potential of the experimental areas. Among the factors causing the low average productivity in the RS, there is the condition of stress by excess iron in the soil. This problem is accentuated with the flooding, which promotes the reduction of ferric oxides (Fe^{3+}) to ferrous oxide (Fe^{2+}) in the compounds, with consequent increase of the solubility and availability in the soil solution, causing toxicity to plants. An efficient alternative to overcome this stress is to use cultivars tolerant to high levels of iron in the soil. This study aimed to evaluate the behavior of inbred lines, the breeding program of Embrapa rice, subjecting them to stress by iron, in harvest 2011/12. The experiment was conducted at the Experimental Station of Embrapa Temperate Lands, in Capão do Leão, RS. The test consisted of 49 genotypes, and four controls (BR IRGA 409, IRGA 417, BRS Taim and BRS Querencia 7). The genotypes were distributed through the experimental design of randomized blocks with three replications and plots with 4 rows of 3 meters in length, spaced 17.5 cm. Irrigation was continuous, starting 10 days after emergence of the plants (DAE) to maintain reducing conditions of the soil. The evaluation of symptoms of iron toxicity (indirect toxicity) was performed in three seasons, 40, 70 and 100 days after plant emergence. The evaluation scale was based on the symptoms of leaves and varies alaranjamento 1-9, with 1 to 3.5 tolerant; tolerant average 3.6 to 5.5; sensitive average 5.6 to 7.5 and 7.6 to 9 sensitive. Four inbred lines (AB10004, AB11047, AB10571 and AB11004) showed tolerance to stress, similar to the control BRS Querencia. Shown as medium tolerant genotypes 28 and 13 as medium sensitive strains showed the character, similar to the controls, BR IRGA 409 and IRGA 417.



3339 - Crop Breeding & Genetics

Giovanni Orlando Cancino Escalante

PARTICIPATORY SELECTION OF BLACKBERRY RUBUS GLAUCUS BENTH IN THE NORTH EASTERN REGION OF COLOMBIA, SOUTH AMERICA

Cancino-Escalante,GO; Quevedo-Garcia,E; Villamizar,CE; Díaz-Carvajal,C;

Universidad de Pamplona;

Participatory plant selection of heterogeneous varieties is one strategy to address the loss of crop diversity which may restrict the adaptive potential of agricultural species. This strategy is valid to address this issue by bringing together the skills and knowledge of farmers and scientists. Promising *Rubus glaucus* Benth materials using participatory diagnostic assessment were selected from commercial properties of four blackberry growers association in the municipalities of Pamplona and Chitagá (North of Santander, Colombia). 3 - 5 specimens, established in 51 commercial farms, aged 9 to 24 months that presented accessions during their fruiting stage were collected. A total of 58 accessions and 9 variables such as morphological, agronomical and nutritional (yield, degrees Brix degree, percentage of acidity, pH, fruit length, fruit diameter, fruit weight, maturity, farmers rating) were evaluated. Principal component analysis, contingency matrix and Ward's conglomerate analysis method was applied to the 9 variables. Results of the conglomerate analysis showed that accessions were reorganized in 3 main groups which explain the 71.7% of total variability. First group: fruit diameter, maturity, yield and Brix degree; Second group: fruit length, fruit weight and Third group: farmers rating. The participatory diagnostic assessment determined that a total of 15 promising accessions of the four blackberry growers association analyzed should be selected for mass plant tissue culture micropropagation. In addition, on-farm breeding and conservation of crop populations gives value to genetic diversity by maintaining diversity within and among populations. Key Words: *Rubus glaucus*, participatory diagnostic assessment, component and conglomerate analysis.



3326 - Crop Breeding & Genetics

Guilherme da Silva Pereira

ESTIMATION OF GENETIC AND PHENOTYPIC PARAMETERS FOR FRUIT TRAITS IN A FULL-SIB FAMILY OF SWEET PASSION FRUIT USING MIXED MODELS

Pereira,GS; Gazaffi,R; Nunes,ES; Laperuta,LC; Geraldi,IO; Vieira,MLC; Garcia,AAF;

Department of Genetics, "Luiz de Queiroz" College of Agriculture, University of São Paulo, Piracicaba, São Paulo, Brazil;

Sweet passion fruit (*Passiflora alata*) is a tropical outcrossing species native to Brazil. Despite of the increase interest in the crop, there is limited genetic information to establish a breeding program. This study aimed to estimate genetic and phenotypic parameters for fruit traits in a full-sib family of sweet passion fruit in order to select promising genotypes. A population of 100 individuals, derived from a cross of two divergent accessions of sweet passion fruit, was planted in 2008 at two locations (Piracicaba and Descalvado, São Paulo, Brazil), and was evaluated in two harvest years (2009 and 2010) for seven fruit traits. The field experiments were installed as lattice design with two or three replicates. Averages of up to ten fruits per plot were obtained for diameter (DF, in mm), length (LF, in mm) and weight (WF, in g) of fruit, thickness (TS, in mm) and weight (WS, in g) of the shell fruit, and weight (WP, in g) and soluble solid contents (SS, in °Brix) of the pulp fruit. The data were analyzed using mixed models in GenStat 13th edition. Genetic and residual variations were estimated as well as the coefficients of heritability for each trait; the adjusted means were used to obtain phenotypic correlations. A multivariate mixed model was used to rank the genotypes, and the predicted gain was calculated based on selection rate of 30%. Unbalanced data were due to the loss of plots with anthracnose disease in the second harvest year; missing data were 3.2% in 2009 and 48.3% in 2010. Genetic and residual variation ranged from 4.82 (SS) to 20.39 (WS) and from 4.58 (SS) to 23.22 (WP), respectively. Coefficients of heritability were moderate, being the smallest value 0.241 to WP, and the largest 0.543 to WS. In general, the correlations for the six traits (DF, LF, WF, TS, WS and WP) were significantly high, ranging from 0.400 (LF-TS) to 0.984 (WF-WS), with exception to TS-WP (0.219); most of correlations with SS were low and negative. Based on multivariate selection, the expected gain ranged from -0.33% (SS) to 12.40% (WS); however, increase of WS is undesired. For univariate selection in a favorable scenario of SS, the expected gain was 2.70%, while for WS was -0.75%. Breeding programs to improve fruit traits of sweet passion fruit should consider jointly all traits evaluated as well as their correlations. Thus, based on our results, the seven traits used to characterize the full-sib family can be taken in a breeding program for this species.



2840 - Crop Breeding & Genetics

Hatem Mohamed Ali Abd EL-Ghany

EVALUATION OF SOME EXOTIC DURUM WHEAT (TRITICUM DURUM DESF.) GENOTYPES IN EGYPT 2. CORRELATION AND PATH COEFFICIENT ANALYSIS OF GRAIN YIELD RELATED TO YIELD COMPONENTS

Abd El-Ghany,HM; Ibrahim,MM; El-Gharbawy,MM;

National Research Centre; Genetic & Cytology. Dept., National Research Centre, Giza, Egypt; Wheat Res. Dept., Field Crops Res. Instit., Agricultural Research Center, Giza, Egypt;

Two field experiments were carried out at National Research Station, in 2008/2009 and 2009/2010 winter season. Twenty nine genotypes, from 1 to 28 introduced from International Maize and Wheat Improvement Center and local variety (Bani Swef 1) No. 29., Theses genotypes were cultivated in randomized complete block design with three replications and plot size was 10.5 m² (3.5 m.; length and 3 m.; width) to study the relative importance of wheat yield components in so far as they affect grain yield. The average of two seasons was subjected to calculate correlation and path coefficient analysis between grain yield and yield components of 29 bread genotypes wheat. The results revealed that positive and significant correlation was found between flag leaf blade area and No. of leaves / tiller , No. of grains / spike and grain weight / spike, No. of spikelet / spike and grain weight, spike length and grain weight, spike length and No. of spikelets / spike, finally between No. of leaves / tiller and No. of grains / spike. Grain yield was significantly and negatively corrected with to 50% heading. High positive direct effects of grain yield with straw yield, No. of leaves / tiller and with grain weight / spike. Negative direct effects with grain yield showed in No. of grain/ spike, grain index, flag leaf blade area and spike length. Thus selection for grain yield in durum wheat through these characters and its positive correlation, direct and indirect effect with grain yield would be effective.



2909 - Crop Breeding & Genetics

Hee-Jong Koh

QTLs FOR HYBRID FERTILITY AND THEIR ASSOCIATION WITH FEMALE AND MALE STERILITY IN RICE.

Koh, KHJ; Kim, KHY; Reflinur, RB;

Seoul National University;

Hybrid sterility is one of the major barriers to the application of wide crosses in plant breeding and is commonly encountered in crosses between indica and japonica rice varieties. Ten mapping populations comprised of two reciprocal F₂ and eight BC₁F₁ populations generated from the cross between Ilpumbyeo (japonica) and Dasanbyeo (indica) were used to identify QTLs and to interpret the gametophytic factors involved in hybrid fertility or sterility between two subspecies. Frame maps were constructed using a total of 107 and 144 STS markers covering 12 rice chromosomes in two reciprocal F₂ and eight BC₁F₁ populations, respectively. A total of 15 main-effect QTLs and 17 significant digenic-epistatic interactions controlling spikelet fertility (SF) were resolved in the entire genome map of F₂ and BC₁F₁ populations. Among detected QTLs responsible for hybrid fertility, four QTLs, qSF5.1 and qSF5.2 on chromosome 5, qSF6.2 on chromosome 6, and qSF12.2 on chromosome 12, were identified as major QTLs since they were located at corresponding positions in at least three mapping populations. Loci qSF5.1, SF6.1 and qSF6.2 were responsible for both female and male sterility, whereas qSF3.1, qSF7 and qSF12.2 affected the spikelet fertility only through embryonic factors, and qSF9.1 did through pollen factors. Five new QTLs identified in this study will be helpful for understanding the hybrid sterility and for breeding programs via inter-subspecific hybridization. Keywords: rice, hybrid sterility, QTL, digenic-epistatic interaction, gametophytic factors



2869 - Crop Breeding & Genetics

Henrique de Souza Luche

ADAPTIVE TRAITS IN OAT BREEDING IN BRAZIL

Luche,HS; Olivo,M; Nornberg,R; Kavalco,SAF; Tessmann,EW; Santos,RL; Silva,JAG; Maia,LC; Oliveira,CA;

Plant Genomics and Breeding Center at Federal University of Pelotas - CGF/UFPel;

In search of superior genotypes, breeding programs have sought, besides the accumulation of favorable alleles productivity also incorporate improved traits in populations that provide better adaptation to culture conditions, called adaptive traits. These traits, when combined with high yield, tend to form superior genotypes. Therefore, they are often the target of breeding programs. Thus, the objective of this work was to study the performance of Brazilian and exotic oat cultivars released since the 80s till today, on the main adaptive traits and yield. The experiment was conducted in the winter of 2011 in the county of Capão do Leão, Rio Grande do Sul, Brazil. The experimental design used was randomized blocks employing four replications, each experimental unit consisted of an area of 1.2 m². A total of 25 oat cultivars, which were representing 22 Brazilian cultivars that were released from 1981 to 2011, and three exotic cultivars, which were Assiniboia (Canada), Hi-Fi and Leonard (United States). The population density and arrays, as well as cultivation, fertilization, and application of pesticides occurred according to the technical recommendations for the crop. In this study, the variables grain yield (GY in kg ha⁻¹), cycle of the planta (CLE, in days), plant height (PH, in cm), number of fertile tillers per linear meter (NFT, in units) and harvest index (HI, dimensionless) were assessed. After tabulating the data, they were subjected to analysis of variance and mean comparison test of Scott-Knott, with the help of the GENES software. Looking at the yield, it is possible to highlight that Brazilian cultivars released after 2000 tend to have higher values, although some cultivars released before that year also had a great performance. It was also observed that the newer cultivars tend to have smaller PH and CLO, also higher NFT. No pronounced changes were observed for HI, indicating that this variable has taken a lesser importance for breeding programs. The exotic cultivars underperformed for the adaptive traits, however, showed intermediate productivity. Therefore, genetic improvement in oats has changed over time both productivity and adaptive characteristics of the genotypes. Making difficult the direct introduction of alien genotypes because of their lower performance on adaptive traits.



3337 - Crop Breeding & Genetics

Hérika Chagas Madureira

OVERCOMING SELF-INCOMPATIBILITY IN PASSIFLORA EDULIS SIMS BY CHEMICAL TREATMENT OF STIGMAS

Madureira,HCM; Pereira,TNSP; Cunha,MC;

UENF;

The present study focuses on alternative chemical treatments to overcome self-incompatibility (SI) in passion fruit plants (*Passiflora edulis* Sims). In order to evaluate the response suppression of SI, eight treatments of stigma were considered followed by manual pollination. The effects of chemical compounds sodium chloride (5%, 8%, 10%), sucrose (1%, 3%), ammonium sulphate (20%), urea (15%, 20%) in attenuating the response of SI passion fruit, were evaluated by analysis of the growth of pollen tubes in vivo through the pistil previously treated, using fluorescence microscopy. As a control, distilled water was applied on the stigma, and after the same time the flower was self-pollinated. The results obtained indicated that stigmas exposed to chemical compounds before self-pollination, showed different rates of SI suppression. Sucrose 3% and urea 20% treatments were more effective in attenuating of the response of incompatibility. In this cases, it was observed that the incompatible pollen tube was able to growth trough the stigma cells, without being recognized and rejected, reaching the region of the ovary 15 hours after pollination. The ammonium sulfate 20% and sodium chloride solution 10% were less effective, however, also showed positive results. In the cases, although the pollen tubes has been issued in small amounts, were able to achieve the ovary 15 hours after pollination. The other treatments were ineffective. Moreover, in the control treatment, incompatible pollen was unable to perform the ovules fertilization. These results suggest that the SI can be effectively suppressed by chemical treatments during the flowering period. Accordingly, it is possible to obtain genetically homogeneous genotypes with superior agronomic characteristics by using chemical compounds which overcome the SI.



3131 - Crop Breeding & Genetics

João Dimas Garcia Maia

NOVEL CULTIVARS OF BRAZILIAN SEEDLESS GRAPES

Maia,JDG; Camargo,UA; Souza,RT; Quecini,V; Ritschel,P;

Embrapa Grape and Wine, Experimental Station of Tropical Viticulture - EVT;

The problems faced by Brazilian tropical regions grape growers are low fertility, high susceptibility to diseases and berry skin cracking during the rainy season. In order to contribute to solving these problems, Embrapa Grape and Wine has initiated in 1997 a breeding program aiming the development of seedless grape cultivars. The breeding program is based on sexual hybridizations to obtain segregating populations, which undergo several field evaluation and selection cycles, in tropical conditions at the Tropical Viticulture Station, Embrapa Grape and Wine, in Jales, SP. In order to simulate the juvenility period, successive trimming practices during plant formation are carried out to reduce the time necessary to develop a novel cultivar. The basic germplasm stock used for the crosses are *Vitis vinifera* for quality attributes and *V. labrusca*, interspecific hybrids and wild *Vitis* species, mainly *V. shuttleworthii* and *V. gigas*, along with *V. caribaea*, *V. candicans*, *V. smalliana* among others, as source of genes for adaptation and fungal diseases resistance. Forty to 50 progenitor combinations are performed yearly according to the demands from viticulturists. Six weeks after the hybridizations, embryo rescue and regeneration is performed at the Plant Tissue Culture Laboratory. Approximately 1,000 hybrids of seedless grapes are evaluated per year and selected to further evaluation, when meeting the planned goals for each specific progenitor combination. Subsequently, the selected plants are submitted to progressively more strict selection during 6-7 cycles. The final evaluation step consists in semi-commercial scale testing, in growers' vineyards, to evaluate the material adaptation and acceptability by the market. Approved cultivars are released and made available to viticulturists. Cultivars 'BRS Clara', 'BRS Morena' and 'BRS Linda', released in 2003, exhibit firm berry consistency, high fertility and precocious cycle. In 2010, validation tests of 15 novel selections of seedless grape material under subtropical and tropical climate were initiated. The selections display high fertility, berries with strong cluster adherence, firm texture, adequate size and high sugar contents. From those, three selections are tolerant to mildew, the main grapevine disease in Brazil. Two novel seedless grape cultivars for tropical and subtropical conditions in Brazil will be released by Embrapa Grape and Wine breeding program, until 2015.



2758 - Crop Breeding & Genetics

Julia Lambret Frotté Silva

ISOLATION AND EXPRESSION PATTERN CHARACTERIZATION OF TWO COTTON (*GOSSYPIUM HIRSUTUM*) FLOWER-SPECIFIC PROMOTERS

Lambret-Frotté,JS; Artico,S; Nardeli,SM; Grossi-Sa,F; Alves-Ferreira,M;

UFRJ;

Cotton boll weevil (*A. grandis*) is the main devastating pest on cotton (*G. hirsutum*) crops in Brazil, it attacks the cotton fruit and the flower buds causing its fall. Losses can reach 75%. Due to the problems to control the boll weevil by conventional methods the alternative would be the development of a GM plant expressing the Cry protein. Although, the available promoters in cotton triggers ectopic expression of the Cry protein, which has a high cost to the plant metabolism and can also impact non-target species. Since the boll weevil attacks mainly flowers buds, the main goal of our research is to identify and characterize the upstream sequences of flower-specific genes that are good candidates to be used as regulatory region of Cry expression in cotton. In silico analysis identified 2 genes, named GhPGFS2 and GhPGFS3 with putative flower and fruit specific expression. Experiments of qPCR were conducted to better characterize their expression pattern. Promoter isolation was made through genome walking and characterization was performed using 3'Racer and in silico tools to identify putative cis elements and TIS. Three promoter deletions of GhPGFS2 and GhPGFS3 were fused to the reporter gene uidA (GUS). Both, transient transformation of *G. hirsutum* flower buds and stable transformation of *A. thaliana* were performed to evaluate the activity of the promoter fragments. Colorimetric assays and also fluorimetric and qPCR analyses were conducted to characterize in vivo expression pattern of the promoter regions. qPCR analysis of GhPGFS2 gene during *G. hirsutum* reproductive development showed a high expression in flower while GhPGFS3 is expressed also in fruits. Both genes have a high expression in stamens and petals. GhPGFS2 has the higher expression in 6mm flower buds whereas GhPGFS3 has also a high expression at 2 and 4 mm stages. GhPGFS3 expression is constant during fruit development. The promoter region of GhPGFS2 e GhPGFS3 revealed several putative cis regulatory elements related to flower and fruit specific expression. All 6 transient transformations of *G. hirsutum* flower buds show GUS staining mainly on stamen and pollen. *A. thaliana* harboring the 351bp fragment of GhPGFS2 present GUS staining on stamens at late stage of flower development, confirmed by quantitative assays. Our results show that the regulatory regions of GhPGFS2 and GhPGFS3 may be used as biotechnological tools, when associated with genes encoding toxic proteins, against *A. grandis*.



3216 - Crop Breeding & Genetics
Karina Elizabeth D'Andrea

GENETIC VARIATION IN A MAIZE POPULATION OF RILS: II- HERITABILITY STUDY OF THE ECO-PHYSIOLOGICAL DETERMINANTS OF KERNEL WEIGHT.

Piedra,C; Bender,R; Dandrea,K; Cerri,A; Cirilo,A; Otegui,M;

FAUBA-IFEVA-CONICET;

In maize (*Zea mays* L.), final kernel weight (KW) is determined by the rate (KGR) and the duration (KFD) of grain filling. The genetic control of these traits is currently unknown. The aim of this work was to study the genotypic variation in final KW and its physiological determinants, KGR and KFD during the active grain-filling period. We phenotyped these traits for a collection of 180 recombinant inbred lines (RILs) derived from two contrasting parental inbreds (B100: American semident; LP2: Argentine flint). The collection, both parents and a tester line were grown under irrigation during two seasons (Exp.1: 2009-2010, Exp.2: 2011-2012). The experimental layout was always a completely randomized block design with two replicates. At the start of silking, a total of eight plants were tagged in each plot. Silking date was registered for each tagged plant. Apical ears of these plants were collected on 18, 23, 28, 33, 38, 43, 48 and 53 days after silking, and 15 grains were sampled from each ear at the position 10 from the bottommost spikelet. Grains were oven dried and weighed for the determination of KW. Significant genotypic variation ($p < 0.001$). For tested environments, grain yield was strongly associated with kernel number and to a less extent with KW. Therefore, inbreds with highest KW were not among those that reached highest grain yields. Nevertheless, we identified some inbreds that combined high kernel numbers and high KW (i.e., within the uppermost quartile of grain yield). The selection of these inbreds would allow for the improvement of both grain yield components simultaneously, avoiding the apparent trade-off between them. The observed phenotypic variation in this mapping population will be used for the detection of candidate QTLs that control final KW.



3292 - Crop Breeding & Genetics

Karine Chenu

LARGE-SCALE CHARACTERIZATION OF DROUGHT PATTERN: CURRENT AND FUTURE TRENDS IN THE AUSTRALIAN WHEATBELT

Chenu,K; Chapman,SC;

The University of Queensland - QAAFI;

Drought frequently limits Australian wheat production and the expected future increase in extreme temperatures and rainfall variability will further challenge productivity. A modelling approach captured plant x environment x management interactions to simulate drought patterns experienced by wheat crops for representative locations and managements across the wheatbelt. Simulations were performed for 123 years of 'current' climate (1889-2011) and eight future climatic scenarios for 2030 and 2050, accounting for predicted shifts in sowing dates and soil water content at sowing. Across the wheatbelt, four main drought-environment types have been identified for the 'current' climates, ranging from stress-free/light-stress to severe stress with terminal drought. The frequency of occurrence of these environment types greatly varied across seasons and locations, and these variations tended to accentuate in future climate. For 2030, frequency of the most-severe (terminal) drought type was predicted to increase by 10 to 77% on average across the wheatbelt for the studied future climatic scenarios, with some high spatial variability among regions. While the Wet & Low emission scenario had no substantial impact on drought frequency in most regions, the Dry & High emission scenario more than doubled severe-drought frequency in several regions and substantially impacted the others (>25% increase). The characterisation performed here is proposed as a tool for breeders and agronomists to better understand the current and future targeted environments. It can also assist in design and analysis of trials and in evaluation of the relevance of multi-environment trials. Further study is needed to assess alternative options (genotype and management) to reduce future drought impact, in particular for the Dry & High emission scenario.



2828 - Crop Breeding & Genetics

Katharina Schneebeil

INVESTIGATING DIFFERENCES IN RESPONSE TO RHIZOCTONIA SOLANI AG 8 IN THE DIVERSE WILD BRACHYPODIUM DISTACHYON POPULATION TO DISCOVER MECHANISMS FOR RESISTANCE TO RHIZOCTONIA ROOT ROT IN WHEAT.

Schneebeil,K; Chochois,V; Mathesius,U; Watt,M;

CSIRO Plant Industry;

Many agricultural soils have pathogens that can severely reduce root length and function. Crops require healthy root systems to access water and nutrients to maximise yield, especially in drought-prone and nutrient-poor conditions. Few resistance and tolerance mechanisms have been discovered for root diseases. The aim of this project is to discover mechanisms for resistance to Rhizoctonia root rot in wheat using the new model Brachypodium distachyon. Rhizoctonia solani AG 8 is the causal pathogen of Rhizoctonia root rot, producing 'bare patches' of severely stunted plants in the field. Control of the fungal disease is difficult, particularly as there is no effective genetic resistance available in commercial wheat cultivars. During root invasion R. solani AG 8 secretes an extensive range of enzymes, however specific requirements for pathogenesis are not yet clearly understood. Brachypodium is used in our laboratory as a model plant to study root development of bread wheat, as the two species are closely related. There has been a rapid increase in the use of Brachypodium as a research tool, with the genome sequence published in 2010. Diverse wild accessions are being resequenced and resources including T-DNA insertion lines and recombinant inbred lines have been developed. Brachypodium wild accessions exhibit genetic diversity for resistance to several biotrophic foliar pathogens. With shorter root and shoot growth than wheat, Brachypodium is particularly suitable for studying root traits, allowing disease progression to be studied further into plant development in controlled environment assays. We developed a screening method to compare host-pathogen interaction between Brachypodium accessions in response to R. solani AG 8. Root length and leaf measurements at harvest are used to determine disease severity and the ability of plants to resist infection. A toothpick bait is used to check for the presence of inoculum and contamination between pots. Our results show that Brachypodium and wheat develop a similar disease phenotype and severity in response to R. solani AG 8. The diversity in the available Brachypodium germplasm and its susceptibility to the disease make it a useful model plant to study resistance mechanisms for root rot in wheat. Variation in response to R. solani AG 8 identified among wild Brachypodium accessions is being further investigated. The goal is to identify disease resistance mechanisms in Brachypodium that may also be present in wheat.



3271 - Crop Breeding & Genetics

Liu Luxiang

Agronomic Traits and Photosynthetic Characteristics of the Chlorophyll-Deficient Wheat Mutant Mt6172 Derived from Spaceflight Mutagenesis

Guo,HJ; Zhao,HB; Zhao,LS; Gu,JY; Zhao,SR; Li,JH; Liu,LX;

Institute of Crop Science, Chinese Academy of Agricultural Sciences /National Center of Space Mutagenesis for Crop Improvement /National Key Facility for Crop Gene Resources and Genetic Improvement;

Identification of new chlorophyll-deficient mutants will provide materials for studying signaling components and pathways between plastid and nucleus. A novel chlorophyll-deficient mutant, named Mt6172, was obtained by spaceflight mutagenesis. Preliminary genetic analysis showed that the mutated leaf color trait was controlled by recessive nuclear and cytoplasmic genes. Leaf color of its self-fertilized progenies was always composed of albino, narrow-white striped and green. Only a few cells with abnormal chloroplasts were observed in albino plants and white section of narrow-white striped plants. These chloroplasts had obvious flaws in inner structure, and granum lamellae was extremely disordered. The narrow-white striped plants were characterized with green-and-narrow-white striped leaves, and the width of stripes between different plants was even, their plant height, number of productive tillers, and 1 000-grain weight were lower than those of the wild type. The narrow-white striped plants and the wild type had significant difference in the value of potential activity of photosystem II at all tested stages. At elongation stage, which was impacted the most seriously, effective quantum yield significantly decreased, whereas the energy for photoprotection and photodamage significantly increased. Under different photosynthetic active radiation conditions, changes of electron transport rate, photochemical dissipation, and effective quantum yield were different, electron transport rate was more impacted than other parameters. It was concluded that the leaf morphology and inheritance of mutant Mt6172 was different from the other reported mutants in wheat. Genomic and proteomic characterization for the mutant Mt6172 and its wild type H6172 are in progress.

Correspondence E-mail: luxiang@263.net.cn?. This work was funded by National 863 Program (2012AA100402), National Key Technology R & D Program (2009BAA24B05) of China and International Atomic Energy Agency project (CRP14195 and RAS5056).



3247 - Crop Breeding & Genetics

Maico Savoldi

VIABILITY OF TOTAL POLLEN IN POTATO DIPLOID CLONES AND FREQUENCY OF 2N POLLEN AFTER COLD STORE

Savoldi,M; Bock,JL; Almeida,N; Suzin,M; Augustin,L;

Universidade de Passo Fundo - UPF;

Potato wild diploid species are source of useful genes that can be transferred into tetraploid cultivated potato through interspecific crosses. This scheme 4x-2x depends on non-reduced gametes formation (2n pollen) in diploid species. This study aimed check the 2n pollen frequency, the total pollen viability and fertility, after cold store, in two potato diploid clones (DLB1-140 and DLB1-150). Viability analyses were performed with fresh pollen and stored pollen for 3, 6 and 33 months, using the method of acetic carmine coloration. In vitro germination tests were carried out to determine the fertility of fresh and 33 months stored pollen. To analysis pollen viability it was prepared 4 slides of each clone. One thousand pollen grains were analyzed in each slide considering: a) normal (viable) pollen, those showing well stained and intact; b) 2n pollen, those showing diameter above 20 μ m. The data obtained were submitted to ANOVA and the averages compared by Duncan 5%. The time of store influenced the normal and 2n pollen viability. The highest frequency of normal pollen was obtained from 33 months storage (67.5%) and the less with fresh pollen (50.02%), which could suggest inadequacy of the coloration test applied. The 2n pollen frequency was greater in fresh pollen (31.95%) and smaller at 33 months (13.06%). For in vitro fertility test, pollen of two clones were germinated in slides containing two drops of culture medium described by Brewbaker and Kwack (1963). Four slides of each clone were placed in moisture chamber and incubated at 25°C, in the light, for 18 hours and after analyzed in optical microscope with 5x increased. It was photographed four fields of each slide to count the germinated pollen (with emission of the pollen tube) and non germinated. At 33 months no pollen germination was observed in any clones. It was observed in fresh pollen a greater germination percentage in DLB1-150 (31.07%) clone against DLB1-140 (29.39%) clone. According to literature, coloration tests can overestimate viable pollen percentage, that has been confirmed in this study, since no pollen germination of DLB1-140 and DLB1-150 clones was observed after 33 months cold storage. Further studies are required to check how long the pollen stays viable without reduction of 2n pollen frequency after store.



3333 - Crop Breeding & Genetics

Marcio Andrei Capelin

ESTIMATES GENETIC AND GENERAL COMBINING ABILITY OF YIELD IN SEGREGATING POPULATIONS OF SPRING WHEAT

Capelin,MA; Hagemann,TR; Munaro,LB; Sassi,LHS; Dalló,SC; Oliveira,L;
Benin,G; Costa-Oliveira,A;

Universidade Tecnológica Federal do Paraná;

Diallel crosses generate information on the genetic correlates of the traits evaluated and assess the combining ability of genitors and segregating populations (Iqbal et al. 2007). The objective of this study was to evaluate general combining ability (GCA) and specific combining ability (SCA), in generations F1 and F2 in a full diallel cross of wheat for grain yield per plant. Eight wheat cultivars (1 - BRS Tangará, 2 - BRS Guamirim, 3 - Fundacep Cristalino, 4 - Quartzo, 5 - Mirante, 6 - Vaqueano, 7 - CD 114 and 8 - CD 117), were crossed in diallel form without reciprocals, totaling 28 hybrids combinations. In 2010 crop season, the hybrids F1 and F2 and their parents were sown in the field in a randomized block design with three replications. Grain yield per plant (GYP) was evaluated. The data were submitted to diallelic analysis according the methodology proposed by Griffing (1956), using the Genes statistical software (Cruz, 2006). The graph with best crosses was constructed using the GGE Biplot software (Yan et al., 2001). BRS Guamirim (1.36) and Vaqueano parents (1.90) showed the highest values of GCA respectively in F1 and F2 generations (Table 1), suggesting that effective selection of promising hybrids could be performed efficiently based on GCA effects (Gowda et al., 2010). The estimations of the best crosses of the F1 and F2 generations are presented on the Figure 1. Genotypes that are the furthest away from the origin are connected with straight lines forming a polygon, leaving the labels of the other genotypes within the polygon. Genotypes that are perpendicular on the sides of the polygon divide biplot into several sectors, with every tester belonging to one sector. All testers within a sector produce the best cross for de grain yield with a common genotype (Yan et al., 2000). This analysis explained 64.3% and 81.6% of the total variation respectively F1 and F2 generations. In F1 generation, Quartzo parent shows the best results when crossed with testers Vaqueano, whereas Mirante combines best with testers BRS Guamirim and F. Cristalino. However in the generation F2 the best crosses were Quartzo x BRS Guamirim, Quartzo x F. Cristalino. Similar results in diallel crosses were reported by Yan & Hunt,(2002) and Bo?anski, et al., (2011).



3341 - Crop Breeding & Genetics

Maria Elena Otegui

GENOTYPIC VARIATION FOR BRITTLE-SNAP SUSCEPTIBILITY IN MAIZE (ZEA MAYS L.): PHENOTYPING OF STALK BREAKAGE AND RELATED TRAITS IN A RILS POPULATION

Rodriguez,JG; Kussrow,N; Pirchi,IL; Cirilo,AG; Cerri,AM; Otegui,ME;

UNNOBA;

Winds stronger than 45 m s⁻¹ are known to cause severe brittle-snap of maize (*Zea mays* L.), with stalks breaking near the uppermost ear node, particularly in crops undergoing active stem elongation immediately before anthesis. Early studies on this trait focused on genotypic variation among commercial hybrids and the effect of management practices. They concluded that the best strategy is to plant hybrids less prone to breakage, but breeding against this constraint is limited by the lack of accurate methods for simulating brittle-snap. The aim of this work was to study the genotypic variation in maize susceptibility to stalk breakage. Primarily, for providing robust data for QTL analysis, and additionally for evaluating its relationship with several morphometric traits. These traits were plant height to the uppermost ear and to the uppermost collar, estimated stem volume at ear and uppermost collar heights, and stalk diameter at ground level. We phenotyped mentioned traits for a collection of 180 recombinant inbred lines (RILs) derived from two contrasting parental inbreds (B100: American semident; LP2: Argentine flint). Inbreds were sown in the field at three different sowing dates (14, 18 and 23 Nov, 2011) for avoiding the confounded effect of their variation in time to anthesis (surveyed during 2009-2010). The experimental layout was a completely randomized block design with two replicates. Stand density was 7 plants m⁻², and plots had 10.5 m². A severe wind storm (winds > 45 m s⁻¹) took place on 23-Jan-2012. It was immediately before anthesis of the experiment, which spanned between 24-Jan and 7-Feb. Stalk breakage ranged between 0 (28% of inbreds) and >50% damage (1.1% of inbreds, with maximum of 55.6%), it was not normally distributed.



6th International Crop Science Congress

August 6th to 10th, 2012

Fundaparque Event Center
Bento Gonçalves - RS - Brazil

3174 - Crop Breeding & Genetics

Om Parkash Yadav

ENHANCING CROP PRODUCTIVITY IN SEVERELY WATER-LIMITED ENVIRONMENTS ? AN EXAMPLE OF PEARL MILLET IMPROVEMENT IN INDIA

Yadav, OP;

All India Coordinated Pearl Millet Improvement Project, Jodhpur 342 304, Rajasthan, India;



3132 - Crop Breeding & Genetics

Patricia Ritschel

NOVEL BRAZILIAN GRAPE CULTIVARS FOR JUICE PROCESSING

Ritschel,P; Camargo,UA; Maia,JGG; Zanús,MC;

Embrapa Grape and Wine;

In recent years, the marketing of grape juice has increased 117%. The production is mainly located in Southern Brazil, with a strong trend of expansion towards tropical areas recently. The traditional group of cultivars used by the grape juice industry, consisting of 'Isabella', 'Concord' and 'Bordô' ('Ives'), can be complemented by the development of novel cultivars exhibiting higher sugar contents, intense violet color, wide adaptation range and distinct phenology. In Brazil, genetic breeding aiming to develop novel grape cultivars for juice production is based on the diversity maintained at the Grapevine Germplasm Bank, constituted of approximately 1000 accessions that have been characterized and evaluated for the most important agronomical and industrial traits, such as disease responses and must features. The program employs sexual hybridizations, followed by evaluation and field selection cycles, along with clonal selection. During the final steps of developing novel cultivars, advanced selections are tested in semi-commercial scale, under real production conditions, and the agronomical characteristics and the features of the juice elaborated from the potential cultivar are evaluated, alongside with growers. In the last years, a group of grape cultivars for juice elaboration ('BRS Rúbea', 'Concord Clone 30', 'Isabel Precoce', 'BRS Cora', 'BRS Violeta' and 'BRS Carmem'), exhibiting distinct productive cycles or noteworthy contents of colored compounds, high sugar contents and suitable aroma and flavor, have been developed and released by the Grapevine Breeding Program. Further information on the cultivars is available on the open-access Embrapa Grape and Wine website. Four novel advanced selections for grape juice elaboration are under validation in partnership production sites in the states of Mato Grosso, Pernambuco, and Rio Grande do Sul. In general, the novel genetic material display one or more of the following traits: rusticity, wide adaptation, intense violet color, high glucometric potential and high contents of health-related compounds (anthocyanins and total phenolic compounds) and distinct growth cycles. At least two novel cultivars for grape juice elaboration will be released in the near future. They will add and complement the group of traditional varieties available to Brazilian producers, increasing and diversifying the options of grape cultivars for the juice industry.



3114 - Crop Breeding & Genetics

Patricia Ritschel

NOVEL GRAPE CULTIVARS ADAPTED TO BRAZILIAN GROWTH CONDITIONS SUITABLE FOR QUALITY-WINE PRODUCTION

Ritschel,P; Almeida-Camargo,UAC; Garcia-Maia,JD; Zanús,MC; Guerra,CC;

Embrapa Grape and Wine;

Embrapa Grapevine Breeding Program aims to develop disease resistant, productive and widely adapted interspecific hybrid cultivars for wine-making, exhibiting organoleptic characteristics similar to those of *Vitis vinifera* grapes. Varieties with these features will be, in the future, the basis for the development of organic wine production. The breeding program is based on sexual hybridizations to obtain segregating populations, submitted to field evaluation and selection cycles. During the final stage of the program, the selections are tested in semi-commercial scale, under real production conditions; and the agronomic performance and the characteristics of the wine made from the potential cultivar are evaluated, alongside by breeders, growers, winemakers and enologists. The basic germplasm used in the crosses consist of *V. vinifera* cultivars, to provide quality attributes, and *V. labrusca*, interspecific hybrids and wild species of *Vitis* as sources of adaptative traits and resistance to fungal diseases. In recent years, three novel grape varieties for wine making ('Moscató Embrapa', 'BRS Lorena' and 'BRS Margot') were developed and released by the Grapevine Breeding Program. They are hybrid grapes whose wine refers to the product made with *V. vinifera* grapes. Further information on the cultivars is available on the open-access Embrapa Grape and Wine website. Three advanced selections of white grapes with muscat flavor are under development by the Breeding Program, in recent years. Agronomically, the selections display high productivity and good disease tolerance. Sensorial analysis of the wine obtained by microvinifications of berries from the advanced selections resulted in a final product with appropriate color, aroma and flavor. The taste analysis highlighted the predominance of muscat aroma, with subtle fruity and herbaceous ones, lacking the bitter flavor or taste. The elaborated wines are similar to *V. vinifera* wines. The advanced selections for wine-making are under validation in partnership with growers from the states of Rio Grande do Sul and Goiás. Conclusions Partial results of grapevine plant performance under field conditions (yield, adaptation, disease resistance and maturation indices), chemical analysis and sensory features of the wine, during the last three growing seasons, suggest that, at least, one novel Brazilian grapevine cultivar for wine elaboration, exhibiting muscat flavor, will be released in the near future.



3080 - Crop Breeding & Genetics

Paula Wietholter

IDENTIFICATION OF QTL ASSOCIATED WITH TASSEL AND FLOWERING TRAITS IN CORN

Wietholter,P; Terra,TF; Fuller,TN; Rodrigues,JA; Tessele,C; Sereno,MJCM; Barbosa-Neto,JA;

Embrapa Trigo / Faculdade Meridional - IMED;

Most corn presently cultivated in the world are hybrids. The chances to introduce genetic variability in this material are small due to market requirements in terms of productivity. For this reason corn breeders in general use their own elite germoplasm as source of genetic variability, maintaining therefore the standard characteristics of their population. However, the variability of these genotypes might be insufficient, requiring the use of germoplasm from different locations that often do not have wide environment adaptation. The landraces, besides being rich in genetic variability, are naturally adapted to their sites of origin. The disadvantage of these materials is that they are agronomically inferior, limiting their direct use as commercial varieties or as germplasm source. For this reason one of the main challenges of genetic breeding has been to create strategies that allow a rapid and efficient incorporation of variability in elite materials. In corn the main agronomic characters are of quantitative nature. The QTL identification may help breeders to check the introgression of superior alleles in elite materials. The objective of this study was to identify quantitative trait loci (QTL) associated with tassels and flowering traits in maize. Two backcrosses and two self-fertilization cycles were carried out after crossing the elite line LA67 with the Argentino Flint landrace. The progeny was genotyped with 177 microsatellites loci and phenotyped for length of the tassel of the main stem, length of the secondary stem of the first lateral branch of the tassel, total number of stems of the tassel, tassel emergence days, silking days, pollen shedding date and flowering interval (days). The phenotypic traits significant at 5% probability in the analysis of variance were selected for the simple linear regression analysis with molecular markers. Among all the microsatellite loci tested, only 34 showed polymorphism. The total number of stems of the tassel, silking days, pollen shedding date and flowering interval traits were significant in the analysis of variance. Three QTL for total number of stems of the tassel accounted between 4 and 26% of the phenotypic variation. Two QTL for pollen shedding accounted approximately for 13% of the phenotypic variation. The use of these markers flanking the QTL of major effects may represent a strategy for introgression of superior alleles for landraces in elite maize materials.



3377 - Crop Breeding & Genetics

Paulo Ricardo Reis Fagundes

REACTION OF IRRIGATED RICE GENOTYPES TO BIOLOGICAL NITROGEN FIXATION

Fagundes,PRR; Mattos,MLT; Magalhães-Júnior,AM; Severo,ACM; Azambuja,VV; Krunt-Júnior,E;

Embrapa Temperate Climate Center;

Nitrogen (N) is an indispensable element to synthesis of proteins and essential enzymes for plant metabolism and life. This mineral participates in numerous biochemical processes in soil-plant system. In addition to high cost from economics and environmental aspects, this can be easily lost by leaching in the form of nitrate (NO₃-), due to volatilization as ammonium (NH₃) or denitrification. The replacement of artificial inputs by natural inputs with lower cost of production and conservation of natural resources, is a worldwide trend. In last decades, a considerable amount of information was published on diazotrophic bacteria, indicating the possibility of using it as biological input. The ability of this bacteria to colonize and transfer fixed nitrogen in symbiosis with plants of rice, as well as the occurrence and understanding of the mechanisms of interaction plant/microorganism/environment and the existence of genetic variability in both the microorganism and potentially nitrogen-fixing genotypes rice, have been widely demonstrated and discussed. However, biological nitrogen fixation (BNF) in different cultures is dependent on a complex interaction between plants, microorganisms and the ecosystems. In the subtropical lowlands in Rio Grande do Sul (RS) State, colonies of aerobic diazotrophic endophytic) bacteria (DEB) with potential for BNF were isolated from leaves, stems and roots of BRS-7 "Taim" and BRS Pelota cultivars. In the season 2010/11 a study was conducted at the Lowland Experimental Station of Embrapa Temperate Climate, located at the city of Capão do Leão, RS. In this study were evaluated 78 genotypes from Embrapa rice breeding program with and without inoculation with DEB. The variables analyzed were the chlorophylla real index (CRI) and dry matter of stalks (DM/S). The results shown that inoculation of genotypes with DEB promoted an increase of approximately 12% in CRI and 14% in dry matter yield of stalks. There was also a positive trend for the differential response of genotypes, especially strains AB10005, AB09021, AB09006, AB09002 and AB09044, in which the inoculated plants shown CRI and DM/S higher than the best control (commercial cultivar BRS 7 "Taim").



12058 - Crop Breeding & Genetics

Qifa Zhang

RICE BIOTECHNOLOGY: HOW CAN WE FEED THE BILLIONS?

Zhang,Q;

National Key Laboratory of Crop Genetic Improvement, Huazhong Agricultural University;

Rice is the main staple food for a large segment of the world population. In the last half century, rice yield has undergone two big leaps, primarily as the result of genetic improvement: increasing harvest index by reducing plant height making use of the semidwarf gene and utilization of heterosis by producing hybrids. Consequently, rice yield has more than doubled in most parts of the world and even tripled in certain countries. However, rice production is facing even greater challenges in the next half a century because of high demands in both quantity and quality, and ever increasing pressures on resources and environments. At the same time, advances in genomics, biotechnology and genetic studies have brought about unprecedented opportunities for crop genetic improvement. In my presentation, I will address the main issues that we have encountered as challenges, describe the demands for increased production for future needs, present current understanding on the progress in the researches in relevant areas, and provide prospect how the advance in research can be translated into technologies and activities for rice genetic improvement.



3344 - Crop Breeding & Genetics

Rafael Nornberg

ESTIMATE OF HETEROSIS AND INBREEDING DEPRESSION FOR CHARACTER FALLING NUMBER WET IN WHEAT

Nornberg,R; Luche,HS; Tessmann,EW; Olivo,M; Zimmer,CM; Figueiredo,R; Maia,LC; Costadeoliveira,A;

Plant Genomics and Breeding Center at Federal University of Pelotas;

The pre-harvest sprouting (PHS) detracts from the quality of wheat flour, enzymes responsible for the germination, which degrade the starch. Evaluation of Falling Number Wet (FNW) has been a measure of the activity of the enzyme alpha-amylase, and expresses the intensity of germination of wheat grains. Therefore, the importance of elucidating the contribution of the hybrids and understanding the effects of inbreeding in the selection process. So, the objective of this study was to estimate heterosis, inbreeding depression and indicate the best combinations. In 2010 hybridizations were performed, with the parents: BRS 220, MARFIM, SUPERA, VALENTE, BRS 194, FRONTANA, ITAIPU and QUARTZO. In the cold season of 2011, the experiment was conducted on the experimental field of the Plant Genomics and Breeding Center at Federal University of Pelotas (CGF/UFPel) located in the city of Capão do Leão. The FNW was measured in seconds for parents, F1 and F2 generations and their reciprocal randomized block design with three replications. The spikes were placed immersed in distilled water for two hours, and rolled in germination paper, moistened with distilled water and placed for incubate for three days at $25^{\circ}\text{C} \pm 1^{\circ}\text{C}$ in a germination chamber. After this period were placed to dry in an oven at 50°C for 72h, with the end of drying the threshing was done and the grains were ground to produce whole-wheat flour. The falling number wet was evaluated with an automatic apparatus falling number of Hagberg mark PERTEN 1500. The analysis of variance was performed on software GENES and heterosis, inbred depressions were calculated. Significant differences were evidenced in both generations. The populations evaluated presented results of heterosis and inbreeding depression for character variables. The verification of crosses with heterosis of high magnitude significant positive allows its recommendation for use in breeding programs, with this, the populations of combinations MARFIM x FRONTANA, MARFIM x ITAIPU and their reciprocal, with high heterosis for falling number wet have the specific combinations transgressives, and may be recommended to increase the falling number, and decreased activity of the enzyme alpha-amylase in wheat grains. High estimates of heterosis and reduced inbred depressions are observed for the falling number in these populations and have potential sources of recovery of individuals higher. It has pronounced effect reciprocal, which should be considered.



2832 - Crop Breeding & Genetics

Ram Chandra Sharma

RELATIONSHIP BETWEEN NORMALIZED DIFFERENCE VEGETATION INDEX (NDVI) AND GRAIN YIELD IN WINTER WHEAT UNDER TERMINAL HEAT STRESS

Sharma,R; Hazratkulova,S; Alikulov,S; Yuldashev,T; Khalikulov,Z; Ziyadullaev,Z; Turok,J;

ICARDA-Central Asia and the Caucasus Regional Program;

Heat stress during grain-filling period is an important constraint to wheat (*Triticum aestivum* L.) production in Central Asia. The normalized difference vegetation index (NDVI), defined as the ratio of the difference between near-infrared and the red bands to the sum of the two bands, is a measure of greenness. It is used to assess the effect that factors have in limiting plant growth, including growth stage, genotype, and environmental stress. A study was conducted to determine genotypic variation for NDVI and its relationship to grain yield winter wheat. A set of genetically diverse 30 winter wheat genotypes was included in the study. The field experiments were conducted at two locations (Kibray and Karshi) in 2010 and 2011 in Uzbekistan. NDVI was measured at booting, heading, milk and dough stages. Average maximum temperatures at the two sites in the two years were between 28.8 and 32.9°C in May and 35.3 and 38.8°C in June. Wheat genotypes differed significantly for NDVI at each growth stage. Mean NDVI values ranged from 0.76 to 0.82, 0.73 to 0.80, 0.64 to 0.73 and 0.47 to 0.67 during booting, heading, milk and dough stage, respectively. Mean grain yield varied between 3.95 and 6.13 t ha⁻¹. All genotypes showed a decline in NDVI from booting to dough stage with mean reductions ranging from 15 to 41%. However, several high-yielding genotypes maintained relatively higher NDVI than the low yielding genotypes when heat stress was evident due to high temperatures during the grain-filling period. The genotypes with low reductions in NDVI that possessed high grain yield were 'Gozgon' (15% reduction in NDVI and 5.95 t ha⁻¹ yield), Kuyalnik (19% reduction in NDVI and 5.57 t ha⁻¹ yield), 'Elomon' (20% reduction in NDVI and 6.13% yield), 'Kiryas' (21% reduction in NDVI and 5.54 t ha⁻¹ yield) and MV17-3/Croc-1/Ae. squarrosa (205)//Kauz' (22% reduction in NDVI and 5.69 t ha⁻¹ yield). NDVI showed a significant positive correlation coefficient ($r = 0.62$ to 0.78 , p) with grain yield at milk and dough stage. The correlation coefficients were higher in the warmer year 2011 compared to 2010. Regression analysis showed that more than 60% of the grain yield variability could be estimated on the basis of NDVI values at the milk and dough stages. The results suggest that relatively higher NDVI could be a measure of genotypic tolerance to heat at terminal growth stages, which could be used as an indirect selection criterion for identifying high-yielding wheat genotypes.



3379 - Crop Breeding & Genetics

RAQUEL DALLA LANA CARDOSO

ARTIFICIAL HYBRIDIZATION IN GÉRBERA: SEED FORMATION AND SEGREGATION OF THE OBTAINED PROGENY

Cardoso,RDL; Milach,SCK; Grando,MF; Augustin,L; Susin,M; Scorteganha,A; Machado,C;

IFRS Campus Ibirubá/ UPF; IFRS Campus Ibirubá/ UPF;

To provide subsidies for the gerbera breeding, this study had as aim: evaluated the occurrence of self-incompatibility and incompatibility in gerbera, and analyze segregation and inheritance of vegetative and morphological capitulum character that are commercially important, and access the combining ability of crosses to produce seeds. To evaluate the self-incompatibility occurrence, capitulum of cv. Green White Center, A8 e A7, were pollinated with pollen of the same plant evaluating the seed production. In order to verify the incompatibility and maternal and paternal effect on seed production, two different set crossing carried out, one testing the paternal parents (A7, A8 and the cvs. Ave Maria, Chili Pepper, Dream, Essandre, Feria, GWC, Isimar and Opium), and other the maternal effects using GWC and a non commercial access A8 as mother. The general and specific ability for seed production were checked using a diallel between the genotypes GWC, A8 e A8. The seeds were germinated and evaluated at nine months for vegetative and morphological capitulum characters. Herdability was estimate in the broad sense based on the environmental variance. It was confirmed the occurrence of geitonogamy, self-incompatibility absence and the inhibition of self-pollination within the chapter is due to protogyny. The general and specific combining ability to seed production did not have statistical significance due the high coefficient of variation of the experiment. The heritability estimates were moderate to high. The variability observed in the progeny obtained to vegetative plant character and in the capitulum character, confirms that the progenies from performed crosses is not originating from self-cross. It is possible to perform hybridization and generate fertile seeds and progenies of gerbera by both, inbreeding and outbreeding, to develop new materials in gerbera breeding.



3075 - Crop Breeding & Genetics

Ricardo Lima de Castro

PERFORMANCE SCORE AS A TOOL FOR CHOICE AND SELECTION OF WHEAT CULTIVARS

Castro,RL; Caierão,E; Silva,MS; Scheeren,PL; Cargnin,A; Moresco,ER;
Guarienti,EM; Miranda,MZ;

Embrapa Trigo;

About 80% of the wheat produced in Brazil is used for domestic and industrial products such as bread and pasta which requires gluten strength above 220×10^{-4} J. The remaining 20%, with gluten strength lower than 220×10^{-4} J, is used for baking cakes, biscuits and confectionery products in general. The technological quality requirements are decisive on wheat grain sales, which associated to grain yield define the suitability of cultivars for farmers. This work proposes the use of a performance score (EF) based on the average of grain yield (EP) and technological quality parameters (EQ) to rank wheat cultivars in the state of Rio Grande do Sul, Brazil: $EF = (EP \times 0.5) + (EQ \times 0.5)$. Because both factors are economically important it was given an equal weight to EP and EQ. In addition, there is no market for cultivars with high grain yield and low quality requirements or cultivars with quality requirements and lower grain yield. EP scores range from 0 to 10, ranked according to the grain yield percentage relatively to the best control, as follows: below 70%, scores zero, while above 110%, scores 10. For relatively grain yield values between 70% and 110%, every 1% is equivalent to 0.25 on the EP score. EQ is based on the gluten strength (W), tenacity /extensibility ratio (P/L) and flour color (Minolta L*) parameters, as follows: $EQ = (W \times 0.6) + (P/L \times 0.2) + (\text{color } L \times 0.2)$. For gluten strength, W 1 and



2857 - Crop Breeding & Genetics

Rodrigo Danielowski

INDIRECT SELECTION OF OAT GENOTYPES (*AVENA SATIVA* L.) IN RESPONSE TO IRON STRESS

Danielowski,R; Peters,JA; Kavalko,SAF; Nornberg,R; Costa-Oliveira,A; Maia,LC;

Federal University of Pelotas; Federal University of Pelotas;

Oat (*Avena sativa* L.) is one of the major crops in Rio Grande Sul State, Brazil, which produces more than half of Brazilian's oat production. The use of oats in rotation with rice in lowland areas would provide an important alternative for rice farmers, with a potential use in over five million ha in the State. However, lowland soils in the presence of iron oxides and low redox potential, increase the availability and subsequent toxicity of iron (Fe^{2+}). The use of correlation estimates in the indirect selection of characters is an important tool for breeders to improve the efficiency of selection. This work aimed to evaluate the effect of excess iron in oat cultivars in the vegetative phase, through Pearson's coefficient of correlation estimates between characters. The experiment was carried out at the Federal University of Pelotas, Pelotas-RS, with 18 white oat genotypes. Oat seedlings were watered over a period of 21 days with regular Hoagland and Arnon nutrient solution, supplied with iron (T1 = 0.9 mM and T2= 9.0 mM) in the form of ferric sulphate,. The experimental design was in randomized blocks in a factorial arrangement of 18 X 2 with three replications. The characters analyzed were shoot (MFS/MDS) and root (MFR/MDR) fresh and dry mass, shoot length (SL), root volume (RV), number of leaves (NL) and tillers (NT). The data were subjected to ANOVA and correlation calculations were obtained using the software GENES. Significant differences ($p \leq 0.05$) were observed for the characters studied, therefore correlation estimates were performed between the characters. The Pearson coefficients were positive with high magnitude for correlations between SL and MFS (0.6352; 0.678); RV and MDR (0.7212; 0.6944); MFR and RV (0.7322; 0.8114); MDR and MFR (0.6519; 0.8171) respectively for the two treatments. The correlation between MFS and MFR (0.7232) produced positive and high values for T2, suggesting high influence of the treatment on these characters. For the correlations RV and NT (-0.6242) and in NT and MFR (-0.7475), changes in the direction and magnitude of correlations occurred. The correlations between characters RV and MFS (0.593) and NT and MDR (-0.7249) showed an increase in magnitude in T2 compared with T1, becoming significant at $p \leq 0.01$ by the t test. The treatments caused changes in the direction and magnitude of correlations analyzed and the characters SL, RV, and MFR can be used for indirect selection for iron stress in oat.



3207 - Crop Breeding & Genetics

Rosemeire de Lellis Naves

RESISTANCE OF SEEDLESS TABLE GRAPES CULTIVARS AND SELECTIONS TO DOWNY MILDEW

Naves,RL; Ritschel,P; Santana,APS; Camargo,UA; Maia,JDG;

Embrapa Uva e Vinho;

Downy mildew caused by *Plasmopara viticola* (Berk. & Curt) Berl. Toni is a devastating disease of grapes worldwide mainly in hot and humid regions. Because of its destructive nature and economic importance, the Breeding Program of Embrapa Grape and Wine is actively trying to enhance resistance to downy mildew in its breeding material. The objective of this study was to evaluate the resistance of seedless table grapes cultivars and selections to downy mildew under natural infection. Two experiments were conducted in April/May and November/December 2006 in Tropical Viticulture Experimental Station in Jales, São Paulo, Brazil. Ten selections and one cultivar developed by the Genetic Grape Breeding Program of Embrapa Grape and Wine were assessed for resistance to downy mildew under natural field conditions. Traditional hybrid Seyve Villard 12375 and cultivar Thompson Seedless were used as resistant and susceptible controls, respectively. The experimental design was on randomized blocks with 13 treatments and five replications, each plot presenting four plants. Downy mildew resistance was determined by evaluating the disease severity on the leaves, employing a scale with notes from 1 to 9 defined by UPOV and OIV, during 53 and 38 days without spraying fungicide in the first and second experiment, respectively. The analysis of the area under the disease progress curve (AUDPC) indicated that the selection Embrapa 102 as well as the cultivar Seyve Villard 12375 was highly resistant to downy mildew, while the selections Embrapa 96, Embrapa 42, Embrapa 50 and the cultivars BRS Clara and Thompson Seedless were highly susceptible. The selection Embrapa 200 was classified as resistant, the selections Embrapa 47 and Embrapa 116, as moderately resistant and the selections Embrapa 92, Embrapa 179 and Embrapa 91, as susceptible. The downy mildew resistance of the analyzed genetic material together with the desirable agronomic characteristics make it a promise of future seedless table grapes cultivars. Also, it can be used in future crossings which aim to develop new cultivars.



3406 - Crop Breeding & Genetics

Shreekant S Patil

DEVELOPMENT AND EXPLOITATION OF HETEROTIC GROUPS IN COTTON

Patil,SS; Manjula,SM; Rajeev,S; Pranesh,KJ; Ranganath,HM; Swathi,P; Pooja,VGOANKAR;

University of agricultural sciences, dharwad;

To enhance heterosis it is necessary to increase genetic distances among parents. The concept of developing heterotic populations among cross pollinated crops has never been employed in self pollinated crops. Progress made in developing heterotic groups and exploiting them in cotton is presented here. Developing heterotic groups of cotton and exploiting them through reciprocal selection for combining ability. Evaluation of intra hirsutum crosses and comparing them with the ruling commercial checks were followed over a decade in identifying number of potential crosses. The reason for the potentiality of crosses was assessed based on the complementation of different traits. Reciprocal selection for combining ability has been practiced by deploying heterotic box of stay green v/s compact genotypes in F₄ generation. Based on the pattern of complementation for plant type traits, efficiency of physiological processes etc., broad heterotic groups of cotton genotypes (Stay green, Robust, High relative growth rate types (RGR) Compact etc.,) were made in which the crosses between the heterotic groups in general gave productive crosses. The plant type differences seen between robust and compact types have led to better packing of bolls on a robust frame. The crosses of Stay green v/s high RGR/Compact show increased harvest index and rejuvenation. Two elite combiners of each group were involved in developing heterotic boxes. The segregating F₄ lines of opposite pairs of selected heterotic box deployed in reciprocal selection for combining ability showed increase in variability for combining ability against opposite testers. Some transgressive segregants for combining ability were selected. Progress of work on developing broad based populations is discussed. The heterotic groups can be maintained and distributed to public and private sector breeders. Reciprocal selection for combining ability helps in enhancing the heterosis between the chosen groups.



3402 - Crop Breeding & Genetics

Shreekant S Patil

TARGET GENOTYPE BASED CHOICE OF BREEDING METHODS IN VARIETAL DEVELOPMENT OF SELF POLLINATED CROPS

Patil,SS; Manjula,MS; Rajeev,SUNDAR; Kenchareddi,HG;

University of agricultural sciences, dharwad.;

The concept of target genotype is defined in terms of proportions of alleles of the parents desired in the varietal line targeted to be developed after hybridization. After hybridization, two broad approaches of backcross breeding (where the target genotype is say 98:2) or selection in selfed generations are presently in vogue. Theoretical basis is explained here on how the 50:50 (or nearly) types occur with high frequency in selfed segregating generations while limited backcross derived populations are potential when there is unequal distribution (say around 75:25) of desirable alleles among parents. A mismatch between the target genotype and the approaches leads to failure in getting the desired potential variety in self pollinated crops. Developing an approach of conceptualizing the target genotype for self pollinated crops. Comparison of B1, F2 and B2 generations and their succeeding selfed generations (B1F2, F3 and B2F2) was carried out in three intra hirsutum cotton crosses. Data on seed cotton yield was used for determining potentiality of these populations. Results: One of the three crosses revealed superiority of F2 and F3, over the corresponding backcrossing populations indicating that relatively equal proportion of desirable alleles were present at the two parents. In the other two crosses, back cross populations were relatively more potential confirming the unequal distribution of desirable alleles between the parents. The trend of superiority of these populations was continued in the subsequent selfed generations. This confirmed the theory of relationship between potentiality of these generations with distribution of favorable alleles between parents. The proposed approach of comparing B1 B2 and F2 is helpful to assess the relative potential of the populations which in turn gives an idea of the distribution of desirable alleles between parents and also the target genotype desired to be developed after hybridization in self pollinated crop.



3105 - Crop Breeding & Genetics

Sohn, Jae-Keun

QTL DETECTION FOR LIPID CONTENT IN BROWN RICE OF A HIGH-LIPID RICE

Kim,NH; Kim,TH; Sohn,JK;

Kyungpook National University;

High lipid content is one of the characteristics of high quality rice and has become an important target trait in breeding programs. This study was conducted to determine the fatty acid analysis and to detect the QTL for lipid content in brown rice of a high-lipid rice. The lipid content of a high-lipid line 'P31-2-2-2-B-B' in brown rice was 4.42% whereas that of a donor cultivar 'Dongjin' was 2.56%. The unsaturated fatty acid composition of a high-lipid line was oleic acid(2.73%), linoleic acid(2.74%), and linolenic acid(0.34%) but those of 'Dongjin' was oleic acid(1.30%) and linoleic acid(0.99%). The continuous frequency distributions and transgressive segregations of lipid content were observed in the F3 family(Seed) derived from a cross between a high-lipid japonica line 'P31-2-2-2-B-B' and a indica type cultivar 'Samgang'. A significant QTL, qRLC5, was located on chromosome 5 with LOD scores of 2.37 flanked by STS markers 5007 and 5014. The present study should be useful for improving rice nutritional quality by means of marker-assisted selection.



2906 - Crop Breeding & Genetics

Solange Ferreira da Silveira Silveira

PHENOTYPIC AND MOLECULAR ANALYSIS IN SEGREGATING POPULATION (F2) WHITE OATS FOR THE CONTENT OF β -GLUCAN IN GRAIN

Silveira,SFS; Oliveira,DCS; Crestani,M; Luz,VK; Viana,T; Wolter,DD; Zimmer,CM; Fegueiredo,R; Gutkoski,LC; Maia,LC; Oliveira,AC;

Federal University of Pelotas;

High levels of *B*-glucans in oats (*Avena sativa* L.) are desirable when they are intended for human consumption, whereas when destined for animal consumption, low levels of these fibers are required. This study aimed to analyze a segregating population of oats phenotypic and molecular, generating support for a subsequent mapping of character. The analyzes were performed in an F2 population (130 individuals) originated from a cross between the cultivars ALBASUL and UPF 15, with high and low content of *B*-glucan, respectively. The kernels were ground and analyzed on a spectrometer of near infrared reflectance. The extraction of DNA (parents and population) was performed on leaves of 70-day old plants. Based on phenotypic evaluations of population, groups were formed by pooling DNA from plants that showed *B*-glucan content equal to average more than 1.5 standard deviation and from plants with *B*-glucan content equal to the mean minus 1.5 standard deviations, respectively. The high *B*-glucan group was composed by seven and the low *B*-glucan by 5 individuals. After, amplifications were performed by polymerase chain reaction, testing 141 combinations of microsatellite primers, 65 retrotransposon-microsatellite amplified polymorphism (REMAP) and 10 combinations of primers designed for genes of the route of starch synthesis in rice. The reaction product was seen in 6% polyacrylamide gel. It was observed that for the population under study the average content of *B*-glucan (5.32 g 100 g⁻¹) was intermediate to parents which showed 6.28 and 3.35 g 100 g⁻¹. This population had 5/130 transgressive individuals with underperformance and 30/130 individuals with superior performance to parents with lower and higher content of *B*-glucan, respectively. Analyses with molecular markers had four polymorphic combinations of primers among the parents and among groups contrasting for the character in question. It was found that a combination of primers is related to a wheat microsatellite marker, a combination refers to the gene OsCslF2 and two REMAP combinations, where the forward primer was designed on the transposable elements Ping and Pong of rice, combined with an ISSR primer -(GA)_n(C). The population studied presents a large number of transgressive segregant individuals for the content of *B*-glucan. The markers displayed polymorphism in the study, are likely associated with *B*-glucan content in oat grains and could be used in a future work of mapping QTLs for *B*-glucan.



2872 - Crop Breeding & Genetics

Sydney Antonio Frehner Kavalco

DIALLEL ANALYSIS IN WHEAT GENOTYPES SUBJECTED TO FLOODING STRESS

Kavalco,SAF; Tessmann,EW; Figueiredo,RG; Groli,EL; Zimmer,CM; Santos,RL;
Nornberg,R; Maia,LC; Oliveira,AC;

Plant Genomics and Breeding Center at Federal University of Pelotas - CGF/UFPel;

One of the main steps of a breeding program is the parent selection. This election is bounded by the low ability to predict the genetic intensity effects and how the parents will manifest in the progeny. The breeder challenge is to assemble in only one genotype the favorable alleles, coming from different parents. In GRIFFING (1956) diallel analysis the sums of squares treatments are deployed on the effects of general combining ability (GCA) and specific combining ability (SCA). This work was carried out to determine the GCA and SCA for one group of characters using a diallel cross and multivariate analysis. Six parents (CEP29, IPR 85, JURITI, SAFIRA, FIGUEIRA and BRS 117) and 15 F3 segregating Brazilian wheat populations were used. The experiment was installed in the Experimental Area of Plant Genomics and Breeding Center (CAP/CGF). The stress was performed from tillering initiation to flowering initiation, approximately 20 days. Characters evaluated were Fertile Tiller Number (FTN), Grain Yield per Plant (GYP), Grain Spikelet Number (GSN), the Grain Spikelet Weight (GSW), Thousand Grain Mass (TGM) and the development cycle (CYCLE). The data were subjected to variance analysis and Griffing method 2 diallel analysis. The interaction between genotype and environment was significant for most characters with a



2871 - Crop Breeding & Genetics

Sydney Antonio Frehner Kavalco

GRAIN YIELD PATH ANALYSIS IN WHEAT CULTIVARS GROWN IN PELOTAS

Kavalco,SAF; Figueiredo,RG; Zimmer,CM; Santos,RL; Danielowski,R; Luche,H;
Maia,LC; Oliveira,AC;

Plant Genomics and Breeding Center at Federal University of Pelotas - CGF/UFPel;

There are several methods to obtain correlation estimates for plants, developed according to the experimental design, genetic characteristics and growth environment. To better understand the association between characters, Wright (1921) proposed a method called path analysis that unfolds the estimated correlations in direct and indirect effects of each character on a basic variable. This study aimed to estimate the path coefficients for the productivity of wheat cultivars through the analysis of genotypic correlations among traits of grain yield. A complete randomized block experiment was installed in the experimental area of the Plant Genomics and Breeding Center (CGF). A total of 30 wheat cultivars recommended for use in southern Brazil were used. Path analysis was performed based on the genotypic correlation matrix, with the help of GENES software (Cruz, 2006), considering the character Productivity (PROD) as the dependent variable, and Number of Fertile Tillers (NFT), Hectoliter Weight (HW), Thousand Grain Weight (TGW), Plant Average Height at Tillering (PAHT), Plant Average Height at Flowering (PAHF) and Development of Plant Height between the tillering and flowering (DPH) as explanatory variables. The NFT, HW, PAHT and PAHF characters gave major contributions to the productivity, and there was still high expression of the direct effect of genetic correlations between NFT and PROD (1.14). The NFT, PAHT and PAHF characters through significant positive indirect effects (0.47, 0.26 and 0.11 respectively) were those who promoted the $r_g = 0.73$ between HW and PROD. The direct effect of TGW on PROD was positive, but lesser (0.46) and NAF indirect effect contributed negatively (-0.52) resulting in $r_g = 0.05$. Positive direct effect on PAHT to PROD was observed (0.63), but the negative indirect effect of NFT (-0.45) and positive of DPH (0.29) were responsible for $r_g = 0.51$. The direct effect of PAHF on PROD was positive (0.22), and the positive contribution of NFT (0.62) and negative of DPH (-0.3589) jointly responsible for $r_g = 0.46$. Direct negative effects can be observed for DPH on PROD (-0.45), but positive indirect effects of NFT (0.74), PAHF (0.18) and negative of PAHT (-0.41) influenced the low magnitude of $r_g = 0.04$. These results justify the importance of path coefficient correlations deployment, only then it's possible to visualize the true association between the characters. NFT is the major character responsible for the grain yield in wheat.



3157 - Crop Breeding & Genetics

Tae Heon Kim

DETECTION OF QUANTITATIVE TRAIT LOCI (QTL) ASSOCIATED WITH RESISTANCE TO WHITE BACKED PLANTHOPPER USING DOUBLED HAPLOID POPULATION IN RICE

Kim,THK; Sohn,JKS;

Kyungpook national university;

The white backed planthopper (WBPH), *Sogatella furcifera* (Horvath) is a most serious insect pest in rice growing region of the world. The nymphs and adults suck the phloem sap which causes reduced plant vigor, stunting, yellowing of leaves. We employed a mapping population composed of 94 doubled haploid (DH) lines, derived from a cross between resistant cultivar 'Cheongcheong' and susceptible cultivar 'Nagdong', to identify the quantitative trait loci (QTL) associated with WBPH resistance. A linkage map was constructed with 137 SSR markers using the MAPMAKER/EXP 3.0b software program. The DH population was evaluated for resistance to WBPH using seed box screening test. The WBPH resistance of each plants was estimated when susceptible check 'TN1' was killed using 1-9 scale according to Standard Evaluation System for Rice (IRRI, 1988). The WinQTLcart 2.5 program was used for detection of QTL associated with WBPH resistance. The composite interval mapping (CIM) was operated for the whole genome scanning on QTL detection by WinQTLcart 2.5 at a threshold of LOD 2.5. The WBPH resistance score showed a continuous distribution from 0.4 to 9.0 in the DH population. Two significant QTLs conferring resistance to WBPH, qwbph1 and qwbph4, were detected on the chromosome 1 and 4, respectively. The qwbph1 was detected in the region of RM1287-RM449, RM595 on chromosome 1 with LOD scores of 2.6 and explained 9% of phenotypic variation. The qwbph4 was detected in the region of RM1205-RM1305 on chromosome 4 with LOD scores of 3.6 and explained 25% of phenotypic variation. These two QTLs have large effects on WBPH resistance and may be useful for establishment of marker assisted selection (MAS) in the rice breeding programs.



3471 - Crop Breeding & Genetics

Toi Tsilo

POLYMERIC PROTEINS AND THEIR ASSOCIATION WITH GRAIN YIELD IN HARD RED SPRING WHEAT LINES

Tsilo,TJ; Hareland,GA; Ohm,JB; Anderson,JA;

Agricultural Research Council - Small Grain Institute, Private Bag X29, Bethlehem, 9700;

Development of high yielding wheat (*Triticum aestivum* L.) varieties with acceptable end-use quality is a major focus in breeding programs worldwide. Variations in molecular weight (Mw) distribution of wheat endosperm proteins are known to influence end-use quality traits. In this paper, we report the relationship of the size-exclusion high performance liquid chromatography (SE-HPLC) profile of important fractions of endosperm proteins with grain yield. Flour samples were previously analyzed for Mw distribution of sodium-dodecyl sulfate (SDS) extractable and unextractable proteins using the SE-HPLC protocol. Correlations were calculated between grain yield and HPLC absorbance data obtained at 0.01-min retention time intervals. Although both SDS-extractable and unextractable proteins had positive correlations with grain protein content, only SDS-unextractable very high Mw polymeric proteins (UVHP) had no negative association with grain yield and yield components, while SDS-extractable fractions rich in low Mw polymeric proteins had a negative correlation ($r = -0.41$) with grain yield. These results suggest that in an effort to increase grain yield, breeding programs should target grain yield as a primary trait and also increase levels of UVHP and decrease SDS-extractable polymeric proteins, thereby, maintaining acceptable bread-making quality.



2823 - Crop Breeding & Genetics

Vanessa Galli

GENETIC VARIABILITY OF SACCHARUM SPP. USING SSR MARKERS

Galli,V; Kneib,RB; Silva,SDA;

Universidade Federal do Rio Grande do Sul/Embrapa Clima Temperado;

The objective of the present study was to evaluate genetic variability of sugarcane collection using microsatellite markers in order to provide information for breeding process of this crop. Total genomic DNA was isolated from young leaves of 224 genotypes and SSR-PCR was performed using GoTaq Green Master Mix (Promega). The touchdown amplification was as follow: first round: 18 cycles at 94 °C for 1 min followed by a decrease of 1 °C each 2 cycles (64 °C to 55 °C) and 72 °C por 1 min; second round: 30 cycles at 94 °C for 1 min followed by 55 °C for 1 min and 72 °C for 1 min. PCR products were subjected to electrophoresis on 3.5% agarose gel, and visualized using Gel Red (Biotium®). The polymorphic alleles obtained with each primer pair were scored for their presence (1) or absence (0). From the data matrix, a dendrogram was constructed using the unweighted pair group method using arithmetic averages (UPGMA), the Dice similarity coefficient, and the software NTSYS 2.15. The generated dendrogram was sectioned in the mean similarity value to evaluate the resulted groups. A cofenetic correlation coefficient (r), according to Sokal & Rohlf (1962) was estimated in order to verify the adjustment between the similarity matrix and the dendrogram. Because of their abundance, hypervariability and uniform dispersion in the genome, SSR markers usually reveal high levels of polymorphism. In fact, in this study, 9 SSR markers generated 239 polymorphic bands, showing the efficiency of this technique and the presence of a large genetic variability among sugarcane analyzed. The mean similarity coefficient of 0.16 was used as reference to generate six groups: Group I was composed mainly by varieties and clones with short lifecycle; Group II, III and IV presents the clones with middle lifecycle, while Group V includes varieties and clones with middle lifecycle. Group VI surprisingly included only one contrasting clone (middle lifecycle) that will be investigated for its agronomic characteristics. The copenetic correlation coefficient of the dendrogram ($r = 0.896$) revealed a high correspondence between the graphical representation of genetic similarity and the similarity matrix, which shows the robustness of the inferences. There is a great genetic variability among the sugarcane evaluated that will be important for the breeding process, specially related to lifecycle duration.



2894 - Crop Breeding & Genetics

Vanessa Galli

MAIZE LANDRACES WITH POTENTIAL TO ZEAXANTHIN BIOFORTIFICATION

Galli,V; Labonde,J; Borowsky,J; Silva,SDA; Messias,RS;

UFRGS/Embrapa Clima Temperado;

The aim of this study was to characterize maize landraces for their total carotenoid content and identify promising candidates for biofortification, according to the expression of genes coding for *B*-carotene hydroxylase (*hyd3*) and ϵ -carotene hydroxylase (*lut1*), related to zeaxanthin levels. Twenty seven maize landraces were grown on field at Pelotas, Rio Grande do Sul, Brazil and pollinated manually. Total RNA was extracted from cobs collected 21 days after pollination, with a CTAB-based method, cDNA synthesized using MMLV and the gene expression was performed by RT-qPCR using ubiquitin as housekeeping gene. *Hyd3*/*lut1* ratio was obtained after calculate the fold change according to 2-Ct method. Total carotenoid content was quantified in grains collected at harvest by the method adapted from Rodriguez-Amaya and Kimura (2004) and compared to a β -carotene standard curve. Maize landraces evaluated showed a great variability in total carotenoid content, ranging from 0.14 $\mu\text{g/g}$ (Açoriano Baiano) to 23.59 $\mu\text{g/g}$ (Dente de Ouro Amarelo), with a mean value of 12.13 $\mu\text{g/g}$. This content had no correlation with any of the genes whose expression was verified. Landraces with the highest levels of *hyd3* transcripts were 'Amarelão' and 'Roxo Índio', and those with the highest expression of *lut1* were also 'Amarelão', followed by 'Mato Grosso'. Curiously, all landraces showed *hyd3* expression higher than *lut1*, probably because *hyd3* also play a role in both branches of the carotenoid metabolic pathway. Furthermore, yellow grains are usually correlated with the highest values of zeaxanthin/lutein ratio, but until this date there were no reporter of this behavior in landrace maize. 'Tupi Laranja' and 'Mato Grosso' showed the lowest *hyd3*/*lut1* ratio, while 'Rico Ouro' and 'Dente de Cão' stood out for their *hyd3*/*lut1* ratio, suggesting that are promising candidates for biofortification strategies aiming increase levels of zeaxanthin, a carotenoid associated with prevention against age-related yeas diseases, and also a precursor of the important phytohormone abscisic acid. The variability in carotenoid content as well as the trade off in carotenoid biosynthetic pathway observed in the landraces evaluated in the present study allowed identifying candidates to increase zeaxanthin levels in maize grains by conventional breeding or metabolic engineering.



2822 - Crop Breeding & Genetics

Vanessa Galli

MOLECULAR CHARACTERIZATION OF JATROPHA CURCAS ACCESSIONS

Galli,V; Kneib,RB; Borowsky,JM; Silva,SDA;

Universidad Federal do Rio Grande do Sul;

In this study, the genetic diversity of *Jatropha curcas* accessions was analyzed using microsatellite markers aiming to help in the breeding process of this crop. Total genomic DNA was isolated from young leaves of 146 genotypes from different origins, by the method described by Dart (2008). PCR reactions were developed in a 20- μ l reaction mixture that contained 5 μ l of GoTaq Master Green Mix (Promega), 50 ng of DNA and 1.4 μ M of each primer. The amplification was as follows: 94°C for 5 min, followed by 30 cycles of 94°C for 1 min, 52 °C for 2 min and 72°C for 2 min, and final extension of 72°C for 5 min. PCR products were subjected to electrophoresis on 3.5% agarose gel, and visualized using Gel Red (Biotium®). The polymorphic alleles obtained with each primer pair were scored for their presence (1) or absence (0). From the data matrix, a dendrogram was constructed using the unweighted pair group method using arithmetic averages (UPGMA), the Dice similarity coefficient, and the software NTSYS 2.15. The generated dendrogram was sectioned in the mean similarity value to evaluate the resulted groups. Using six primers, a total of 21 polymorphic bands were observed. The similarity between the genotypes ranged from 0.34 to 1.00, with mean similarity value of 0.83. Samples were separated into 10 groups, according to their similarity, allowing the identification of the 6 more genetic distant genotypes that will be used as candidates in further breeding processes. The cophenetic correlation coefficient of the dendrogram ($r=0.98$) revealed a high correspondence between the graphical representation of genetic similarity and the similarity matrix, which shows the robustness of the inferences. Although the variability of this population showed to be small, a higher variability was observed in previous studies using accessions from Embrapa Clima Temperado germplasm (Moreira et al., 2009); however a limited variability was observed in samples from China (Sun et al., 2008) and from India (Basha and Sujatha (2007), indicating that the origin of *Jatropha* (South America and Mexico) can be the determining factor in the variability found in genotypes from south america, such as these from Embrapa Clima Temperado. The microsatellite markers are efficient to detect the genetic variability among the accessions of *Jatropha curcas*. The germplasm evaluated allowed to select potential candidates for crop breeding.



3227 - Crop Breeding & Genetics

Vania Moda Cirino

BREEDING BIOFORTIFIED COMMON BEAN CULTIVARS AT IAPAR

Moda-Cirino,V; Pavan,MA; Sousa,RA;

Iapar;

Aiming to develop new common bean cultivars with good agronomic performance and grain with high levels of protein and minerals, mainly iron and zinc a representative sample formed by 1,480 accessions from the common bean germplasm bank of IAPAR, representing different centers of origin and gene pools were sowed in four locations of Paraná State, South of Brazil, in the crop season 2009/2010. A sample of 100g of seeds without injury or damage, of each experimental plot, was sent to the Chemical Analysis Laboratory of IAPAR. These samples were first washed with distilled water in order to remove any residual soil or other material, and then were dried at the constant ventilation of 65°C for 48h and ground to produce particles of less than 1 mm in diameter. The protein content was quantified spectrophotometrically by the Kjeldahl method, first reading was carried out in N UV-VIS spectrophotometer. The factor 6.25 was used to convert the total nitrogen in the seed to crude protein ($N \times 6.25$), and later corrected to dry basis. To determine minerals content, a nitroperchloric digestion was made and reading of minerals was obtained by atomic emission spectrometry coupled plasma. The results obtained showed the presence of high genetic variability for protein and mineral levels in the grains, and the influence of the environment in related characters for nutritional quality. The concentrations of Iron varying from 39.71 to 149.90mg.kg⁻¹ and from 20.11 to 59.76mg.kg⁻¹ for Zn. The concentration of protein varying from 10,08% to 31,25%. Thirty accesses which performed well for high content of protein, Iron and Zinc were selected as potential sources and crossed for introgression of these traits in promising advanced lines, in order to develop and release new common bean cultivars combining good agronomic performance and good grain nutritional quality. The selected F3 progenies were evaluated for nutritional quality and the best were intercrossed starting a new selection cycle. The best 13 progenies (F7), from the initial population and that had good agronomic performance in relation to control were coded with the initials LP11-500 to LP11-512 and are being evaluated in Preliminary yield trials and adaptability conducted in four environments in the Paraná State on the crop season 2011/2012. New cultivars with high nutritional quality will be released in the next years to increase the nutritional status of the Brazilian population health.



2904 - Crop Breeding & Genetics

Viviane Kopp da Luz

VARIABILITY FOR AGRONOMICALLY IMPORTANT TRAITS IN RICE MUTANT FAMILIES

Luz,VK; Fonseca,GM; Groli,EL; Neves,CG; Figueiredo,R; Baretta,D; Silveira,SFS;
Kopp,MM; Magalhães-Júnior,AM; Maia,LC; Oliveira,AC;

Federal University of Pelotas; Federal University of Pelotas;

Over 160 million hectares are cultivated with rice annually in the world, producing around 688 million tones. The genetic variability constitutes the essence of the evolutionary processes and plant breeding, being essential for natural and/or artificial selection. The use of physical mutagens such as ionizing radiation and chemicals such as alkylating substances (ethylmethanesulfonate-EMS) may be of fundamental importance for the development and incorporation of new genes and/or alleles of agronomic interest, and may result in more stable and adapted genotypes to climatic conditions in Southern Brazil. The objective of this study was to evaluate the effect of chemical mutagen EMS on the characters length of main panicle, weight of main panicle and width of flag leaf, in rice mutant families. A total of 145 M3 families of rice belonging to the genebank CGF/FAEM / UFPel obtained from the genotype BRS Querência by treatment with the chemical mutagen EMS, at a concentration of 1.5% (v/v) were studied. The genotype BRS Querência was used as control. Seeds of rice in the M3 generation were sown in the experimental field at Embrapa Clima Temperado. The experimental design was a completely randomized block with four replications. Were evaluated the characters: length of main panicle (LMP) in cm, weight of main panicle (WMP) in g and width of flag leaf (WFL) in cm. The data were subjected to analysis of variance ($p \leq 0.05$), and comparison of means was performed by Dunnett's test at 5% probability. The variance analysis has highlighted significant differences between the means of genotypes for all traits. Character in relation to the LMP, most families presented significantly means equal to the control (24.72cm), but seven families presented average higher than the control and only one family showed LMP lower than the control. For the character WMP, four families presented means higher than the control (3.19g) and only one family mean lower showed that is character, and the other families presented significantly WMP equal to the control. For the WFL, there were only three families with averages lower than the control, and the remaining families presented means that did not differ from the control (1.67cm). Induction of mutation with EMS at a concentration of 1.5% is effective for generating mutants in rice for the characters length of main panicle, weight of main panicle and width of flag leaf.



3403 - Crop Breeding & Genetics

yanal alkuddsi

Correlation and Path Coefficient Analysis of Yield Components in Cotton (*Gossypium Hirsutum* L.)

Alkuddsi, YANAL;

University of Agricultural Sciences Dharwad;

Kapas yield per plant was significantly and positively genotypic correlation with days to 50 per cent flowering (0.359), plant height (0.443), bolls per plant (0.590), mean boll weight (0.422) and ginning per cent (0.379) but significantly and negatively correlated with seed index at genotypic level. The phenotypic correlation values also revealed that kapas yield per plant had highly significant and positive phenotypic correlation with bolls per plant (0.624), significantly and positively phenotypic correlation found between kapas yield per plant and mean boll weight (0.327). The path analysis indicated high positive direct effect of monopodia per plant (0.619) and mean boll weight (0.321) on kapas yield. Sympodia per plant exhibited high positive indirect effect on kapas yield via seed index (0.374) the result of this mean boll weight had high positive correlation with kapas yield and sympodia per plant recorded low positive correlation with kapas yield.



3404 - Crop Breeding & Genetics

yanal alkuddsi

HETEROSIS STUDIES INVOLVING COMPACT AND ROBUST PLANT TYPES FOR YIELD AND YIELD COMPONENTS IN COTTON (*Gossypium hirsutum* L.)

Alkuddsi, YANAL;

University of Agricultural Sciences;

An investigation was carried out during kharif 2008 in cotton (*G. hirsutum* L.) to evaluate intrahirsutum hybrids produced through Line x Tester mating design using 6 *hirsutum* non Bt lines and 8 *hirsutum* non Bt testers, to generate information on heterosis in respect of kapas yield and yield attributing characters. The analysis of variance among 48 hybrids and 2 checks tested in 2 replications indicated highly significant differences among the hybrids with respect to all characters except, monopodia per plant, mean boll weight and seed index. Two hybrids YHH 134, YHH 133 were superior over standard commercial check hybrid (RAHH 95) for kapas yield, sympodia and , monopodia per plant, bolls per plant and ginning per cent. and hybrid YHH 136 which exceeded best Bt check hybrid (RCH2 Bt) for kapas yield. The present study was helpful in identifying top ranking cotton hybrids viz., YHH136, YHH 134 and YHH 133 which exceeded the commercial check hybrid (RAHH 95) by 105.36, 55.80 & 53.93 per cent and hybrid YHH 136 which exceeded the best Bt check hybrid (RCH2Bt) by 30.09 per cent in respect of kapas yield.



Poster Session

Crop Ecology, Management & Quality



2860 - Crop Ecology, Management & Quality

Alfredo Castamann

DRIS NORMS RELATED TO SOYBEAN GRAIN OIL CONTENT

Castamann,A; Escosteguy,PAV; Berres,D; Zanella,S;

Universidade Federal da Fronteira Sul;

The diagnosis and management of nutrient constraints is a relevant factor in maximizing grain quality or oil production of soybean fields in Brazil. The Diagnosis and Recommendation Integrated System (DRIS) approach evaluates plant nutritional status and is based on DRIS norms. These norms should be locally calibrated and were not established in soybean crops in Brazil. The aims of this paper were develop the DRIS norms related to grain oil content in two consecutives agricultural years and to compare the nutritional diagnosis based on these norms. The soils of the assessed areas have been managed under no-tillage in the Planalto Médio Region of the state of Rio Grande do Sul, Brazil. They were pre-selected in order to have field with low, medium and high soil fertility in the studied areas. BRS 243 RR and Fundacep 55 RR cultivars were evaluated in experimental plots, while 6445 RR, 6001 RR, Apolo RR, Fundacep 53 RR and Fundacep 55 RR cultivars were evaluated in commercial field farms. The leaf concentrations of N, P, K, Ca, Mg, S, B, Cu, Fe, Mn, Zn and the grain oil content were assessed in 207 samples. The DRIS norms were computed from this data bank by analyzing the results of the leaf mineral composition and corresponding grain yield, in 2007/2008 and 2008/2009 soybean season. Leaf samples consisted of 30 newly mature trifoliate leaves, with petioles, randomly collected during full bloom (R2 stage). Samples were analyzed for oil content by using near-infrared reflectance spectroscopy. DRIS norms related to grain oil content could be developed, but they changed between the assessed seasons. The correlation between oil content and nutritional balance index, based on the norm of 2007/2008 season was negative ($r = -0,647$; $p = 0,002$), but a positive correlation was found by using the other season norm. The most appropriate nutritional diagnosis was obtained from the norm of 2007/2008 season. In this season, the high-yield subpopulation was constituted by samples with oil content greater than 18.68%. The increase in the index DRIS value of B, Ca, Mg and S was followed by higher oil content, but the opposite was found for K, N and P. Higher concentrations of K, P and N favored protein formation to the detriment of fatty acid synthesis. This effect possibly explains the negative correlation between the DRIS indexes for nutrients and grain oil content.



3197 - Crop Ecology, Management & Quality

Anelise Christ Ribeiro

RECOVERY OF PHENOLIC COMPOUNDS OF RICE BRAN.

Christ-Ribeiro,A; Costa-Bretanha,C; Giacobbo-Luz,G; Moraes-Souza,M; Badiale-Furlong,E;
FURG;

The biological function of the rice grain to allow the formation of a new individual makes it an excellent source of major nutrients and traces with functional activity. The beneficiation of the rice grain for consumption results in fractions, which highlights the bran, the outer portion of the grain, which carries the components of the germ. The use of bran as a source of functional compounds is viable, because of its availability at the regional level. The carbohydrate content enables the use of bran as a substrate for solid state fermentation by fungi GRAS (Generally Recognized As Safe). For GRAS development, it is released hydrolytic enzymes such as cellulases, amylases, proteases and others that degrade large polymeric networks of biomolecules with availability of phenolic compounds, with antioxidant activity, on the biomass. Therefore, the objective was to provide phenolic compounds of rice bran, through solid state fermentation promoted by *Rhizopus oryzae*, ordering their application as conservative natural food production. To generate biomass has been the standard methodology used by Oliveira et al. (2009). The rice bran, using standard particle size of 32 mesh, was the substrate for fermentation with *Rhizopus oryzae* CCT 7560 from a spore suspension (4×10^6 spores/g of bran) with humidity in the environment adjusted to approximately 50%. The reactors were placed in fermentation chamber at 30 ° C and removed from the 0h, 24h, 48h, 72h and 96h. The extraction of phenolic compounds was performed according to Souza et al.(2009). The content of total phenols was quantified by spectrophotometric method with the Folin-Ciocateau at a wavelength of 750 nm using a standard curve of ferulic acid (1.7 to 12.2 µg/mL). The yield of total phenolic compounds produced during the fermentation process were 1.42 ± 0.02 , 2.47 ± 0.01 , 2.16 ± 0.05 , 2.23 ± 0.07 and 1.94 ± 0.03 for 0, 24, 48, 72 and 96 hours fermentation, respectively. Therefore, the increased availability of phenolic compounds occurred in 24 hours of fermentation, which makes the procedure advantageous, because it requires less time of the experiment and less risk of contamination of the crop. The fermented rice bran doubled availability of phenolic compounds demonstrating, thus, the advantage of starting fermentation with byproducts, besides the affordability and simplicity of implementation of the method of extraction.



3189 - Crop Ecology, Management & Quality

Bon Il, Ku

THE EFFECTS OF LATITUDE CHANGE TO GROWTH DURATION AND HEADING DATE OF RICE ACCORDING TO RIPENING ECOTYPE AND TRANSPLANTING TIME IN KOREA

Ku,BONIL; Choi,MINKYU; Kang,SHINGU; Sang,WANKYU; Park,HONGKYU; Kim,YOUNGDOO; Kim,BOKYEONG;

National Institute of Crop science;

Korea is located approximately between latitude 33~43° and japonica rice is cultivated in most areas of Korea. So the difference of weather conditions of diverse rice cultivation areas are very severe. The increase of global warming gases in the atmosphere after Industrial Revolution force up the earth's temperature gradually. Especially the temperature increase of Korea are more higher because of dense industrial facilities. As temperature increase, we are considering to move transplanting time of rice in order to continue maximum rice yield. But there is not enough study about when the transplanting time changed, what effect break out to early, middle and middle-late ripening Korean rice cultivars. So, here we studied the variation of growth duration and heading date according to rice cultivars, transplanting time and latitude of Suweon which located at 37.2° and Iksan which located at 35.6°. Transplanting times of Suweon were May 2, May 12, May 22, June 2, June 11, June 21 and those of Iksan were May 1, May 16, May 31, June 15 and June 30. In transplanting at Suweon, the growth durations between transplanting and the completion of flag leaf on main culm of Odaebyeo, Hwasungbyeon and Dongjinbyeon with 10 days seedling were 55.7~74.4, 59.1~83.1 and 66.2~91.7, respectively. And those with 30 days seedling were 51.7~67.0, 54.6~74.3 and 60.4~76.7, respectively. In transplanting at Iksan, the growth durations between transplanting and the completion of flag leaf on main culm of Unkwangbyeon, Hwayoungbyeon and Nampyeongbyeon with 10 days seedling were 51.6~74.7, 54.0~88.9 and 57.9~95.6, respectively. And those with 30 days seedling were 47.5~74.3, 51.2~83.3 and 53.8~92.6, respectively.



5356 - Crop Ecology, Management & Quality

Casiane Salete Tibola

DETECTION OF DEOXYNIVALENOL IN WHEAT SAMPLES USING CHROMATOGRAPHIC AND SCREENING METHODS

Tibola,CS; Lukow,OM; Adams,K; Tittlemier,SA; Fernandes,JMC;

Embrapa Wheat;

Fusarium Head Blight (FHB) is a fungal disease that affects cereals and is capable of producing mycotoxins, mainly deoxynivalenol (DON), generating health concerns and economic losses. The objectives were to analyze levels of DON in wheat from various cultivars grown in the Canadian prairies and to compare the results obtained by three methods: gas chromatography-mass spectrometry (GC-MS), enzyme-linked immunosorbent assay (ELISA), and near infrared spectroscopy (NIRS). A total of 96 wheat samples belonging to 16 Canadian Western hard red spring wheat (CWRS) cultivars, obtained from Portage la Prairie, Manitoba, Lethbridge, Alberta and Indian Head, Saskatchewan, were analyzed. The average DON content obtained by GC-MS statistically differed from the results measured by both ELISA and NIRS screening methods. In the chromatographic method, DON concentrations ranged from <50 to 3,040 ppb. The screening methods tended to give higher measurements, which ranged from <200 to 4,550 ppb and <200 to 1,551 ppb for ELISA and NIRs, respectively. ELISA presented adequate correlation with results obtained by NIRS method, no false positive results were observed for uncontaminated samples. Although, screening methods are useful tools on detecting DON in wheat, they are not precise enough to detect all relevant levels of wheat mycotoxins. These methods could be used associated with standard analytical methods, which are applied not only to detect other mycotoxins but also to determine lower levels more precisely, thereby minimizing the risk of including contaminated wheat in the feed and food production chains. DON mean content for Portage la Prairie samples was statistically different from Indian Head and Lethbridge, likewise for the 16 cultivars evaluated, reinforcing the demand for wide and frequent monitoring of representative sets of samples, in order to capture the effects of environment and genetic influence on DON formation.



5355 - Crop Ecology, Management & Quality

Casiane Salete Tibola

QUANTIFICATION OF DEOXYNIVALENOL IN WHEAT USING NEAR INFRARED REFLECTANCE SPECTROSCOPY

Tibola,CS; Fernandes,JMC; Bernardi,CMG;

Embrapa Wheat;

Fusarium graminearum is the main causal agent of Fusarium head blight (FHB) in wheat in Southern Brazil region. The pathogen invades wheat kernel and is capable of producing different mycotoxins, being the deoxynivalenol (DON) the most important because of its high concentration, toxicity and widespread occurrence. Amongst the available methods for rapid screening of contaminated kernel samples, Near Infrared Reflectance Spectroscopy (NIRs) based on the absorption of near-infrared light by organic compounds presents promising results. The objectives of this study were to develop and to validate a NIRs method based on reference chromatographic DON content results. A total of 313 wheat samples from 2009, 2010 and 2011 growing seasons were analyzed. Wheat samples were obtained from commercial fields naturally infected by *F. graminearum* and from breeding trials conducted at Embrapa Wheat. The procedure required, firstly, the whole kernel wheat samples, to be scanned by NIRs. Secondly, the same samples were milled, homogenized and scanned again by NIRs. Finally, the milled samples were analyzed by the reference method liquid chromatography-tandem mass spectrometry (LCMS/MS). The NIRs instrument used was a FOSS XDS - RCA. The accuracy of each calibration model was tested by using cross-validation in groups and was selected based on the highest coefficient of determination in calibration (r^2) and the lowest standard error of cross validation (SECV). The calibrations were performed by modified partial least square (MPLS). Spectral outliers (standardized $H > 3$) were removed and samples with large residuals ($T2.5$) were omitted from the population. In wheat the r^2 obtained for DON content was 0.63 and SECV 646 ppb; in milled wheat r^2 was 0.78 and SECV 622 ppb, indicating a good prediction using the NIRs calibration model MPLS. The accurate prediction of DON levels to meet legal limits may be particularly difficult, due to the influence of fungal strain, the genotype resistance and the environmental conditions. Further studies are necessary before recommending NIRs as a routine screening method. At the moment, the NIRs technique could be applied for screening genotypes and commercial wheat lots highly contaminated with *F. graminearum*.



3389 - Crop Physiology and metabolism

Clovis Arruda de Souza

CHARACTERIZATION OF SOME BAF/UDESC COMMON BEAN LANDRACES TO ALUMINUM AND LOW PH IN SAND CULTURE WITH NUTRIENT SOLUTION

Souza,CA; Tormem,ME; Zanesco,PR; Zilio,M; Faccin,TR; Stefen,DLV; Coelho,CMM;

Santa Catarina State University (UDESC), Lages-SC;

The aim of this research was to evaluate the common bean landraces reaction to low pH and aluminum (Al) in simple nutrient sand culture. The experiment was carried out in a greenhouse pot experiment at UDESC, Lages (SC), between july-august/2010 using 4 liters pot capacity and the substrate sand previously washed. The pot experiment was set up in a randomized complete block design with four replications in factorial design 3x33, consisted by simple nutrient solution (i) pH 5.5 without Al³⁺, (ii) pH 4.2 without Al³⁺ and (iii) pH 4.2+Al³⁺ 50µmol.L⁻¹; using 33 bean genotypes. After sowing and emergence the seedlings received daily 0.2 liter of one of each simple solution above described, as the treatment. Fifteen days after seedlings emergence the were evaluated the following traits: leaf chlorophyll content (LCC), root length (RL), plant height (PH), shoot weight (SW) and root weight (RW). The dates were submitted the variance analysis and the averages were compared by Tukey test (p). The genotype effect was observed to all traits, and effect of pH for root weight e plant height. The LCC to BAF10, BAF23 and BAF112 were highest, and to BAF44, BAF115 and BAF4 were lowest. The highest RL were observed on BAF44, BAF10 and BAF75 and the lowest RH in BAF36, BAF97 and BAF57. The SW of the BAF192, BAF120 and BAF46 were highest and lowest were the BAF102, BAF7 and BAF42. The RW of BAF120, BAF14 and BAF192 were higher and of the BAF59, BAF57 and BAF7 were lower. The PH higher were of BAF120, BAF46 and BAF58 and of BAF26, BAF50 and BAF13 were lowest. The PH were observed at pH 5.5-treatment compared to pH-treatments (with and without aluminum). The root weight from genotypes treated with pH 4.2 without Al were higher than observed to pH 5.5 and pH 4.2 with Al. The higher seedlings performances were observed from BAF192, BAF120, BAF46, BAF58, BAF75 and BAF68. The Al promotes increase on plant shoot and decrease on plant root. However low pH without Al promotes increase of root weight when compared to low pH with 50µmol.L⁻¹ of Al. The Al toxicity lead to lower performance of seedlings in all traits evaluated.



3178 - Crop Ecology, Management & Quality

Gabriela da Rocha Lemos Mendes

ENZYMATIC PROFILE AND INHIBITOR FRACTION FROM SEVERAL WHEAT VARIETIES (TRITICUM AESTIVUM L.)

Mendes, GL; Pagnussatt, FA; Leal, CA; Badiale-Furlong, E;

Universidade Federal do Rio Grande;

Wheat varieties, obtained from the north and northeast regions of Rio Grande do Sul/ Brazil, have different structural and chemical characteristics among themselves, as well as other abiotic variables that affect inhibitory enzymes fractions and availability in the grain. This abiotic specificities may determine each variety susceptibility to fungal infestation. This work objective was to evaluate the enzymatic profile and the presence of substances capable of inhibiting a commercial amylase extract activity (Fungamyl ®) in the wheat varieties Fundacep, Horizonte, Marfim, Guamirim e Codetec, from the 2012 harvest, in order to determinate fungal infestation susceptibility through the observed characteristics. The samples water soluble extracts were submitted to α -amylase activity through starch degradation with a iodometric methodology, β -amylase quantification was realized by the quantification of hydrolyzed maltose with the 3,5 dinitrosalicilic acid (3,5 DNS) colorimetric methodology. Protease activity quantification was accomplished by the liberated amino-acids determination by Folin-Ciocalteau analysis. Lipase was determined with the titration of the free fatty-acids after the extract action. The extracts containing the inhibitors were obtained through the prolamin fraction with ethyl alcohol 70%, were the inhibitory effect was quantify by its action in commercial fungal amylase (Fungamyl ®). Inhibition percentage was estimated by the difference among the velocity in the control experiment and the velocity with the inhibitor, where $\%I = ((V \text{ control} - V \text{ inhibitor})/V \text{ control}) \times 100$.



3175 - Crop Ecology, Management & Quality
Gabriela da Rocha Lemos Mendes

PECTINASE AND AMYLASE PRODUCTION BY RHIZOPUS ORYZAE E TRICHODERMA REESEI FERMENTATION UTILIZATING RICE HUSK AND BRAN

Mendes, GL; Kupski, L; Silvello, MAC; Lima, TS; Fontes, MRV; Garda-Buffon, J;

Universidade Federal do Rio Grande;

Rice husk and bran were employed as carbon source to *Rhizopus oryzae* CCT 7560 and *Trichoderma reesei* QM 9414 in solid fermentation in order to produce the enzymes pectinase and amylase. This process was realized in tray bioreactors with medias containing substrates constituted by different rice husk proportions, 1, 3 and 5%, in rice bran. The bioreactors were incubated at 30°C for 120 h, sampling was realized each 24 h. Enzymes were extracted with 1:5 (w/v) in NaCl 0,5% and its amylolytic and pectinolytic activities determined by iodometric and 3,5 DNS methods utilizing starch and galacturonic acid as substrates, respectively. An amylase unit was defined as the amount of hydrolyzed starch, as for pectinase such unit was defined as the amount of liberated galacturonic acid per minute in the experiment conditions. Growth was accompanied by glucosamine according to Aiddo (1981) and reducing sugars liberation as described by Miller (1959). The results indicated that, among the studied microorganisms, such enzymes production is more promising with *R.oryzae*, due to its higher productivity of amylase, 0.26 U.g-1.d⁻¹ utilizing 5% rice husk, and pectinase, 2.13 U.g-1.d⁻¹ utilizing 1% husk, both at the 24 h sample. Maximum productivity coincided with the greatest reducing sugars liberation, this being 2.3 to 5.8 larger in the fermentation with *R. oryzae* than in the one with *T. reesei*. This fact may be attributed to *R. oryzae* specific growth, 20 times larger than the one achieved by *T. reesei*, in these substrates. This growth rate provided a rapid substrate consumption and the release of carbohydrate structures with lower degree of polymerization for energy attainment due the higher enzyme activity. These results also indicate that *Rhizopus oryzae* CCT7560 adapted well to media used in this study, such behavior was expected, since this strain was isolated from rice husk. The results showed that is possible to add value to rice industries residues, widely found in the southern region of Rio Grande do Sul for hydrolytic enzymes production.



3176 - Crop Ecology, Management & Quality

Gabriela da Rocha Lemos Mendes

PROMISING ANTIFUNGAL EFFECT OF PHENOLICS EXTRACTED FROM SPIRULINA ON FUSARIUM GRAMINEARUM GROWTH

Mendes, GL; Pagnussatt, FA; Filoda, PF; Darley, F; Delponte, EM; Garda-
Buffon, J; Badiale-Furlong, E;

Universidade Federal do Rio Grande;

Phenolic compounds (PC) extracted from the *Spirulina* LEB-18 had its antifungal activity evaluated through in vitro inhibitory assay against 12 *Fusarium graminearum* strains. *Spirulina* LEB-18 biomass was cultivated in RS/Brazil with Mangueira Lagoons water. To extract phenolic compounds, 6 g of cyanobacterium were homogenized with 40 mL of methanol. The extracts were then filtered, the solvent evaporated in rotary evaporator, the filtrated portion was dissolved in distilled water (20 mL) and clarified. PC in the extract were determined by spectrophotometry using the Folin-Ciocalteu reagent and employing a gallic acid calibration curve (4 a 50 mg mL⁻¹). All toxigenic fungal strains were obtained from the collection of the Departamento de Fitossanidade (Brazil). *F. graminearum* strains 14C-1, 18C-2, 46C-1 and 39C-2 were originally isolated from infected barley grains, A-3, A-6, B-8, B-10, C-4, 702-01, 702-25 and 730-10 from infected wheat grains. Dissolved extracts were diluted in potato dextrose agar (PDA) at different concentrations (10%, 8%, 6%, 5% and 3,5%). The prepared Petri dishes were aseptically inoculated with an assay disc cut from the periphery of a 7-day-old culture of the target fungi. The control sets were prepared using an equal volume of distilled water without extracts. The plates were incubated at 25°C for 7 days. Inhibition percentage was calculated by the radial growth from the target fungi according to the following formula: percent inhibition = (DC - DT) / DC x 100, where DC is the colony diameter of the control sets and DT is the colony diameter of the treated sets. The median inhibitory concentration (MIC50) was considered as the PC concentration that resulting in 50% inhibition of the visible growth when compared with control sets. The fungal growth inhibition effect was different among the 12 fungal species. *Spirulina* LEB-18 PC affected fungal growth and was sufficiently effective against the *F. graminearum* mycelial growth. According to the results, the MIC50 was 3% for 702-01, B10, C4, 702-25, 46C-1, 18C-2, A-3 fungal species; to B-8, 730-10 and 14C-1 the MIC50 was 4%, while for 39C-2 and A-6 highest concentrations (> 8%) should be tested to obtain MIC50. In summary, microalgae PC have an inhibitory effect on *F. graminearum* growth and the glucosamine, enzymes and ergosterol content in fungal biomass will be determined to the action mechanism identification.



3186 - Crop Ecology, Management & Quality

Germán Wies

PHOTO-MORFOGENIC PROCESS REGULATED BY B-PHYTOCHROMES AND THEIR EFFECTS ON PLANT-TO-PLANT VARIABILITY OF MAIZE (ZEA MAYS.L) CROPS

Wies,G; Maddonni,GA;

Facultad de Agronomía, Universidad de Buenos Aires;

In maize crops, inter plant variability of several traits is established at early ontogenic stages and enhanced in response to increased plant population density. These responses may be determined by genetic and/or environmental factors. Among the latter, subtle changes in the reflected light (specially the red-far red ratio; R/RL) perceived by plants, trigger several plant responses to colonize empty spaces and avoid mutual shading (i.e. the shade avoidance syndrome). The objectives of this work were to elucidate the role of phytochrome B1 and B2 on i) some maize plant response previously described in the "shade avoidance syndrome" (e.g. shoot stem elongation, thinning stem, azimuthal leaf orientation) and ii) the inter plant variability of mentioned traits. A split-split-plot experiment was conducted in Vegetal Production department experimental field of FA-UBA without water and nutritional limitations. A wild type line (Wt) and their isogenic lines with mutations of B phytochromes (phyB1-PhyB2 and PhyB1-phyB2) were cultivated at low and high plant densities. Results: At high plant density, Wt exhibited lower plant biomass ($p < 0.1$) were not affected. By contrast, phyB1-PhyB2 line had similar plant biomass at both densities ($p = 0.26$). Only Wt showed a higher inter-plant variability of plant biomass at high plant density. Plant architecture described in the shade avoidance syndrome seem to be regulated by both B phytochromes. Thus, B1 phytochrome played a role in stem thickness. On the other hand, stem elongation and leaf re-orientation capacity were only regulated by B2 phytochrome. Consequently mutations of B phytochromes reduced the early capacity of plants to detect neighbors which was reflected in a similar inter-plant variability of plant biomass at both densities.



3171 - Crop Ecology, Management & Quality

Kaori FUJITA

DETECTION OF FUSARIUM MYCOTOXIN IN WHEAT GRAIN USING FLUORESCENCE FINGERPRINT

Fujita,K; Tsuta,M; Sugiyama,J; Nakagawa,H; Yoshimura,M; Kokawa,M; Shibata,M;

National Food Research Institute;

Fusarium mycotoxins are produced in wheat, corn and other cereal grains when exposed to Fusarium genus. It is particularly notable in wheat when affected by Fusarium head blight. Not only does it reduce yield and quality but also causes symptoms such as vomiting, diarrhea and headaches upon human and animal ingestion. A new method to detect mycotoxins quickly, easily and accurately has been demanded. The objective of this study is to develop a nondestructive method for simultaneously detecting mycotoxins using fluorescence fingerprint (FF). FF is also called an excitation-emission matrix (EEM), which has three dimensional data composed of excitation wavelengths $\times$ emission wavelengths $\times$ fluorescence intensities. Three Fusarium mycotoxins (deoxynivalenol (DON), nivalenol (NIV), zearalenone1 (ZEA)) and four phase of diseased wheat were examined. The wheat flour samples were made from the diseased wheat using a mill. Total 32 flour samples composed of 8 repeats and 4 diseased phases were prepared. The FFs were measured with a fluorescence spectrometer. The measurement range for the excitation and emission wavelengths was 200-900 nm, with 10 nm wavelength increments. The concentrations of three mycotoxins for the same samples were measured by liquid chromatography-tandem mass spectrometry (LC/MS/MS). The FF data was preprocessed to remove scattered lights and noisy signals. They were set as explanatory variables for PLS regression. Then, the concentration of the mycotoxins was set as the response variable. The FFs of the mycotoxins showed some fluorescent peaks and contour patterns. FF of ZEA was quite different patterns from the others. On the other hands, the other two mycotoxins were similar patterns. 16 of the 32 samples were selected for the calibration dataset, and the rest were used for the validation dataset. The PLS correlation coefficients, which represent the degree of contribution to the model at each wavelength condition, indicated that the prediction were mainly based on the fluorescence of each mycotoxin. Therefore, we concluded that as follows; Three Fusarium mycotoxins have different fluorescent signals. The combination of FF measurement and PLS method could successfully predict each mycotoxin in the wheat flour. These results indicate that FF measurement can be extended to imaging work to visualize Fusarium mycotoxins. Possibility of mycotoxin visualization will be shown in the presentation.



3293 - Crop Ecology, Management & Quality

Kyu-Jong, Lee

DIAGNOSIS OF RICE GROWTH AND NITROGEN NUTRITION STATUS USING DIGITAL CAMERA IMAGE ANALYSIS

Lee,KJ; Choi,DW; Park,SJ; Lee,BW;

Seoul national university;

Most of the monitoring methods for crop status are destructive and resource-consuming. Alternatively, the use of digital cameras as a low-cost and high efficient tool has been used with some success in diagnosis of crop growth and nitrogen (N) nutrition status. The objectives of this study were to develop a non-destructive method for monitoring crop growth and N nutrition status with digital camera image analysis at the canopy level of rice. The field experiments were conducted from early tillering to panicle initiation stage of rice from 2006 to 2009 at the experimental farm of Seoul National University, Korea. Four rice cultivars were grown under various nitrogen applications with seven different timings of panicle N fertilization. Digital images of rice canopy were taken with a conventional digital camera and at the same time plants were sampled to measure dry weight (DW), leaf area index (LAI), and shoot N accumulation (Nup). The first step for analyzing digital images of rice canopy is to segment the crop plant from variable background. Three mosaic images for rice plant, flooded/bare soil, and algae-infested background were prepared from digital camera images of algae-infested paddy field. An image analysis program was developed in Visual Basic to extract Red, Green, and Blue (RGB) features from the mosaic images, calculate RGB-based color indices, and compute the minimum segmentation error. Modified excessive green index (MEGI) showed the highest performance for segmenting rice plant from flooded/bare soil background. However, discriminant function (DF) of $1.2553\text{EGI} + 0.01735\text{G} - 0.01474\text{B}$ was successful in segmenting rice plant from algae-infested background. The percent rice canopy cover (CC) were estimated based on the threshold value of MEGI and DF and also manually using commercial software. Both estimates of CC showed good agreement. The second step is to develop models for diagnosing rice growth and N nutrition status. Thirteen color indices were calculated from digital images using image analysis program developed in Visual Basic. More than eight color indices and CC showed significant correlations with DW, LAI, and Nup. Models for estimating DW, LAI, and Nup were derived from stepwise multiple linear regression analysis using color indices. These models showed relatively high R² of more than 0.7, promising the applicability of digital camera to diagnosing growth and N nutrition status of rice plant.



2601 - Crop Ecology, Management & Quality

Ma Zhongming

EFFECTS OF PLASTIC FILM MULCHES ON SOIL TEMPERATURE AND MOISTURE AND WATERMELON PRODUCTION IN GRAVEL-MULCHED LAND IN SEMIARID AREA

Zhongming, ZHM;

Gansu Academy of Agricultural Sciences, Lanzhou 730070, China;

Key Observation and Experiment Station of Agro-ecological Environment in Zhangye Oasis Irrigation Region, Ministry of Agriculture, Zh;

Gravel-mulched land was the unique and conventional farming system and its planting area was enlarged year by year in semiarid region of northwest China. Gravel-mulched watermelon reached more than 33% of total area of gravel-mulched land but the stresses of lower temperature in early spring and water shortage during growth period of watermelon were major limiting factors for yield increasing. To find the ways improving soil temperature and WUE, field trials with full plastic film mulch (FM), soil bed-forming and much plastic film for collecting rainfall (RM), half soil plastic film mulch (HM) and no plastic film mulch (CK) were conducted in gravel-mulched land in semiarid area of Gansu to study the effects of soil temperature, soil water and yield as well as quality of watermelon. The results indicated that the daily soil temperature in 0-25cm soil layer changed as "S" and transferred from soil surface layers to deeper layers, the time of maximum and minimum soil temperature appearance delayed 1h as soil depth deepened 5cm. The changes of soil temperature in 5cm soil layer were greater than other soil layers and its changing degree was decreased as soil layers deepened. Soil temperature increasing in 0-25cm soil layer followed as FM>RM>HM>CK and the daily average soil temperature of FM, RM and HM increased by 2.8-2.0 and 1.8, compared to CK, respectively. FM and RM were the key plastic film mulches influencing soil water. The effects of rainfall collection were obvious for RM as its bed forming from sowing to seedling stage and the effects of soil water conservation were significant for FM treatments after extending stage as soil water evaporation decreasing. Compared to CK, the average soil water content for FM and RM increased 1.1-2.2 percentage points from sowing to extending stage. Compared to CK, the length of main vines were increased by 12.7%, 11.5% and 8.8% and leaf area index were increased by 67.8%, 31.4% and 25.6% for FM, RM and HM in fruit stage, respectively. The chlorophyll content of leaf reached highest value in vines stage and increased by 14.1%, 13.7% and 12.2%, the watermelon yield was increased by 145.81%-99.32% and 95.46% for FM, RM and HM compared to CK, respectively. The content of soluble solid and soluble sugar changed as FM>RM>HM>CK. But the content of Vc, fiber and effective acid were influenced slightly by plastic film mulches. By analysis comprehensively FM and RM treatments were optimum mulching options in gravel mulched land.



2902 - Crop Ecology, Management & Quality

MARTHA ZAVARIZ DE MIRANDA

RELATIONSHIP BETWEEN WHEAT GLUTEN COLOR AND WHEAT QUALITY: PRELIMINARILY RESULTS

Miranda,MZ; Caetano,VR; Scheeren,PL; Tiggemann,L; Tatsch,P; Oro,T;

Embrapa Wheat;

Wheat genotypes in breeding programs are subjected to an array of quality tests. However, the desirable quality depends on the wheat end-use. In general, for wheat quality evaluation, most of the equipment is expensive, a large amount of sample is used and usually are time-consuming procedures. Wheat quality determination is essential in breeding programs, so any method able to use a small amount of sample, in a simple way, will be of a great use. The objective of this study was to investigate the relationship between wheat gluten color and other wheat quality parameters, aiming to verify the possibility to use gluten color analysis as an indicator of wheat quality, especially for genotype selection. Forty wheat cultivars with different quality characteristics were experimentally milled. Official methods for wheat quality evaluation were used, employing colorimeter (CIEL*a*b* system), glutomatic, alveograph, farinograph and grain hardness equipment. Samples showed significant differences among each other, especially samples with high (clearer) and low (darker) gluten brightness (L^*) corresponding to wheat cultivars with weak and strong gluten strength, respectively. The results oscillated in a wide range of values for all parameters evaluated: experimental milling (55-71%); brightness flour, L^* (91.03-95.38), flour a^* value (-0.83-0.39), and flour b^* value (5.01-10.2); gluten index (49-100), wet gluten (20-40%), and dry gluten (6-13%); gluten L^* (56.97-82.05), gluten a^* value (-0.39-4.50), and gluten b^* value (17-29); deformation energy, W (124-467x10⁻⁴J), tenacity/extensibility ratio (0.38-2.53), and elasticity index, le (0-77%); grain hardness, GH (23-89); water absorption, WA (49-63 %), dough development time (2-22min), stability time (3-25min), and mixing tolerance index (11-84FU). Wheat gluten L^* was positively correlated with le ($r=0.63$) indicating that the stronger the cultivar is ($>le$), the clearer the gluten color is. Flour and gluten b^* values were positively correlated with GH ($r=0.95$ and 0.80 , respectively) suggesting that yellow flour and gluten were obtained from wheat with stronger texture. These results suggest that gluten color analysis can be used as a good quality indicator and that it is possible to use this parameter to determine wheat quality in a first moment. Besides that, gluten analysis could also be officially performed by manual method, and colorimeter is one of the cheapest equipment used for wheat quality evaluation.



2903 - Crop Ecology, Management & Quality

MARTHA ZAVARIZ DE MIRANDA

SOLVENT RETENTION CAPACITY TEST DETERMINED BY NEAR INFRARED LIGHT TECHNOLOGY TO INVESTIGATE WHEAT QUALITY PERFORMANCE

Miranda,MZ; Tibola,CS; Bordignon,JR; Delanora,R; Elkhouri,M; Pieri,FLZ; Tatsch,PO; Guarienti,EM; Caierão,E;

Embrapa Wheat;

Evaluation of end-use quality is an important component of wheat breeding programs (WBPs). Rapid methods and those which use small amount of samples are important for early generation selection, where grain quantity is limited. Wheat flour can be quickly evaluated for certain quality parameters by using near-infrared (NIR) spectroscopy which is based on the absorption of near-infrared light by organic compounds. The solvent retention capacity (SRC) test is useful for evaluating wheat end-use quality in small scale, and it measures the flour capacity to retain four different solutions. The SRC combined values can establish a flour quality/functionality profile. The aim of this work was to perform SRC test using NIR to investigate wheat technological quality performance. The SRC values of 641 wheat flour samples were analyzed at Kraft Foods, using water (WA influenced by all flour constituents), sodium carbonate (SC related to damage starch), sucrose (Suc linked to pentosans and gliadin characteristics), and lactic acid (LA joined to gluten quality), according to a reference method, being acid ratio (AcR) calculated: $LA/(SC+Suc)$. At Embrapa Wheat the same samples were analyzed by NIR. The equipment FOSS XDS-RCA coupled with the module XDS monochromator with double detection system (silicon 400-1100nm and lead sulphide 1100-2500nm) was used. The spectrum was scanned using the software ISScan TM, and all spectral data acquired in reflectance mode and recorded as $\log 1/R$. The reference SRC values were used to develop a NIR calibration curve (CC). For the validation test, 46 unknown flour samples were performed by NIR. The accuracy of each CC was tested by using cross-validation in four groups. The best CC was selected based on the highest determination coefficient (R^2) of calibration and the lowest standard error of cross validation. The NIR CCs were performed by modified partial least square calibration models. The spectral outliers were removed, and samples with large residuals omitted from the population. The validation R^2 values (and curve ranges) obtained for SRC solvents were: WA= 0.92 (48.53-77.19%), SC= 0.91 (45.20-107.69%), Suc= 0.85 (79.81-113.28%), LA= 0.79 (62.14-181.02%), and AcR= 0.65 (0.42-1.02%). The calibration models showed a very good prediction for WA, SC, and Suc, and an acceptable prediction for LA and AcR. These suggest that SRC test by NIR can be successfully used for quick screening of wheat quality in early generation of WBPs.



3181 - Crop Ecology, Management & Quality

Renata Heidtmann Bemvenuti

DETERMINATION OF MYCOTOXINS PRODUCED BY FUSARIUM GRAMINEARUM IN PRESENCE AND ABSENCE OF ESTROBIRULINS FUNGICIDES

Heidtmann-Bemvenuti,R; Nora,NS; Kraide,LE; Manetti,KO; Badiale-Furlong,E;

Universidade Federal do Rio Grande;

Nivalenol (NIV), deoxynivalenol (DON) and zearalenone (ZEA) are mycotoxins produced by fungi of the genus *Fusarium* and are frequently found in cultures that predominates the high water activity during cultivation. Some studies have shown that toxigenic fungi can produce more mycotoxins in presence of fungicides because these chemical products can cause stress to the fungus, that produces mycotoxins as a defense mechanism. The objective of this work was to evaluate in vitro the effect of the use of azoxystrobin and trifloxystrobin in the production of NIV, DON and ZEA produced by *Fusarium graminearum*. A mycelial disc of 5 mm of diameter was inoculated on petri dishes containing 15 mL of potato dextrose agar (PDA) 39 g/L, which is the control medium. In the experiment containing the fungicides, azoxystrobin (0.1 mg/kg) and trifloxystrobin (0.2 mg/kg) were added to the PDA medium before inoculation of the fungus. The plates were placed in a incubator chamber (12 h light and 12 h dark) for 10 days at 25°C. The extraction of mycotoxins was based on the methodology described by Vaclavik et al., (2010) with modifications. Quantification was performed using thin layer chromatography with high efficiency (HPTLC) using the photometric procedure developed by Hoeltz et al., (2010). The vat elution containing toluene:ethyl acetate:formic acid (30:20:5). For development, HPTLC plate was rapidly immersed in aluminum chloride (15%) and taken to 130°C for 10 min. The production of NIV, DON and ZEA by *F. graminearum* was higher when fungicides were present in the medium, being higher in medium containing trifloxystrobin. Regarding the control medium containing *F. graminearum*, the increase in the production of mycotoxins were present when the fungicide azoxystrobin and trifloxystrobin were, respectively, 42.6% and 44.3% to NIV, 49.3% and 60.4% to DON and 24.5% and 35.4% to ZEA. It was demonstrated that the use of chemical fungicides stimulates the production of mycotoxins, such as other studies have reported for other sources of mycotoxins.



3180 - Crop Ecology, Management & Quality

Renata Heidtmann Bemvenuti

MEASURE OF GLUCOSAMINE AND ERGOSTEROL AS AN INDICATOR OF INHIBITION OF FUSARIUM GRAMINEARUM BY ESTROBIRULIN FUNGICIDES

Heidtmann-Bemvenuti,R; Nora,NS; Kraide,LE; Manetti,KO; Badiale-Furlong,E;

Universidade Federal do Rio Grande;

Fusarium graminearum is a toxigenic fungal that commonly contaminated grains and other plants in the field, especially when there is a predominance of high water activity, eg in rice cultivation. Fungicides azoxystrobin and trifloxystrobin are widely used for the cultivation of this cereal. The objective of this study was to evaluate in vitro inhibition of *Fusarium graminearum* by using azoxystrobin and trifloxystrobin and employing determination of ergosterol and glucosamine. A mycelial disc with 0.5 cm of diameter was placed in the center of the petri dishes containing 15 ml of potato dextrose agar (PDA) 4%, this was the blank of experiment. In the experiment with the inhibitor, the fungicide azoxystrobin (0.2 mg/kg) and trifloxystrobin (0.4 mg/kg) were added to the PDA. The plates were incubated in BOD (12 h light and 12 h dark) for 7 days at 25°C. The measure of halo was performed in quadruplicate on the 3th, 4th, 5th, 6th and 7th day of growth in three directions. The glucosamine and ergosterol determinations were performed on 7th day of fungal growth. By halo measuring, the greatest inhibition of the fungus by azoxystrobin was observed in 4 th (27.4%), and by trifloxystrobin on the 5th day (35.8%). At 7th day, the plates containing azoxystrobin were completely filled with the mold, while the plates with trifloxystrobin showed inhibition of 13.6%. The rate of fungal growth in a medium containing azoxystrobin was higher (1.18 cm/day) than in medium containing trifloxystrobin (0.98 cm/day). The glucosamine measure showed inhibition of 48.3 and 48% and ergosterol of 15.1 and 10.5%, by azoxystrobin and trifloxystrobin, respectively. These results show that measurement of the halo is not efficient to measure the fungal development, because this measuring the volume of mycelium and does not quantify components of wall or membrane fungal, such as glucosamine and ergosterol. The legislation of Brazil to fungicide in rice requires that the replacement of the fungicide must be after 30 days for azoxystrobin and 15 days for trifloxystrobin at concentrations of 0.1 and 0.2 mg/kg, respectively. With this study was possible to observe that a replacement would be in a shorter period. However, these compounds are toxic to humans, and therefore would be interesting to find an alternative to application of the fungicides, such as the use of antifungal agents from natural sources, which does not harm the environment and would not be toxic to humans and animals.



3161 - Crop Ecology, Management & Quality

Silmara da Luz Correia

WINTER COVER CROPS TO PADDY RICE SUSTENTABILITY

Luz-Correia,S; Boeni,M; Silva,PRF; Anghinoni,I; Carmona,GI; Maass,MB;

UFRGS;

The objective of this study was to evaluate paddy rice agronomic performance in succession to four cover crop systems in the winter, grown under three fertilization rates. A field experiment was conducted during two years (2010/11 and 2011/12), in Cachoeirinha, RS, Brazil. Treatments were composed by four winter cover crop systems (ryegrass (*Lolium multiflorum*), a leguminous species (*Ornithopus micranthus*), a system with simultaneous cropping of ryegrass and *Ornithopus* and a fallow soil check) and three fertilizer rates in rice growing in succession, according to the soil analysis (without fertilizer and expectations to medium and to very high response to fertilization). The experimental design was a randomized complete block, disposed in split-plot, with four replications. In the first year, initial plant population was higher in the fallow treatment in relation to the other soil cover systems, while in the second year plant population was higher with the mixture of the two winter crops. Regardless of crop cover and year, plant population was within the recommended range for rice crop, which is 150 to 300 plants m⁻². The number of panicles m⁻² varied with soil cover systems only in the second year, being higher in rice in succession to *Ornithopus*. In both years, this yield component increased up to the application of fertilizer to very high expectation of response, especially in the second year. In the first year, rice grain yield was affected by cover crops and fertilization levels, being lower when rice was grown in succession to ryegrass, in relation to the other systems. In the second year, there was interaction between the two factors. Only in the treatment with fertilization to obtain medium response, grain yield also was lower when in succession to ryegrass, compared to other systems, but it was verified a trend to obtain lower grain yield in the treatment without fertilization. In both years, grain yield increased up to the application of fertilizer to the expectation of very high response, principally in the second year. The results obtained for two consecutive years show that the use of ryegrass as a cover crop in winter reduces rice grain yield grown in succession. In the second year, there is a beneficial effect on rice grain yield grown in succession to *Ornithopus*, resulting in the fertilization response to obtain medium response, while in the other systems there was response to fertilization application to very high response.



2825 - Crop Ecology, Management & Quality

Wei-li LIANG

HOW MUCH IS TOO MUCH: A SYSTEM ANALYSIS ON PRODUCTIVITY AND NITROGEN INTENSITY OF THE WHEAT-MAIZE SYSTEM IN NORTH CHINA PLAIN

Liang,WL; Carberry,P; Chen,F; Whish,J; Wang,GY; Li,RX; Xia,AP;

Agricultural University of Hebei;

Farmers have been blamed of applying too much nitrogen (N) in the wheat-maize double cropping system in the North China Plain (NCP), and it has been said crop yields could be increased by reducing N input level. These statements are misleading against ecological principles. This paper aims to clarify this issue using a system approach. On-farm crop production data of 351 farmers were collected in a survey. Annual productivity of the cropping system at various nitrogen input levels on a typical soil of the survey area with no water and other nutrients constraints was simulated with APSIM using weather data during the same time period of the surveyed cropping season to create a production frontier of crop productivity responding to nitrogen input level. On-farm data and demonstration data from 6 sites in the same year were then compared against simulated data which served as a benchmark. Results: Simulated maximum annual production of the wheat-maize system during the research cropping season was 22.8 t ha⁻¹ with a corresponding N input of 500 kg ha⁻¹. Average annual yield of the demonstration plots was 19.6 t ha⁻¹ with a corresponding N input of 470 kg ha⁻¹. Average on-farm annual yield was 14.8 t ha⁻¹ with a corresponding N input of 372 kg ha⁻¹, corresponding to a simulated annual production of 20.0 t ha⁻¹ - 88% of the simulated maximum N rate. The average annual on-farm production was only 65% of the simulated maximum despite the level of N applied, owing to various problems in management. The average annual yield of the demonstration plots achieved 86% of the simulated maximum which provides good evidence that crop yields can be lifted to higher levels by implementing better field agronomic measures. In current practice, for wheat, 66.7% of the farms used too much N and 6.6% applied inadequate N (i.e. less than 55% of N demand for achieving the simulated maximum yield). For maize, 27.4% of farms over-applied N and 31.6% used inadequate N. Annually across both crops, 43% of farms used too much N and 9.1% of them applied inadequate N. The correct way of addressing reasonable N input level is to relate it to crop productivity. Therefore, the current farm yields of the wheat-maize system in NCP are too low compared to levels of N input and potential yield. Productivity of the system could be increased before reaching the currently available potential by 32.4% with an annual N input increase by 26.3%.



3089 - Crop Ecology, Management & Quality

Yongmin, Jin

ANALYSIS OF SOIL ORGANIC CARBON AND RICE YIELD, QUALITIES IN 21 YEARS NO-TILL AND TILLAGE PADDY FIELD

Youngmin-Jin,JYM;

Gyeongnam agricultural research and extension service;

The soil organic carbon(SOC) plays an important role in enhancing crop production and mitigating the net rate of greenhouse gas emissions. No-till(NT) agriculture is one of the management practices that conserves SOC, and lowers the cost of production by compensating labor, fuel and equipment cost when compared with conventional tillage(CT). In this study, we investigated physicochemical characteristics to find content of SOC and rice growth, yields components and qualities to examine the characteristics of mechanical transplanting culture in the 21 years no-till paddy field. All the crop residues were restored to the soil. Soils were sampled (0-30cm) from NT and CT paddy field at each. SOC was calculated based on equivalent soil biomass. Rice growth, yield components, yield and quality were examined in NT and CT paddy system using testing variety, dongjin 1. Organic matter layer was approximately 5.5cm in NT paddy field, available P and exchangeable cation content in NT were higher but the pH level was lower than CT in the cultivation layer, SOC content in NT paddy field was 8.7ton/10a, it was 87.5% higher than CT paddy field. Planting depth when mechanical transplanting in NT paddy field was 2.2cm depth, it showed the significant shallow planting depth than CT paddy field, 3.3cm(p



Poster Session

Crop Physiology and metabolism



3258 - Crop Physiology and metabolism

Adriana de Andrade Figueiró

BIOCHEMICAL MECHANISMS INVOLVED IN PARTIAL CROWN RUST RESISTANCE IN OAT

Figueiró,AA; Reese,N; Gonzalez,J; Pacheco,MT; Delatorre,CA;

UFRGS;

Crown rust caused by *Puccinia coronata* f. sp. *Avenae* (PCA) is the most widespread and damaging disease in oat (*Avena sativa* L.), occurring in all environments where this cereal is cultivated. Traditionally, the resistance exploited by oat breeder completely prevents reproduction of the fungus on the host and generally it segregates as a single or few genes. However, this practice leads to a strong selection pressure on pathogen, contributing to fast emergence of new races capable of overcoming the resistance. Therefore, complete resistance has a short durability, reducing the useful life of cultivars. It has been suggested that partial resistance should be more durable. The Brazilian oat cultivar URS21 is partial resistant and has remained resistant to crown rust since its release in 2000 to the present. URS21 allows the presence of a small amount of disease throughout the crop cycle. Elucidation of the resistance mechanism could be useful in the selection of parents in breeding programs. This study aimed to identify the mechanisms involved in the partial resistance of URS21 to crown rust. URS21 was studied in comparison with the genotypes Leggett (complete resistant), URS22 and Clinland (both susceptible). First fully expanded leaf from the oat seedlings was inoculated with a spore suspension in mineral oil (105spores/mL). Leaf samples of each cultivar were collected at 0, 6, 24, 48, 72, 120 and 240 hours after inoculation (hpi). The evaluations included phenolic compounds, chlorophylls, carotenoids, hydrogen peroxide contents and catalase (CAT), glutathione reductase (GR) and ascorbate peroxidase (APX) activities. The results showed that the interaction between URS21 and PCA caused an increase in the synthesis of phenolic compounds at 24 hpi followed by reduction, whereas in URS 22, the levels of phenolic compounds were gradually reduced until 72 hpi, after that a large increase was observed probably associated to the fungus colonization. H₂O₂ levels reduced at 24 hpi in URS21, at 6 hpi in Leggett, and in the susceptible cultivars, only at 48 hpi. The three enzymes analyzed involved in the quenching of the oxidative stress had, in general, the smallest activities in URS21 and the largest ones in Clinland, after inoculation. URS21 showed the highest levels of chlorophylls and carotenoids. The data suggest that ROS does not play any important role and phenolic compounds may be involved in this partial resistance mechanism.



3253 - Crop Physiology and metabolism

Alexandro César Faleiro

PROTEOMIC ANALYSIS OF ZEA MAYS VARIETY DKB240 INOCULATED WITH AZOSPIRILLUM BRASILENSE FP2

Faleiro,AC; Espíndula,E; Pereira,TP; Arisi,ACM;

Universidade Federal de Santa Catarina;

The *Azospirillum* genus consists of spirillum-shaped, Nitrogen-fixing, Gram-negative alpha-proteobacteria often living plant rhizosphere. It is involved in the promotion of secondary roots and plant growth by phytohormones production and other metabolic compounds involved in the plant defense. The aim of this work is to investigate the influence of *Azospirillum brasilense* FP2 in development of maize seedlings in relation to the number of secondary roots, main root length and weight, root total weight (adventitious + main root), weight and number of adventitious roots, leaf length and weight and to identify differential proteins involved in the plant-bacteria interaction. Seeds of *Zea mays* var. DKB240 were germinated in test tubes containing 14 mL of Plant Medium (Egener et al., 1999) kept in the dark for three days in germination chamber. After three days of growth, the seedlings were inoculated with 10⁵ CFU of *A. brasilense* FP2 strain for 30 min, at 30 °C and 120 rpm. The bacterial counts were taken 1, 4, 7, 10 days after inoculation in three biological repetitions. The collected plants were evaluated at each time in relation to the above traits. The samples were stored at ultra-freezer at -80 °C for protein extraction and subsequent proteomic analysis. Results obtained did not show significant differences among the evaluated traits. However, small variations were observed among repetitions of the same experiment suggesting that this maize variety has a significant natural variability. Root protein extraction protocol and IEF and SDS-PAGE conditions were optimized for subsequent proteomic analysis. **Keywords:** Plant-Bacteria Interaction; *Azospirillum brasilense*; *Zea mays*; Proteomics



3200 - Crop Physiology and metabolism

ANA CLAUDIA PEDERSEN

PLANT GROWTH REGULATOR AND DENSITY: EFFECTS ON THE LEAF AREA INDEX OF CORN

Pedersen,AC; Mello,N; Giacomini,R; Chavarria,G;

Universidade de Passo Fundo;

The corn crop is widespread in Brazil due to its multiplicity of uses and also the tradition of cultivation this cereal by Brazilian farmers. The leaf area index (m^2 of leaf area per m^2 of ground area) of cultivated plants is a key information for obtaining optimal levels of photosynthetic leaf area and high productivity. Trinexapac-ethyl has been widely used in wheat in order to restrict the plant growth and reduce the bending down. The reason of the use of trinexapac-ethyl in maize is to reduce the height in the early stages of development, giving the possibility of greater interception of solar radiation and also diverting carbon from vegetative growth to reproductive structures. However, in maize there is no information in the scientific literature. The objective of this study was to evaluate the effects of trinexapac-ethyl and variations in plant density on the leaf area index in corn. The work was carried out in Passo Fundo/RS in 2010. The hybrid Status at 45 cm spaced sown and variations in density of 60, 70, 80 and 90 thousand plants per hectare, with and without applications of trinexapac-ethyl (1.2 L ha^{-1}) at four true-leaf stage. The experiment used a randomized block design, plots were 6 m long and 3.15 m wide, four replications. 250 leaves were collected randomly and measured the length and width of the leaf, and the leaf area was determined using a leaf area meter (LI-3100C). After measurements leaf area measurements were correlated with biometric parameters (length and width), to estimate leaf area in a nondestructive method. In each plot 10 plants were selected and their leaves measured to estimate the leaf area index. According to the correlation between leaf length and width, as a tool for estimating the leaf area, was observed that the most suitable biometric parameter, for the hybrid Status, was the length through the linear equation ($y = 9.8083x - 182.18$ $r^2 = 0.87$). Trinexapac-ethyl did not affect the leaf area index of corn in any sowing density evaluated. According to the sowing density was observed a increase in leaf area index in plants grown at 90 thousand plants per hectare. Trinexapac-ethyl does not affect the leaf area index of corn in sowing densities of 60, 70, 80 and 90 thousand plants per hectare. The density of 90 thousand plants resulted in higher leaf area index in corn plants.



3313 - Crop Physiology and metabolism

Ana Paula Schwantes

EFFECT OF STROBILURIN PYRACLOSTROBIN IN THE RATE OF CARBON ASSIMILATION, NITRATE REDUCTASE ACTIVITY AND YIELD OF SOYBEAN

Schwantes,AP; Dourado-Neto,D; Fagan,EB; Rodrigues,MAT; Martins,KV; Galdi,G;

University of São Paulo;

The incidence of diseases compromises the yield of cultures and the quality of the grains. There are many agricultural practices used by farmers to control these diseases, including the use of fungicides. Beyond the control of fungal diseases, studies have shown that the use of strobilurin Pyraclostrobin fungicides causes physiological changes in many cultures, reflecting on increases in production of dry matter and grain yield. With the purpose of studying the effect of the strobilurin Pyraclostrobin application on physiological and phenometric variables on soybean crop, this experiment was carried out at University of São Paulo, Escola Superior de Agricultura "Luiz de Queiroz", in Piracicaba - SP, Brazil, from November 2005 to May 2006. Evaluations of gas exchange (net photosynthesis and respiration), dry mass of aerial part and roots, and leaf area were taken. Based on these results, the gross rate of carbon assimilation and the net rate of carbon in the pods were calculated using models proposed by VAN KEULER e WOLF (1986). The activity of nitrate reductase enzyme, mass of 1000 grain and yield were also evaluated. The experimental design was randomized blocks with three treatments (T1 - no fungicide application; T2 - two applications of Pyraclostrobin at R1 e R5.1 soybean phenological stages and T3 - two applications of Tebuconazole - triazol - at R1 and R5.1), with four replications. Strobilurin Pyraclostrobin application increased the gross rate carbon assimilation and the net assimilation in the pods. The nitrate reductase enzyme activity increased by the application of Pyraclostrobin at the 15th day after the first application. Plants treated with Pyraclostrobin increased 7 to 8% in the mass of 1000 grains, and 13 and 14 bags ha⁻¹ in productivity, when compared to the untreated and to the treatment with triazole (Tebuconazole), respectively. The results indicate that Pyraclostrobin affects the rate of carbon and nitrogen assimilation in soybean, which is reflected in grain yield.



3316 - Crop Physiology and metabolism

Ana Paula Schwantes

PHYSIOLOGICAL CHARACTERIZATION OF STROBILURIN PYRACLOSTROBIN ACTION ON GAS EXCHANGE IN CORN AND SOYBEAN

Schwantes,AP; Dourado-Neto,D; Fagan,EB; Rodrigues,MAT; Martins,KV; Lacerda,MP;

University of São Paulo;

Studies have been demonstrating that strobilurin Pyraclostrobin fungicides have been providing productivity increase, even in sites without disease pressure. This effect is attributed to physiological alterations caused by fungicide use. With the aim of a better understanding of the effects of strobilurin Pyraclostrobin application, two experiments were carried at University of São Paulo, Escola Superior de Agricultura "Luiz de Queiroz", in Piracicaba - SP, Brazil: one with the soybean cultivar BRS Valiosa RR and the other with the corn hybrid DKB 390. The statistical design was complete randomized blocks with three treatments (T1 - untreated, T2 - two strobilurin Pyraclostrobin applications in R1 and R5.1 growth stages and T3 - two applications of triazole Epoxiconazole in R1 e R5.1 growth stages) and four replications. The gas exchanges determinations were programmed for three hours after products application and then in 1, 3, 7, 8, 10, 15 and 24 days after fungicides application, from 9am to 11am in sunny days. These measures were taken with an Infra-red Gas Analyzer (IRGA) model LI-6400 (Li-cor®) in two plants for each plot. Based on the results it was noticed that the net photosynthesis increased in plants treated with the strobilurin Pyraclostrobin due to partial inhibition of cellular respiration. It was observed that the internal concentration of CO₂ evaluated during the respiration process (Ciresp) was reduced when the strobilurin was applied, for both crops. However corn is a plant from C4 photosynthetic group, in which the Ciresp alterations are lower, showing a more stable metabolism, what can explain the better adaptation of these plants to stress conditions. There was also reduction of water loss by transpiration process in soybean when the strobilurin Pyraclostrobin was applied. On the other hand, there was not any influence of the fungicide use on corn transpiration. Although the physiological effect of the strobilurin is more significant on soybean, the use of this fungicide has shown higher yield in both crops of the study, what means that the physiological effect resulted in increased productivity.



3268 - Crop Physiology and metabolism

Bon Il, Ku

GROWTH RESPONSE AND NITROGEN USE EFFICIENCY OF HIGH YIELD JAPONICA RICE TO VARIABLE NITROGEN FERTILIZATION

Kang,SG; Hassan,MS; Park,HG; Choi,MK; Ku,BI; Kim,YD; Park,TS; Kim,BK;

National Institute of Crop Science, RDA, Iksan 570-080;

Nitrogen (N) is often limiting factors for high yield in rice (*Oryza sativa* L.) production. This study was conducted to determine the responses to different levels of nitrogen application on rice growth at National Institute of Crop Science (NICS), Iksan, 2011. Three N application rates (90, 150, 210 kg N ha⁻¹) were evaluated on two high yielding japonica rice varieties (Boramchan and Deuraechan) and Dongjin2 as control. Only the single year this study was conducted, N application effect on yield was not evaluated. Higher photosynthetic rate (Pn) was resulted in higher nitrogen levels than optimum dose. Rice varieties showed significant variations in Pn and Deuraechan ranked the top. Total nitrogen uptake varied significantly among N levels and varieties. Higher nitrogen levels showed significantly lower nitrogen use efficiency (NUE). Around 57 kg grain yield (rough rice) was produced by the utilization of one kg nitrogen input. Variety Dongjin2 showed the highest nitrogen uptake efficiency while Deuraechan was the lowest but Boramchan and Deuraechan was the top in nitrogen utilization efficiency. Boramchan ranked the top in producing nitrogen harvest index (NHI). Higher amount of yield (rough rice) was obtained from higher levels of nitrogen. Varietal differences were observed in yield under optimum to very high nitrogen levels. Boramchan and Dongjin2 produced significantly higher yield which mainly due to higher number of panicles per m² but comparatively higher number of spikelets per panicle of Deuraechan didn't compensate the yield due to lower number of panicle per m².



3118 - Crop Physiology and metabolism

Camila Pegoraro

GENE EXPRESSION CHANGES ASSOCIATED WITH WOOLLINESS PREVENTION IN PEACH, FOLLOWING PRE-HARVEST APPLICATION OF GIBBERELIC ACID

Pegoraro,C; Tadiello,A; Chaves,FC; Trainotti,L; Oliveira,AC; Rombaldi,CV;

Federal University of Pelotas;

Chimarrita peach (*Prunus persica* Batsch.) fruit have high metabolic rates and a short postharvest life. Cold storage (CS) is one of the most frequently employed methods for extending shelf-life of peach. However, prolonged storage at low temperature can negatively affect fruit quality causing woolliness. Recently, Pegoraro et al. (2010) observed that gibberellic acid (GA3) sprayed at the beginning of pit hardening prevents woolliness. In order to evaluate the molecular mechanism of GA3 on woolliness prevention, Chimarrita peach plants were treated as follows: Control - without GA3; and GA3 - spraying GA3 solution (50 mg L⁻¹) at the beginning of the pit hardening stage (45 days after anthesis). For each treatment, peach fruit were harvested when fruit color was light green, corresponding to the pre-climacteric stage. Fruit were stored at 4°C and 92% relative humidity (RH) for 30 days, then exposed to 23°C and 75% RH for two days. Samples evaluated by microarray analysis were collected at harvest and at the end of the two-day ripening after CS. Microarray analysis using gene chip μ PEACH 3.0 followed the Agilent Gene Expression oligo microarrays One-Color protocol. Analysis steps in brief: cDNA synthesis; cRNA synthesis; labeling with cyanine 3-CTP; hybridization; washing; scanning; data extraction; normalization and statistical analysis; data analysis and interpretation. When compared to control fruit at harvest, GA3 fruit showed up-regulation of 63 genes and down-regulation of 74 genes. Some representative down-regulated pathways in GA3 fruit were fatty acid metabolism, *B*-linolenic acid and linoleic acid metabolism, while representative up-regulated pathways in GA3 fruit were sphingolipid metabolism, glycerophospholipid metabolism, and glycerolipid metabolism. Cold stored control fruit had 714 genes up-regulated and 233 genes down-regulated when compared to control fruit at harvest. Cold stored GA3 fruit had 449 genes up-regulated and 170 genes down-regulated when compared to GA3 at harvest. Cold stored GA3 fruit did not exhibit woolliness, and had 1174 genes up-regulated and 1725 genes down-regulated when compared to cold stored control fruit (wooly). Different pathways have been shown to be associated with woolliness development and prevention. Here, membrane lipid metabolism was among the main pathways that were differentially expressed. Given the enormous amount of data generated, processing is still underway and new insights into other pathways may arise.



3362 - Crop Physiology and metabolism
Carla Andrea Delatorre

MOLECULAR MECHANISMS INVOLVED IN PARTIAL CROWN RUST RESISTANCE IN OAT

Figueiró,AA; Reese,N; Gonzalez,J; Pacheco,MT; Delatorre,CA;

Universidade Federal do Rio Grande do Sul;

Crown rust (*Puccinia coronata* f.sp. *avenae*) (PCA) is the main problem to oat production in the world. Traditionally, the resistance exploited by oat breeder completely prevents reproduction of the fungus on the host and generally it segregates as a single or few genes. However, this practice leads to strong selection pressure on pathogen, contributing to fast emergence of new races capable of overcoming the resistance. It has been suggested that partial resistance should be more durable. Secondary metabolites as phenolic compounds and saponins are associated to disease resistance. The Brazilian oat cultivar URS21 is partial resistant and has remained resistant to crown rust since its release in 2000 to the present. This study aimed to verify if phenolic compounds and saponins are involved in the partial resistance of URS21 to crown rust. URS21 was studied in comparison with the susceptible genotype URS22. Flag leaves fully expanded were inoculated with a spore suspension (105spores/mL). Leaf samples of each cultivar were collected at 0, 6, 24, 48, 72, 120 and 240 hours after inoculation (hpi). The evaluations included total phenolic, steroidal saponin and the quantitative relative expression for RTPCR of some genes involved in production of avenanthramides (phenolic compound), such as the key enzymes anthranilate synthase (Anthsy), caffeoyl-CoA3-O-methyltransferase (CCoAOMT) and hidroxi antranilato hidroxicinamoil transferase (HHT), and one gene involved in the production of avenacoside (steroidal saponin), coding the key enzyme cycloartenol synthase (CS). The 18S ribosomal RNA was used as endogenous control. The results showed that the interaction between URS21 and PCA caused increase in the synthesis of total phenolics at 24 hpi followed by reduction, and increase at 72hpi for saponin. In URS22, the levels of phenolic compounds were gradually reduced until 72 hpi, after that a large increase was observed probably associated to the fungus colonization. There was increase at 48 hpi for saponin in URS22, however lower than that found in URS21. The expression of Anthsy was smaller in URS21 and, in URS22 the highest expression was found at 6hpi. URS21 had the highest levels of expression of CCoAOMT, mainly after 48hpi. The HHT gene showed low levels of expression for both cultivars. CS gene had high levels of expression at 6 and 24hpi in URS21. The data suggest that saponin and phenolic compounds may be involved in this partial resistance mechanism



3388 - Crop Physiology and metabolism

Cássio Barcellos Hervé

SEARCHING FOR ALUMINUM-TOLERANCE MECHANISMS IN AVENA SATIVA

Delatorre,CA; Schneider,AB; Hervé,CB; Islamovic,E; Jackson,EW;

Universidade Federal do Rio Grande do Sul;

Aluminum (Al) toxicity is a limitation to yield in acid soils. Oats are considered one of the most Al tolerant small grains but the tolerance mechanism has not been elucidated yet. The mechanisms are commonly related to external chelation by exudation of organic acids or to internal detoxification. Al tolerance in oat has been considered monogenic. Several genes involved in Al tolerance have been isolated in other species. This study aimed to identify in oat ortholog genes related to Al in other species, compare their sequence and expression in contrasting genotypes, and evaluate the Al content and the ability to increase organic acid secretion under Al exposure. The sequences of nine Al-related genes were obtained from NCBI and compared to the USDA CORE Oat EST Database. The genotypes UFRGS17 (tolerant) and UFRGS930598 (sensitive) were used for isolation of the gene sequences. Expression analysis were conducted for UFRGS17, UFRGS930598, four RILs from their crossing, and the cultivars, Belle, Baker and Sesqui, considered, in the literature, tolerant, tolerant and sensitive, respectively. The Al content and organic acid secretion were measured for UFRGS17 and UFRGS930598. Only ALMT1 sequence has been isolated until now. The ALMT1-like gene was successfully cloned from UFRGS17 and has 2,496bp containing five exons and four introns. It showed high similarity to ALMT1 from *Aegilops tauschii*, rye and barley. Only a partial sequence was obtained from UFRGS930598. The difficulties in cloning the gene from UFRGS930598 suggest the existence of significant differences between the genotypes. Changes in sequence may render a gene nonfunctional. Expression data is currently being analyzed to verify if there are differences between the sensitive and tolerant genotypes. Smaller amounts of Al were found in UFRGS17 shoots compared to UFRGS930598, and malate secretion may be responsible for this reduction in uptake. Quantification of malate and citrate secretion is currently being performed. UFRGS17 accumulated less Al in the internal root tissue than UFRGS930598. The data obtained until now suggest that the difference in Al-tolerance between genotypes is at least partially due to differences in the ALMT1 gene, which causes Al-exclusion. However, it may not be the only mechanism. It has been shown that UFRGS17 and UPF91Al share one major gene as the responsible for Al tolerance and UPF91Al does not limit Al entrance. But both genotypes showed reduced oxidative stress.



2819 - Crop Physiology and metabolism

Ciro A Rosolem

COTTON LEAF GAS EXCHANGE AS AFFECTED BY LEAF AGE AND PHOTOSYNTHETIC PHOTON FLUX DENSITY

Rosolem,CA; Echer,FR; Werle,R; Sirtoli,L; Rodrigues,JD;

São Paulo State University;

This work has no conflict of interests. To evaluate the cotton leaf gas exchange in different leaf ages under distinct photon flux density. The experiment was carried out in a glasshouse at Botucatu, São Paulo State, Brazil (22°51' S, 48°26'O). Cotton plants (Gossypium hirsutum cv. FMT 701) were grown between February and April 2010, in 12 liter pots with soil from the arable layer of a Rhodic Ferralsol (FAO, 2006). Plants were watered daily with half-strength Hoagland's nutrient solution. The experimental design was a 4 x 9 factorial (leaf age x photosynthetic photon flux density- PPFD), in randomized blocks with three replications. Leaf ages were 15, 30, 45 and 60 days while PPFD were 0, 50, 100, 200, 300, 600, 900, 1200 e 1500 mmol m⁻²s⁻¹. Li-COR 6400 was the PPFD source. Measurements of CO₂ assimilation (Pn) of cotton leaves were done using a Li-COR 6400 gas exchange system (LI-COR Inc., Lincoln, NE). Measurements were made from 09:00 to 11:00 am. For statistical analysis, means were compared using t test (DMS, P Results Leaf gas exchange was higher in 15 and 30 days old leaves, but only at PPFD over 600 mmol m⁻²s⁻¹. Fifteen and 30 day old leaves reached the light saturation point (95% of highest Pn) at 900 e 1100 mmol m⁻² s⁻¹, respectively. However, in older leaves the light saturation point was reduced to 700 mmol m⁻²s⁻¹ in 45 day old leaf and to 500 mmol m⁻²s⁻¹ in 60 day old leaf, showing that in old leaves leaf gas exchange is limited by other factors, not related to light intensity. Light compensation point (light intensity where respiration and photosynthesis are null) was lower in oldest leaves, from 19 to 9,5 mmol m⁻²s⁻¹ in 45 and 60 day old leaves, respectively. Furthermore, light compensation point was reached at 26 e 24 mmol m⁻²s⁻¹ in 15 and 30 days old leaves, ratifying the lower light requirement with leaf aging. Conclusions Under low photon flux density leaf age does not affect leaf gas exchange, but changes the light compensation point. The highest leaf gas exchange occurs in 15 and 30 days old leaves at 1000 mmol m⁻²s⁻¹.



3391 - Crop Physiology and metabolism

Clovis Arruda de Souza

EFFECT OF GROWTH RETARDANT ON WHEAT CV. ONIX PLANT MORPHOLOGIC ATTRIBUTES AND ITS YIELD COMPONENTS

Souza,CA; Zanesco,PR; Tormem,ME; Zilio,M; Stefen,DLV; Faccin,TR; Coelho,CMM;

Santa Catarina State University (UDESC);

The objective of this work was to evaluate the effect of different plant growth retardant on the plant morphologic traits and yield componentes in wheat. The experiment was carried out at field conditions, under randomized complete block design with four replications, in 2008 crop year using *Triticum aestivum* L. cv. Onix. The treatments were composed by (i) control (without retardant spray) and the different growth retardant: (ii) mepiquat chloride (MC), (iii) chlormequat chloride (CC), (iv) chlorocholine chloride (CCC) and (v) ethyl-trinexapac (ETP) sprayed when first internode visible stage of the plant. The variables data were submitted to variance analysis by F test and then the mains were compared by Tukey test (p). The traits evaluate were plant height (two and four weeks after plant gorwth retardant spary on plant and, in the harvest), lodging index, tiller number per plant, number of grains per ear, thousand grains weight, hectoliter weight, grains with diameter higher than 2mm and, yield. The plant height due MC, CCC, and ETP-treatment were more short than control, specially on ETP-treatment that decrease plant height in 25.1 cm. The grain yield after ETP-treatment was lower (-773kg.ha-¹) than control. The thousand grains weight was 32.8g. The hectoliter weight was 77.3g. The grains with diameter higher than 2mm was 91%. The number of grains per ear was 134.6. The tillering number per plant was 1.1. The use of growth retardant reduced 11% on lodging; although did differ not from control. In conclusion, these work point to needs continuity in these research to evaluate its effect on the wheat plants.



2898 - Crop Physiology and metabolism

Dr. Pisamai Chantuma

Daily Variable Micro-Climate Affected on Rubber Production

Chantuma,PISAMAI;

Department of Agriculture (CRRRC);

The study aims was assessed the daily variable micro-climate affected on rubber production as well as time of latex flow. The experiment was set up in Chachoengsao Rubber Research Centre (RRIT-DOA) on clone RRIM 600 age 22 years. Harvesting on 5-6th November 2009 which during winter season, tapped trees were divided to 13 groups. Each group,10 trees/group, were tapped with 1/2S d/2 in different time which started from 20.00 pm-12.00 am. The results confirmed the significant effect of micro-climate on yield and latex flow time. The main source of variation was the variable of daily micro-climate. Nevertheless, there were negative correlation between yield and temperature, net radiation, wind speed, evapotranspiration and vapor pressure deficit. On the other hand, there was positive correlation between yield and relative humidity. Also, there was positive correlation between yield and time of latex flow. Yield and latex at first 10 minute, when we tapped at 24.00 pm, were 117.8 g/tree and 7.12 ml respectively and this tapped time was higher than others. Likewise this tapped time spent $4\frac{1}{2}$ hours of latex flow. Daily micro-climate; temperature, wind speed, vapor pressure deficit, evapotranspiration and net radiation were lower. But Relative humidity was high at 24.00 pm.



3417 - Crop Physiology and metabolism

Dr.B.C.Patil

EVALUATION OF YIELD POTENTIALITY AND STABILITY IN G.HIRSUTUM COTTON VARIETIES IN INDIA

Patil,BC; Pawar,KN; Babu,AG; Shaheen,AB;

Agricultural Research Station, Dharwad Farm, University of Agricultural Sciences, Dharwad-580005, Karnataka, India;

Cotton (*Gossypium hirsutum* L.) "The king of fibre" and the leading fibre crop of the world, is an important raw material supplying about 65% requirement of the Indian textile industry. Drought stress is a complex phenomenon affecting the physiology of cotton plant in turn reduces crop growth and yield. An experiment was conducted in 2010-11 and 2011-12 using twenty *Gossypium hirsutum* genotypes grown in RBD design at Agricultural Research Station, University of Agricultural Sciences, Dharwad, Karnataka (India) and evaluated for genotypic variability for growth phenomena, biophysical parameters, yield parameters under irrigated as well as rainfed condition. The two years pooled data in both irrigated as well as in rainfed condition indicated that, the genotypes ARBH-2004, ARBH-813, Sahana recorded highest numbers of bolls per plant while GSHV-96/612 recorded the least. Maximum boll weight was recorded by AKH-0205 followed by RCR-102 and the least by GSHV-96/612 in irrigated condition. In both irrigated as well as rainfed condition BS-279 and ARBH-2004 recorded the highest water potential while GSHV-96/612 and HBB-101 showed by least. The genotypes BS-279 and ARBH-2004 recorded highest photosynthesis rate and chlorophyll content, while CDP-168, CPD-231 recorded least. The genotypes BS -279, ARBH-2004 and HBB-101 showed higher LAI while GJHV-358 and NH-635 recorded the least. The Biplot of seed cotton yield under irrigated condition vs DSI showed that genotypes BS-279, BS-30 and RCR-102 recorded more cotton yield in irrigated condition but high drought susceptibility index. The BS-279, ARBH-813, ARBH-2004 and Sahana proved better as they recorded highest seed cotton yield both in irrigated and in rainfed condition and least to moderate drought susceptibility indices. These genotypes maintained higher yield due to higher yield components, photosynthesis rate, water use efficiency and other biophysical and genetic factors. These genotypes can be used as desirable genotypes for drought situations.



12057 - Crop Physiology and metabolism

Eliemar Campostrini

PARTIAL ROOTZONE DRYING IN SUGARCANE: EFFECTS ON GROWTH AND PHOTOSYNTHETIC CAPACITY

Ribeiro,MS; Campostrini,E; Couto,TR; Netto,AT; Nogueira,RJMC;

Universidade Estadual do Norte Fluminense Darcy Ribeiro, Campos dos Goytacazes - Rio de Janeiro;

Universidade Federal Rural de Pernambuco, Recife - Pernambuco;

Sugarcane (*Saccharum officinarum* L.) is known as an effective crop for biomass production and it is used mainly for sugar production and bio-fuel. In addition, irrigation water has become less available in many regions due to global climate change and domestic purposes. To confront this challenge, there is urgent need to develop water-saving irrigation techniques in order to maximize crop water use efficiency (WUE). Partial rootzone drying (PRD) is water-saving irrigation strategies, and involves irrigating only part of the root zone leaving the other part to dry to a predetermined level before the next irrigation. The objective of this study was to examine whether PRD affects photosynthetic capacity and growth in sugarcane plants. The experiment was conducted from January to April, 2011 in greenhouse of the Universidade Estadual do Norte Fluminense, Campos dos Goytacazes, Brazil. At 20 days mini-stalks sugarcane were transplanted into two pots (12L each, 30cm deep) divided, such that water exchange between the two pots was prevented. The pots were filled with soil (oxisol), sand and manure (1:1:1). The sugarcane plants were well-watered in the first 10 days after transplanting. Thereafter, the plants were exposed to three irrigation regimes: (1) FI (control) in which both soil compartments were watered in the field capacity; (2) PRD in which one soil compartment was watered in the field capacity while the other was allowed to dry to 17 days, then the plants were reirrigated; (WI) without irrigation in which both compartments were allowed to dry to 17 days, then the plants were reirrigated. During the experiment, the net photosynthetic rate, stomatal conductance, transpiration, chlorophyll fluorescence parameters, predawn leaf water potential, leaf temperature (thermal imaging), plant height, leaf area, shoot dry weight, root dry weight, root volume, and water use efficiency were measured. The results showed that the PRD did not affect growth, gas exchange, F_v/F_m , photosynthetic index (PI), and leaf temperature. In addition, the WUE was higher in WI (14.3 g total DW L⁻¹) and PRD (12.9 g total DW L⁻¹) than FI (7.48 g total DW L⁻¹). In this study, PRD irrigation reduced water consumption by 38.5% with a total biomass reduction of 10.8% as compared with fully watered plants. In conclusion, the partial rootzone drying may be an efficient irrigation strategy and promising for application in drought-prone regions for saving water where sugarcane is produced.



3223 - Crop Physiology and metabolism

Fabiano Melo de Matos

ROOT DIVERSITY ANALYSIS OF MAIZE INBRED LINES AND HYBRIDS UNDER LOW AND HIGH PHOSPHORUS

Matos,FM; Meirelles,WF; Negri,BF; Mendes,FF; Moreira-Guimarães,LJ; Parentoni,SN; Vidigal-Filho,PS; Sousa,SM;

Embrapa Maize and Sorghum;

Weathered tropical soils are characterized by low availability of nutrients, especially phosphorus (P), which is the second largest consumed nutrient in agriculture and is by far the least mobile and least available nutrient to plants in most soil conditions. The P concentration in the soil solution is often low and, consequently, its diffusion to the root surface is slow. The development of maize cultivars with a root system that acquire P more efficiently would provide an alternative that is more sustainable and relatively inexpensive. The objective of this work was to investigate the diversity in root morphology of maize inbred lines and hybrids to help develop more P efficient genotypes. Nine tropical maize lines (L3, L228-3, L36, L5680079, L51502020, L5680084, L22, L53 and L5680067t) and thirty six F1 crosses derived from these lines were used in this study. The parental lines and the F1s from each of the crosses were evaluated in a paper pouch system with Magnavaca's nutrient solution under low (2.5 uM) and high P (250 uM) conditions. The genotypes were analyzed in a completely randomized experimental design with three biological replicates, each composed of three plants per pouch. ANOVA was performed and means were compared using the least significant difference (LSD).



3329 - Crop Physiology and metabolism

Felipe Brendler Oliveira

PHYSIOLOGICAL CHARACTERIZATION OF STROBILURIN PYRACLOSTROBIN ACTION ON GAS EXCHANGE IN COTTON

Oliveira,FB; Dourado-Neto,D; Fagan,EB; Rodrigues,MAT; Martins,KV;
Soares,LH; Lacerda,MP;

University of São Paulo;

The use of fungicides is a common practice in Brazilian agriculture, with the purpose of controlling diseases and also due to physiological effects attributed to some of these products. Strobilurin effects are described for crops like corn, soybean and wheat for example, but they are not well known for cotton. Therefore, the objective of this experiment was to evaluate the strobilurin Pyraclostrobin effects on cotton, characterizing gas exchange and yield. The trial was carried at the Crop Science Department experimental area of the University of São Paulo, Escola Superior de Agricultura "Luiz de Queiroz", in Piracicaba - SP, Brazil, during crop year 2006/07, without irrigation. Statistical design was complete randomized blocks with three treatments and four replications: T1 -Untreated; T2 - two strobilurin Pyraclostrobin applications 78 and 96 days after sowing (DAS) and T3 - two triazole Epoxiconazole applications, also 78 and 96 days after sowing. Evaluations were taken at 1, 3, 10 and 24 days after fungicide application (DAA). Net photosynthesis, respiration and internal concentration of CO₂ were measured with an Infra-red Gas Analyzer (IRGA), model LI-6400 (Li-cor®), during photosynthesis period - [CO₂]pho - and respiration period - [CO₂]res. The average of all evaluations shows that respiration rate was 3.7 µmol CO₂ m⁻²s⁻¹ in Treatment 2, where the strobilurin Pyraclostrobin was applied, what means that it was 17.8% lower than the other treatments. The reduction of respiration rate resulted on increased net photosynthesis, which was 29.1 µmol CO₂ m⁻²s⁻¹ with strobilurin Pyraclostrobin application, an increase of 8.5 and 18.2% on untreated cotton and treatment with triazole, respectively. The [CO₂]res. was lower when strobilurin was applied and [CO₂]pho was 6% higher than untreated and 8,5% lower than treatment with Epoxiconazole. The strobilurin Pyraclostrobin also has shown an increase of 39.3 and 17.9% in productivity, compared to untreated and Epoxiconazole application, respectively. With the exposed data it can be concluded that the application of strobilurin Pyraclostrobin provides reduction of respiration on cotton and consequently increase of net photosynthesis, by reduction of [CO₂]res. and increase of [CO₂]pho, what also resulted in higher productivity.



3328 - Crop Physiology and metabolism

Felipe Brendler Oliveira

PHYSIOLOGICAL RESPONSE OF SOYBEAN PLANTS IN VEGETATIVE AND REPRODUCTIVE PHASES TO STROBILURIN PYRACLOSTROBIN APPLICATION

Brendler,FB; Dourado-Neto,D; Fagan,EB; Rodrigues,MAT; Martins,KV; Lacerda,MP;

University of São Paulo;

The use of strobilurin Pyraclostrobin fungicides has been demonstrating in addition to the fungicidal action an increase in productivity attributed to the physiological effects provided. These physiological effects are mainly known during the reproductive phase, making still necessary more studies at the vegetative phase. Therefore, this experiment was carried in a greenhouse located at the University of São Paulo, Escola Superior de Agricultura "Luiz de Queiroz", in Piracicaba - SP, Brazil. The objective was to evaluate the time of response of several physiological variables of soybean to the strobilurin Pyraclostrobin application. The cultivar BRS Conquista was sowed in cylindrical pots with 3.8 L capacity, filled with soil from oxisol. Daily watering was performed to restore the soybean plants evapotranspiration. The statistical design was complete randomized blocks with two treatments (T1 - strobilurin Pyraclostrobin application and T2 - untreated) and five replications. Product was applied when plants reached growth stage V2/3, V8/9 (vegetative phase), R1/2 and R5.1 (reproductive phase). At these time three plants of each treatment were selected and leaves net photosyntheses and respiration evaluations were taken with an Infra-red Gas Analyzer (IRGA), model LI-6400 (Li-cor®). Therefore, the activity of nitrate reductase and ethylene synthesis were also determinate. In the vegetative growth stages the physiological effects were observed through the leaf gas exchange until 7 DAA (days after application) and the nitrate reductase activity and the ethylene synthesis were determinate until 16 and 18 DAA, respectively. In the reproductive period increased physiological activity and lower respiration activity were observed until 10 DAA for R1/2 growth stage and until 7 DAA for R5.1. Increase in ethylene synthesis and nitrate reductase activity evidenced strobilurin Pyraclostrobin effects until 7 and 6 DAA for DAA R1/2 and 3 DAA and 16 DAA at R5.1 growth stage, respectively. Based on these results, it was concluded that strobilurin Pyraclostrobin application in soybean leads to greater photosynthetic activity when applied in vegetative growth stages than during reproductive ones. However, the highest response according to nitrate reductase, respiration and ethylene synthesis seem to occur during reproductive phase.



3228 - Crop Physiology and metabolism

Fernanda G Gonzalez

RELATIONSHIP BETWEEN GRAIN WEIGHT AND SPIKE FERTILITY INDEX IN WHEAT

Gonzalez,FG; Gazaba,LN; Terrile,II;

CONICET-UNNOBA-INTA;

The spike fertility index (SFIh), i.e. the number of grains per gram of non-grain spike dry matter at harvest, has been recently proposed as a promising trait to improve wheat yield potential. Nevertheless, a negative relationship has been observed between the SFIh and the average grain weight (GW), questioning the usefulness of the trait to improve wheat yield potential. The objective of the present study was to analyze the relationship between the grain weight and the SFI focusing on the first physiological determinant of potential grain weight, i.e. ovary weight at anthesis (ODWA). The experiment was carried out in the north of Buenos Aires Province (33°51';sl, 60°56';wl), at the Pergamino Research Station of INTA (National Institute for Agricultural Technology and Husbandry). Three adapted cultivars, two of high SFIh (Baguette Premium11 -BP11- and Baguette 19 -B19-) and one of low SFIh (BioINTA 2002 -Bio2002-) were sown at optimum dates under potential growth conditions. All measurements were performed in the main stem spike.



3228 - Crop Physiology and metabolism

Fernanda G Gonzalez

RELATIONSHIP BETWEEN GRAIN WEIGHT AND SPIKE FERTILITY INDEX IN WHEAT

Gonzalez,FG; Gazaba,LN; Terrile,II;

CONICET-UNNOBA-INTA;

The spike fertility index (SFI_h), i.e. the number of grains per gram of non-grain spike dry matter at harvest, has been recently proposed as a promising trait to improve wheat yield potential. Nevertheless, a negative relationship has been observed between the SFI_h and the average grain weight (GW), questioning the usefulness of the trait to improve wheat yield potential. The objective of the present study was to analyze the relationship between the grain weight and the SFI focusing on the first physiological determinant of potential grain weight, i.e. ovary weight at anthesis (ODWA). The experiment was carried out in the north of Buenos Aires Province (33°51'S, 60°56'W), at the Pergamino Research Station of INTA (National Institute for Agricultural Technology and Husbandry). Three adapted cultivars, two of high SFI_h (Baguette Premium11 -BP11- and Baguette 19 -B19-) and one of low SFI_h (BioINTA 2002 -Bio2002-) were sown at optimum dates under potential growth conditions. All measurements were performed in the main stem spike.



3229 - Crop Physiology and metabolism

Fernanda G Gonzalez

SPIKE FERTILITY INDEX IN WHEAT: TRAIT PERFORMANCE UNDER DIFFERENT CROP GROWTH CONDITIONS

Gonzalez,FG; Terrile,II;

CONICET UNNOBA-INTA;

World wheat demand will grow significantly in next decades thus global production needs to be increased. This increment could be achieved through more area under wheat cropping or increasing farm yields, which are highly associated to yield potential in a large range of environments. The study of ecophysiological attributes simpler than potential yield, but functional associated to this, and the understanding of the physiological and genetic basis would be a useful breeding tool to achieve higher genetics gains in wheat yield potential. The spike fertility index at harvest (SFI_h grain number (chaff weight at harvest)-1) is strongly associated to potential grain number in recent wheat varieties released to the market in Argentina. Understanding the performance and stability of the SFI_h under different crop growth conditions would help to determine its usefulness as breeding tool in the future. Three contrasting cultivars for SFI: Baguette Premium 11 (BP11), Baguette 19 (B19) both with high SFI_h vs BIOINTA 2002 (Bio2002) with low SFI_h were sown under three nitrogen doses (N_i, 130kgN.ha⁻¹, 200kgN ha⁻¹), two levels of incident radiation during stem elongation period (both with 200kgN ha⁻¹) and two different sowing dates (early June and late July) during 2010 and 2011 cropping seasons. Grain number per square meter explained the yield variation between cultivars and different crop situation during both years (R²=81%,)



3242 - Crop Physiology and metabolism

Gabriela Abeledo

DIFFERENCES IN GRAIN YIELD GENERATION BETWEEN WHEAT AND BARLEY

Abeledo, LG; Alzueta, I; Miralles, DJ;

Faculty of Agronomy, University of Buenos Aires; CONICET;

Comparative studies between wheat and barley aimed at understanding the ecophysiological basis related to yield generation in response to different nitrogen (N) conditions are scarce. The main objective of the work was to analyze biomass generation and its partitioning to the grains in wheat and barley cultivars under contrasting soil N levels at sowing (from 40 to 200 kg N ha⁻¹). Changes in biomass production (measured in terms of radiation interception and radiation use efficiency), grain yield (GY) and its numerical components were evaluated. GY ranged from ca. 195 to 750 g m⁻² and, independently of the N condition, barley cultivars showed higher or similar GY than wheat cultivars. GY variations were explained by changes in grain number per unit area ($R^2 = 0.78$, $P < 0.001$); however, wheat and barley differed in the way to generate grain yield. While in barley spikes m⁻² was the numerical component that better explained variations in grains m⁻², changes in grain number m⁻² in wheat were associated with variations in spikes m⁻² as well as in grains spike⁻¹. Barley cultivars showed higher harvest index ($P < 0.01$) than wheat (mean of 0.49 and 0.37, respectively). Differences between species in partitioning were associated with variations in the chaff dry weight at maturity as wheat showed a higher proportion of chaff in the spike at maturity than barley (means of 27 and 17%, respectively). Barley also showed higher efficiency than wheat in establishing grains per gram of chaff. The same trend maintained after correcting the data by the proportion of hull in the barley grains. Thus, variations in grain yield between species (or cultivars) were modulated through changes in harvest index (due to mainly variations in the chaff proportion) and the efficiency of establishing grain per unit of biomass of spike at maturity. Despite the lack of differences in total above-ground biomass between species, wheat and barley differed in variables associated with biomass generation. Total photosynthetically active radiation (PAR) absorbed was higher in barley than in wheat, but the efficiency with which absorbed PAR was converted into biomass was superior in wheat than in barley. In both species, N variations modified GY through changes in total biomass generated at maturity without modifications in harvest index. Analysis of the differences between species in yield generation is a tool for improving their performance under farm conditions (by breeding or management).



3245 - Crop Physiology and metabolism

Gabriela Abeledo

WATERLOGGING IN WHEAT AND BARLEY AND ITS EFFECT ON GRAIN YIELD GENERATION

De-Sanceledonio,R; Abeledo,LG; Miralles,DJ;

Faculty of Agronomy, University of Buenos Aires; CONICET;

Waterlogging induces reductions in yield of grain crops, and the magnitude of that loss depends on the crop phenological stage when waterlogging occurs. Under farm conditions, yield losses as a result of waterlogging are often lower in wheat than in barley. However, it is not well-identified the ontogenic stages where waterlogging is more detrimental to reduce yield and the ecophysiological mechanisms involved in the response of wheat and barley to that stress. The objective of the work was to study the effect of short-term waterlogging events during ontogeny of wheat and barley on yield generation in order to indentify the most susceptible period to the stress. For that purpose, two experiments were carried out under contrasting environmental conditions (sowing in July, under greenhouse, and sowing in September, under field conditions), where one wheat and one barley cultivars were exposed to five sequences of waterlogging events from emergency to physiological maturity (L1-L4, L4-L7, L7-L10, L10-At, At-PM; where L: number of leaf appeared in the main stem, At: anthesis, PM: physiological maturity) with a duration of 15-20 days each event. Yield losses were between 0-74% for barley and 4-92% for wheat, depending on sowing date and the moment when waterlogging was imposed. Main losses in yield were, in both species, with treatments immediately previous to anthesis (mean losses respect to the control of 66% in barley and 85% in wheat), and reductions where greater with the latest sowing date. In barley, yield losses were explained by reductions in total biomass at maturity while in wheat yield reductions were associated with decreases in both biomass at maturity and harvest index. Number of spikes per plant was the main numerical component affected in barley, while yield losses in wheat were associated with reductions in number of grains per spike. Grain weight (in main stem and tillers) was also strongly affected in both species with waterlogging events previous to anthesis and during grain filling period. To conclude, waterlogging negatively affected grain yield of wheat and barley with similar magnitude, but the yield sub-components were differently affected between species. Timing around anthesis was identified as the most susceptible period to waterlogging in wheat as well as in barley. Exposing the crop to a more stressful environment, by delaying the sowing date, magnified the response but it did not modify the sensitive timing to waterlogging.



2829 - Crop Physiology and metabolism

Haruto Nagao

Localization of reactive oxygen species and change of antioxidants in mesophyll and bundle sheath chloroplasts of maize under salinity

Omoto,E; Nagao,H; Taniguchi,M; Miyake,H;

Graduate School of Bioagricultural Sciences, Nagoya University;

The localization of reactive oxygen species (ROS) and change of antioxidants in mesophyll cell (MC) and bundle sheath cell (BSC) chloroplasts were investigated in salt-treated maize leaves. In plants treated with 3% NaCl, superoxide ($O_2^{\cdot-}$), hydrogen peroxide (H_2O_2) and hydroxyl radical ($OH\cdot$) increased significantly relative to control. Transmission electron microscopic observation showed that the structure of MC chloroplasts were more vulnerable to salinity stress than that of BSC chloroplasts. $O_2^{\cdot-}$ localization was found in both chloroplasts under salt condition, but the accumulation was much greater in MC chloroplasts. H_2O_2 localization was observed only in salt-treated MC chloroplasts. In isolated chloroplasts, the activities of superoxide dismutase (SOD), ascorbate peroxidase (APX), dehydroascorbate reductase (DHAR), monodehydroascorbate reductase (MDHAR) and glutathione reductase (GR) were increased by salinity. While the enhancement of SOD activity was similar for both chloroplasts, the increase of APX and DHAR activities were more pronounced in BSC chloroplasts than in MC chloroplasts. MDHAR and GR activities were consistently undetectable in BSC chloroplasts. In salt condition, ascorbate content increased dramatically in BSC chloroplasts, but it was little increased in MC chloroplasts. As the glutathione content was significantly increased by salinity, it was higher in MC chloroplasts than in BSC chloroplasts. These results clearly suggested that $O_2^{\cdot-}$ -scavenging capacity, at least in enzyme activities, was comparable between both chloroplasts, whereas H_2O_2 -scavenging capacity was significantly lower in MC chloroplasts than in BSC chloroplasts although MC chloroplasts were more likely to accumulate H_2O_2 . The differences of ROS accumulation and ROS-scavenging capacity in MC and BSC chloroplasts were associated with the degree of their structural damage under salinity.



3284 - Crop Physiology and metabolism

Hossein Soleimanzadeh

Effect of Selenium Levels on Antioxidant Enzymes under Drought Stress in Sunflower

Soleimanzadeh,H;

Pars Abad Moghan Branch, Islamic Azad University;

Drought stress as a major adverse factor can lower leaf water potential, leading to reduced turgor and some other responses, and ultimately lower crop productivity in arid and semi arid zones. Sunflower is one of the main oil seed crops in Iran, where drought stress is the most limiting factor. Drought stress tolerance requires the activation of complex metabolic activities including antioxidative pathways, especially activated oxygen species (AOS) and scavenging systems within the cells which can contribute to continued growth under drought stress. To evaluate the effect of limited irrigation systems and selenium on seed yield, some antioxidant enzymes, the crop was sown in the Research Farm of College of Agriculture, Islamic Azad University, Pars Abad Moghan Branch in 2011. The experimental treatments were arranged as split plots based on a Randomized Complete Block Design with three replications. The main plots were allocated to three different irrigation regimes. The irrigation regimes comprised of: Full irrigation (IR1), Moderate drought stress (IR5) and Severe drought stress (IR2). The subplots were allocated to four selenium levels consisting of S1 = 10, S2 = 20, S3 = 30 and S4 = 40 gr/ha. Plants under drought stress and selenium levels showed a significant increase in SOD, CAT and GPX activity in compared to control plants. In this context, plants with higher levels of selenium showed higher resistance to drought stress conditions and higher yield and dry matter allocation to grain filling process i.e. harvest index. Results of this study suggested that drought stress leads to production of oxygen radicals and oxidative stress in the plant. The scavenging of AOS by the scavenging system especially by SOD, CAT and GPX was done well and damage to membranes was controlled at higher levels of selenium.



3464 - Crop Physiology and metabolism

Jailson Lopes Cruz

EFFECTS OF CO₂ ENRICHMENT AND NITROGEN SOURCE ON DRY MATTER PRODUCTION OF CASSAVA PLANTS

Cruz,JL; Alves,AAC; LeCain,DR; Ellis,D; Morgan,J;

Embrapa Mandioca e Fruticultura;

Under present-day ambient CO₂ concentrations, NH₄⁺ can be detrimental to photosynthesis and accumulation of dry matter in many cultivated plants, include cassava. However, rising CO₂ levels could increase carbon availability and reverse or minimize this negative response due to a positive effect of carbon on NH₄⁺ assimilation in plants. The objective of this research was to evaluate the effect of elevated CO₂ concentrations and the ratio of supplemental NO₃⁻:NH₄⁺ on dry matter accumulation in cassava plants. Cassava variety COL 1468 were grown in pots in a greenhouse (30/25°C day/night) at either ambient or elevated CO₂ levels (390 or 750 ppm, respectively). Three nitrogen treatments were applied: (a) 12 mM NO₃⁻, (b) 6 mM NO₃⁻ + 6 mM NH₄⁺, and (c) 12 mM NH₄⁺. Thus, the experiment involved a 2x3 factorial combination (two CO₂ levels x three nitrogen source) with six replicates per treatment. To limit biological nitrification, 8 ppm of dicyandiamide was added to all treatments. Plants were harvested 92 days after the initiation of treatments, separated into tubers (roots > 1 cm in diameter) and shoots and oven-dried at 70°C until there was no further change in dry weight. Means of the dry mass for each treatment were compared by Scott-Knott test. Total dry matter (TDM) was, on average, 23% higher in plants grown under elevated CO₂ concentrations (750 ppm) and fertilized with NO₃⁻ or NO₃⁻:NH₄⁺, when compared with TDM from plants grown under ambient CO₂ concentrations (390 ppm). Compared to NO₃⁻ and NO₃⁻:NH₄⁺ treatments, plants fertilized with only 12 mM NH₄⁺ reduced TDM and exhibited symptoms of toxicity, including yellowing, chlorosis, and wilting on the oldest leaves at both CO₂ concentrations. The negative effect of NH₄⁺ was lower under elevated CO₂ concentrations, since plants fertilized with only NH₄⁺ produced 37% and 71% more TDM and tuber dry matter, respectively, when grown to 750 ppm of CO₂. Fertilization with only NH₄⁺ also reduced the proportion of dry matter allocated to tubers (harvest index), and again this effect was more pronounced in plants cultivated under ambient compared to elevated CO₂ concentrations. Our results indicate that cassava will respond with increased biomass accumulation in response to raising atmospheric CO₂ levels and that this increasing carbon supply can minimize the negative effect of NH₄⁺ on dry matter accumulation of cassava plants.



3466 - Crop Physiology and metabolism

Jailson Lopes Cruz

ELEVATED CO₂ DELAYS THE EFFECTS OF WATER STRESS ON GAS EXCHANGE OF CASSAVA PLANTS

Cruz,JL; Alves,AAC; LeCain,DR; Ellis,D; Morgan,J;

Embrapa Mandioca e Fruticultura;

In some regions, reduction in rainfall will occur in conjunction with elevated atmospheric CO₂ levels, resulting in increased water stress on plants. Unfortunately, little is known about how water use efficiency in cassava will be affected by high atmospheric carbon dioxide (CO₂) concentrations. In this study we investigated the effect of CO₂ concentration and water stress on gas exchange parameters (photosynthesis, stomatal conductance, transpiration, and instantaneous water use efficiency-WUE) in cassava. The variety COL 1468 was grown in greenhouse conditions in 12 liter pots and maintained with either 390 (ambient) or 750 (elevated) ppm of CO₂. Two water treatments were applied: (i) consistently well-watered (WW) and (ii) periodically water deficit (WS), imposed by withholding irrigation. Thus the experiment involved a 2X2 factorial combination (two CO₂ levels x two water levels) with six replicates per treatment. Five 7-day cycles of water stress were imposed with each cycle followed by irrigation prior to the start of the next cycle. At the beginning of the third stress cycle, measurements of gas exchange parameters were performed on both stressed and well irrigated plants. WUE was calculated by dividing the photosynthesis by the transpiration. Mean comparisons were done using the Scott-Knott test. Three days following the induction of water stress, stomatal conductance and transpiration were reduced in plants grown under 390 ppm of CO₂ (390_WS), and plants grown under 750 ppm of CO₂ (750_WS) had similar stomatal conductance and transpiration values as well-watered plants. Photosynthesis values of 750_WS plants were similar to plants cultivated under 390_WW and 750_WW. Hence, even after three days of withholding irrigation no negative effects on net carbon assimilation were observed for plants grown at elevated CO₂. In contrast, plants grown under 390_WS had 34% less photosynthesis than comparable plants cultivated with 750_WS. Interestingly, when photosynthesis was measured in 390_WS plants at an external concentration (C_a) of 750 ppm of CO₂ the negative effect of water stress was reversed. In general, WUE of 750_WS plants was 1.6 times higher than in 390_WS plants. Five days after the suspension of irrigation, 390_WS plants had a photosynthetic rate of only 2.5 $\mu\text{mol CO}_2 \text{ m}^{-2}\text{s}^{-1}$, a value 61% lower than 750_WS plants. These data confirm that elevated CO₂ delays the onset of water stress in cassava plants cultivated under limited moisture availability.



3409 - Crop Physiology and metabolism

Javad Vafabakhsh

EFFECTS OF DROUGHT STRESS ON RADIATION USE EFFICIENCY AND YIELD OF WINTER CANOLA (BRASSICA NAPUS L.)

Vafabakhsh,J; Nassiri-Mahallati,M; Koocheki,A;

Agriculture & Natural Resources research Center;

A two years field experiment was conducted during growing seasons in the Agriculture Research Station of Torogh, Mashhad to evaluate response of Canola cultivars to limited water. Experimental design was a split plot with three replications in which irrigation regimes were allocated to main plots and cultivars to subplots. Irrigation treatments including 100 (R1), 80 (R2), 65 (R3) and 50 (R4) percent of water requirement based on previously determined water requirement of Canola in Mashhad. Cultivars were Zarfam, Okapi, SLM046 and Licord. The results showed that yield and yield components were significantly affected by drought stress in two years. In R3 seed yield was decreased at first year however, at R4 decreased seed yield was observed in both years. The highest radiation use efficiency (RUE) for Zarfam, Okapi, SLM046 and Licord was obtained at R1, R4, R4 and R3, respectively. This difference was partly due to decreased leaf area index (LAI) with decreasing irrigation levels. The highest and lowest LAI was observed at control (R1) and severe stress (R4), respectively. Harvest index (HI) was affected by drought stress only in R4 treatment. These results showed considerable differences between cultivars in respect to LAI, RUE and HI under drought stress. The lowest and highest RUE of 0.95 and 2.6 g DM MJ⁻¹ were obtained in drought stress treatments. It can be concluded that in this experiment drought resistance in Canola cultivars depends on their higher LAI and RUE. Key words: Canola, radiation, radiation use efficiency, drought stress, harvest index, leaf area index.



3291 - Crop Physiology and metabolism

Karine Chenu

HOW HIGH TEMPERATURE AFFECTS WHEAT GROWTH AND DEVELOPMENT

Chenu,K; Oudin,F; Chapman,SC; Dreccer,MF; Hammer,GL;

UQ -QAAFI;

High temperature and heat-shock events can severely reduce wheat yield by shortening the crop cycle and by affecting different physiological processes influencing grain set and grain filling. While global warming has already increased mean temperatures and the frequency of heat events, these trends are predicted to accentuate in the future. We conducted several growth-chamber and glasshouse experiments at different temperatures to quantify the effect of heat on wheat growth and development for contrasting genotypes. Plants were subjected to increased temperature over their entire cycle or for restricted period of time at different developmental stages. Higher temperature accelerated plant development and reduced yield components through decreased pollen viability, reduced carbon assimilation and accelerated senescence. Genetic variability in heat responses was notable for plant growth, pollen viability, and carbon allocation among organs. Heat stress around flowering greatly impacted yield, affecting grain set and grain size to different extent depending on the timing of the event. Application of such quantitative results to improve crop-model capability in assessing impacts of future climate will be presented.



3217 - Crop Physiology and metabolism

Karla Sabrina Magalhães

ROOT MORPHOLOGICAL ANALYSIS OF A MAIZE DIVERSITY PANEL

Magalhães,KS; Negri,BF; Desousa,SM;

UFSJ, EMBRAPA MAIZE AND SORGHUM;

The modular structure of roots enables them to quickly respond to their surrounding environment, making plants more adaptable to environmental changes, such as water availability and nutrient supply. Certain root system types can help increase the yield due to their higher capacity to acquire nutrients and water. Our work aimed to study root morphological traits of a maize diversity panel, composed of two hundred inbred lines from Embrapa Maize and Sorghum breeding program. The panel was analyzed in a completely randomized experimental design with three biological replicates. Maize seeds were surface sterilized with sodium hypochlorite and germinated in moistened paper rolls. After four days, uniform seedlings were transferred to moistened paper pouches and kept in Magnavaca's solution under controlled conditions. Nutrient solution was changed every three days and the pH was maintained at pH 5.6. In order to analyze and quantify root traits, roots were photographed after 13 days, and the images were processed and analyzed using WhinRhizo software. Four root traits were quantified: length, volume, diameter and volume of fine roots (1-2 mm). Low coefficient of variation, 25.3, 20.2, 7.2 and 24.5% and high heritability 78.2, 79.7, 77.6 and 79.2% were detected for length, volume, diameter and volume of fine roots, respectively. Principal Component Analysis (PCA) was applied, enabling differentiation of genotypes based on the selected root morphology traits. PC1 explained 64.6% and PC2 33.09% of variation of the maize lines. PC1 had positive eigenvector coefficients for all variables, except for root diameter, and was explained mostly by length and volume. PC2 had a negative eigenvector coefficient for length and was explained mostly by root diameter. The information generated by this study will be useful for establishing early selection strategies for selecting maize plants more efficient in water and nutrient acquisition. Supported by Embrapa, CNPq, Fapemig and Generation Challenge Program (GCP).



3314 - Crop Physiology and metabolism

Karla Vilaça Martins

INFLUENCE OF DEFOLIATION LEVELS IN THE YIELD COMPONENTS OF SOYBEAN

Martins,KV; Dourado-Neto,D; Fagan,EB; Rodrigues,MAT; Soares,LH; Schwantes,AP;

University of Sao Paulo;

Soybean is a culture that has monocarpic senescence, what means that it requires the energy from the senescence from old leaves to the vegetative and reproductive development. This way, this study had the purpose to verify the influence of senescence of old leaves to the vegetative and reproductive development of soybean, cultivar NA-7255-RR. The experimente was conducted at Campus II of Centro Universitário de Patos de Minas - UNIPAM, in Patos de Minas, MG, in 2011, and the influence of senescent leaves in the lower level of 0, 25, 50, 75 and 100% of defoliation was evaluated. With the purpose of evaluating the effect of foliar senescence, the plant was divided in three strata, and diferent portions of senescent leaves in the lower strata were maintained (0, 25, 50, 75 and 100%), and this part had 10 leaves in the average. The criteria to determinate the beginning of senescence was the 5% decrease in SPAD index in expanded leaves. Dry mass of pods, total number of pods per plant, weight of 1000 grains and productivity were evaluated. Dry mas of pods and total number of pods linearly decrease with the increase of removing leaves from the lower strata in the beginning of the senescence. Dry mass of pods in plants where 100% of leaves were removed in early senescence, in relation to those the leaves were kept (0% defoliation), presented na average reduction of 28%. The removal of all lower leaves (100% defoliation) caused a loss of 18 pods per plant, when compared to plants where the defoliation level was 0%. The mass of 1000 grains in plants with 0% defoliation was, on average, 146 g, whereas plants with 100% defoliation, the mass was 126 g. Consequently, the yield was reduced when the level of defoliation was increased in the lower strata of the plant, demonstrating the dependance of soybean plants on the energy removed from leaves of the lower strata to grain filling. In plants that a 100% of leaves in early senescence of the lower strata were removed, there was a decrease in productivity of 1545 kg ha⁻¹ compared to plants that weren't defoliated.



3319 - Crop Physiology and metabolism

Karla Vilaça Martins

PHYSIOLOGICAL EFFECTS OF PYRACLOSTROBIN (STROBILURIN) APPLICATION IN SOYBEAN FACTORS PRODUCTION

Martins,KV; Dourado-Neto,D; Fagan,EB; Rocrigues,MAT; Soares,LH; Oliveira,FB; Galdi,G;

University of Sao Paulo;

The Pyraclostrobin (strobilurin) fungicides demonstrate a high capacity for physiological enhancement of crops due to their action in increasing the activity of the nitrate reductase enzyme, decreasing respiratory rate, increasing net photosynthesis, reduction of ethylene synthesis and leaf senescence delay. Thus, this study aimed to evaluate the effect of Pyraclostrobin (strobilurin) fungicides in the number of pods, dry weight of pods and seeds and productivity of soybean, cultivar NA-7255-RR. The experiment was conducted at the Escola Estadual Agrotécnica Afonso Queiroz, Campus II of UNIPAM in Patos de Minas, MG, in 2011. The statistical experiment design was complete randomised block design with three treatments (T1 - no fungicide application, T2 -application of Pyraclostrobin + Epoxiconazole at R1/2 and T3 - application of Epoxiconazole at R1/2) and four replications. The soybean plants in all treatments prioritized the pod yield with 2 and 3 grains which make up around 80% of the total produced pods. The number of empty pods at the T2 treatment in the lower stratum was lower when compared to other treatments. The productivity was higher in treatments with disease control (T2 and T3) compared to no fungicide application (T1). For treatment with application of Pyraclostrobin + Epoxiconazole the increase in yield was 415.14 kg ha⁻¹ when compared to treatment with Epoxiconazole, but when compared to no fungicide application treatment, the increase was 639.89 kg ha⁻¹. According to these results can be considered that the greater number of leafs remaining in the plants treated with Pyraclostrobin + Epoxiconazole, means a higher translocation of assimilates and minerals for the pods growth. The increase in the yield levels is related to the increase in biomass production and consequently photosynthetically active leaf area. Furthermore, the results showed a delay leaf senescence between 8-10 days with the Pyraclostrobin + Epoxiconazole treatment, which became active for a longer period as compared to those treated with only Epoxiconazole, enhancing energy availability for the formation and grain filling.



3088 - Crop Ecology, Management & Quality

Kenji Yamawaki

EFFECT OF RESIDUAL ROOT N OF FABA BEAN ON THE GROWTH, YIELD AND N UPTAKE OF THE SUCCEEDING TURMERIC (*CURCUMA LONGA* L.) CROP

Yamawaki,K; Hattori,R; Matsumura,A; Hossain,MA; Daimon,H;

Graduate School of Life and Environmental Sciences, Osaka Prefecture University;

Turmeric, family Zingiberaceae, which is often used as curry powder and mustard, has recently been popular as a health beverage in Japan. This crop requires a great amount of N fertilizer for higher yield. The chemical N fertilizer demand to this crop could be reduced in some cropping systems including legumes associated with N fixing rhizobia. We focused the N dynamics in the crop rotation system including faba bean crop, in which residual roots might play an important role for N contribution to the succeeding turmeric crop. This study was conducted to evaluate the root deposited N for the succeeding turmeric crop grown in temperate region, Osaka, Japan. Seedlings with 2-3 leaves offaba bean (*Vicia faba* L. cv. Nintoku giant)were transplanted at a density of 5 plants m⁻² in the experimental field on 8 December, 2009. After harvesting pods on late-May, 2010, shoots and/or roots as crop residues were incorporated to the plots. Four treatments of incorporation were as follows; 1) both shoots and roots were incorporated in the faba bean plot (S+R), 2) only roots were incorporated in the faba bean plot (R), 3) shoots were incorporated in the previous fallow plot (S) and 4) no incorporation in the previous fallow plot (C). Seed rhizomes of turmeric were planted at 6.7 plants m⁻² on 14 June, and harvested on 11 December. No chemical fertilizer was applied. Faba bean pod yields of 551 g DW m⁻² and 18.6 g N m⁻² were obtained on late-March. The incorporated shoots of 446 g DW m⁻² contained 8.5 g N m⁻² and the C/N ratio was 21.9. The materials showed traits for rapid decomposition soon after incorporation. Accordingly, 31% of N accumulated in aboveground parts of faba bean was used as green manures. Shoot N contents in S+R and S plots were significantly higher than those in R and C plots after 60 days of planting. Rhizomes were observed after 120 days of planting. At final harvest, rhizome N uptake of turmeric was markedly enhanced in S+R and S plots, as compared with R and C plots, respectively. The differences in N content of rhizome between S+R and R and between S and C plots were 2.1 g m⁻² and 3.7 g m⁻², respectively. On the other hand, the differences between S+R and S and between R and C plots were 0.3 g m⁻² and 1.9 g m⁻², respectively. These results indicated that faba bean residues might be alternative N fertilizer at the rate of 2.1-3.7 g m⁻² in case of incorporation of shoots, and 0.3-1.7 g m⁻² in roots as a basal dressing for turmeric crop.



3226 - Crop Physiology and metabolism

Luis Ignacio Mayer

KERNEL GROWTH AND QUALITY TRAITS OF MAIZE HYBRIDS WITH DIFFERENT END-USE AT CONTRASTING POST-FLOWERING THERMAL ENVIRONMENTS

Mayer,LI; Ordóñez,RA; Savin,R; Cirilo,AG; Maddonni,GA;

Faculty of Agronomy, University of Buenos Aires;

Even though the night time warming is the major trend of world climate change, many productive areas are also subjected to an increment of the mean daily maximum temperature. Knowledge acquisition on the impact of thermal environment on maize kernel weight (KW) and its relative structural and chemical composition would be valuable to maintain or improve grain yield and/or grain quality. We conducted two field experiments (Exp.1 and Exp.2) during 2009-10. Exp.1 was carried out at FA-UBA, (34°35' S, 58°29' W; 26masl) including 3 contrasting grain hybrids (Flint: Mill522, Semi-dent: 2A120HX, Pop-corn: P802) grown under two temperature regimes (control and heated) around mid-day during the effective grain-filling period. Heating (33-42°C at ear level) was applied along two 15-days periods (ES: early stage, LS: late stage). Exp.2 combined a grain hybrid (Pioneer 31N28) and a forage one (Lapopi) grown under 2 nitrogen supplies (non-fertilized and 200 kg N ha⁻¹) at Algerri (41°49' N, 0°38' E; 345masl) and Montferrer (42°20' N, 1°25' E; 820masl). Post-flowering mean temperature at Algerri was 4-6°C lower than at Montferrer. Warmer thermal environments during the active kernel growth, due to either a manipulative treatment (Exp.1) or a geographic difference (Exp.2), determined lighter KWs (between -10 and -15%), which were always promoted by a shorter (pPioneer. The latter hybrid also showed a higher embryo-kernel ratio at the warm location, while an opposite response was exhibited by Lapopi. With respect to kernel chemical composition, oil concentration (only quantified in Exp.1) was reduced (from 7-7,5 to 6-6,5%) by heating only at ES for Mill522 and 2A120HX. Higher temperatures reduced protein concentration only in Exp.2, and the magnitude of this effect was greater for Lapopi. The relative content of zeins always had an increment under cooler thermal environments. Moreover, most of this variation (60-70%) was accounted for by the relative content of B-zeins. In Exp.2 nitrogen restrictions determined lighter KWs due to reductions in grain-filling rate, and lower protein concentrations for all hybrid × location combination.



3320 - Crop Physiology and metabolism

Maíra Paes Lacerda

EFFECTS OF STROBILURIN PYRACLOSTROBIN ON ANTIOXIDANTS ENZYMES IN SOYBEAN

Lacerda,MP; Dourado-Neto,D; Fagan,EV; Rodrigues,MAT; Martins,KV; Soares,LH;

University of São Paulo;

Some studies have been demonstrating that besides disease control, there are also fungicides effects on antioxidant enzymes activity, especially from strobilurin Pyraclostrobin application. However it is still necessary to develop more studies in this research area for a better understanding of these effects. Thus, the purpose of this study was to evaluate strobilurin Pyraclostrobin effect on antioxidants enzymes activity and consequently soybean productivity. Two trials were conducted between November 2006 and may 2007, in the Experimental Area from the University of São Paulo, Escola Superior de Agricultura "Luiz de Queiroz", in Piracicaba - SP, Brazil. The soybean cultivars were M8008 RR (Experiment I) and M7878 RR (Experiment II). The statistical design was complete randomized blocks with 3 treatments (T1: Untreated, T2: two strobilurin Pyraclostrobin + triazole Epoxiconazole applications and T3: two triazole Tebuconazole applications) with four replications. The two applications of fungicides were done at growth stages R1 and R5.1 and leaf samples were collected seven days after each application (7 DAA and 7DA2A). These samples were frozen in liquid nitrogen and taken to the Instituto de Botânica of the Universidade Estadual Paulista (UNESP), in Botucatu-SP, Brazil, with the purpose of determinate antioxidants enzymes activity (specifically catalase - CAT, superoxide dismutase - SOD, peroxidase - POD and polyphenoloxidase - PPO). Soybean productivity was also evaluated in this study. The results were submitted to analysis of variance and compared by Tukey test at 5% level of probability. Average of both experiments has shown that SOD activity increased 45.7 and 34.4% compared to untreated soybean and treatment with only triazole application, respectively. The same trend was observed for CAT and POD. On the other hand, activity of PPO reduced 30.1% compared to T1, indicating low degradation of phenols in plant cells, what means that there was lower stress level than in untreated soybean. The productivity has also shown better results when strobilurin Pyraclostrobin was applied, with an increase of 55 and 16.3% compared to untreated and triazole application, respectively. Based on the presented results it is possible to conclude that strobilurin Pyraclostrobin application provided increase in activity of CAT, POD and SOD and reduction in PPO, what had also influence on soybean productivity, which was higher when this fungicide was applied.



3322 - Crop Physiology and metabolism

Maíra Paes Lacerda

INFLUENCE OF STROBILURIN PYRACLOSTROBIN ON HORMONE LEVELS IN SOYBEAN

Lacerda,MP; Dourado-Neto,D; Fagan,EB; Rodrigues,MAT; Martins,KV; Soares,LH;

University of São Paulo;

Numerous researches have been showing that strobilurin fungicides provides raise of hormone levels, mainly cytokynines, resulting in a direct impact on crops productivity. Considering this, the purpose of this study was to evaluate the effects of strobilurin Pyraclostrobin on cytokynin, gibberellin and auxin levels on soybean. Two trials were conducted between November 2006 and may 2007, in the Experimental Area from the University of São Paulo, Escola Superior de Agricultura "Luiz de Queiroz", in Piracicaba - SP, Brazil. The soybean cultivars were M8008 RR (Experiment I) and M7878 RR (Experiment II). The statistical design was complete randomized blocks with 3 treatments (T1: Untreated, T2: two strobilurin Pyraclostrobin + triazole Epoxiconazole applications and T3: two triazole Tebuconazole applications) with four replications. The two applications of fungicides were done at growth stages R1 and R5.1 and leaf samples were collected seven days after each application (7 DAA and 7DA2A). These samples were frozen in liquid nitrogen and taken to the Instituto de Botânica of the Universidade Estadual Paulista (UNESP), in Botucatu-SP, Brazil, with the purpose of determinate levels of cytokynin, gibberellin and auxin. Soybean productivity was also evaluated in this study. The results were submitted to analysis of variance and compared by Tukey test at 5% level of probability. Strobilurin Pyraclostrobin application raised the level of cytokynin (zeatin and isopentenyl-adenine) in both experiments, what also occurred with gibberellin (gibberellic acid) and the highest increase appears when comparing Pyraclostrobin and untreated plants. The average raise between both applications was 0.004 and 0.0015 ppm when compared to T1 and T3, respectively in Experiment I and 0.002 and 0.0185 ppm in Experiment II. Evaluations of auxin (indolebutyric acid) also shown the same trend. There was an increase of 0.003 and 0.001 ppm comparing to treatments T1 and T3, respectively, for Experiment II. Productivity was also higher when the strobilurin was applied, showing 46.6 and 10% higher results in Experiment I and 63.3 and 22.5% in Experiment II, when compared to T1 and T3. Then it can be concluded that application of strobilurin Pyraclostrobin raises levels of cytokynin, gibberellin and auxin, what results in higher productivities in soybean.



3396 - Crop Physiology and metabolism

Marcos Vily Paladini

PRODUCTION AND CHEMICAL COMPOSITION OF THE ESSENTIAL OIL OF *Artemisia annua* L. VARIETY ARTEMIS SUBMITTED A NPK FERTILIZATION LEVELS

Paladini,MV; Capelin,D; Marchese,JA; Marques,MOM;

Federal Technology University - Paraná (UTFPR);

The objective of this study was to identify changes in the chemical profile of essential oil in plants of *A. annua* var. *Artemis* in response to levels of chemical fertilizer NPK. Plants of *A. annua* grown in the field during the years 2008 and 2009, were subjected to increasing levels of chemical fertilizer NPK in soil with average fertility. The reference dosage of fertilizer was defined based on the recommendations for corn (N: 160 kg ha⁻¹; P2O5: 175 kg ha⁻¹; K2O: 90 kg ha⁻¹), the formulations Urea, Single Super Phosphate and Chloride Potassium, being the control treatments, half dose, one dose and two doses. The essential oil was hydrodistilled in Clevenger apparatus and analyzed by gas chromatography coupled to mass spectrometry (GC-MS) and gas chromatography with flame ionization detector (GC-FID). The essential oil content in leaves decreased linearly with increasing levels of NPK fertilization, with the highest average for the control treatment (9.46 mL kg⁻¹ dry weight of leaves). For oil yield, was not significant adjustment (mean 27.96 L ha⁻¹). Were identified 28 chemical components in the profile, essential oil comprising 94.96%. The majority substances were camphor (44.75%), 1,8 cineol (7.90%), *B*-muuroleno (6.75%), trans-*B*-farnesene (6.51%), myrcene (5.74%). Seven essential oil components showed variation depending on the levels of NPK: p-cymene, camphene, trans-?-terpineol, *B*-pinene, viridifloreno, mirtenila acetate and *B*-pinene, the relative content of these components varied between 0.53 to 2.23% representing approximately 8% of the essential oil profile. The predominant class was monoterpenes (72%). Keywords: NPK fertilizer, essential oils, camphor, 1,8 cineole, chemical fertilization.



2858 - Crop Physiology and metabolism

María del Pilar Vilariño

POST FLOWERING TEMPERATURE AFFECTS YIELD AND OIL CONTENT IN CANOLA (*Brassica napus* L.).

Vilarinho,MP; Rondanini,DP; Miralles,DJ;

Facultad de Agronomía UBA;

Canola (*Brassica napus* L.) is one of the most important edible oils. Even though Argentina has a big potential cropping area, the crop has not been yet fully adopted. Mean harvested area is about 12000 has, with a mean yield of 1400 kg ha⁻¹. Among the reasons for scarce crop adoption is the lack of accurate studies on genotypic adaptation to different environments, which leads to unpredictable and low yields. A research goal is to assess main factors influencing crop yield to elaborate adequate crop management strategies for Argentina. Our objective was to determine how post flowering temperature affects yield and oil in commercial canola cultivars adapted to Argentina. To fulfil this goal, an irrigated and fertilized field experiment, combining genotypes x sowing date, was carried out in Buenos Aires (34°35'S, 58°29'O). Four spring genotypes: 2 short, Hyola 61 (Hy) and BioAureo 2486 (Bi) and 2 intermediate cycle, Jura (Ju) and Gladiator (Gl), and 2 winter genotypes, Barrel (Ba) and Gospel (Go) were sown in 4 dates: 04/30 and 07/01, 2008 and 04/15 and 06/09, 2009 (SD1 and SD2, respectively) in 6-rowed, 3m long plots, with 3 replicates. Measurements included phenology, intercepted radiation, aerial biomass, grain yield and components, and oil grain content. No interactions among factors were found. Results showed differences between years ($p < 0.001$), being yields ca. 80% higher in 2008 (mean extreme values were 3545 kg.ha⁻¹ for Bi SD1, 2008 and 422 for Go SD2, 2009). Significant differences were also found among genotypes ($p < 0.001$); all spring cultivars yielded more than winter cultivars. As expected, SD1 yielded more than SD2. A two months delay in the sowing date, shortened the cycle ca. 20% in all, and exposed post flowering period to higher temperatures (mean temperatures: 14-20°C). Low yield in SD2 was associated to less grain number, the component that better explained variations in yield. During 2009, a rate of reduction of 7000 grains per m⁻² for each 1°C increased ($r^2 = 0.43$) was recorded. Temperature also affected grain weight and oil concentration (1% drop in oil for each 1°C increased), resulting in both less grain and oil yield. We conclude it is possible to obtain good yield and quality in our latitude with early sowings of spring cultivars, avoiding high post flowering temperatures. Further studies on more detailed genotype x environment interactions and breeding for local conditions are needed to match accurately genotype and environment.



3230 - Crop Physiology and metabolism

Maria Paula Laserna

INTER-PLANT VARIABILITY OF PLANT GROWTH AND DEVELOPMENT OF CONVENTIONAL AND TRANSGENIC MAIZE HYBRIDS

Laserna,MP; López,CG; Maddonni,GA;

Cátedra de Cerealicultura, FAUBA, IFEVA-CONICET;

Residual heterozygosis in parental lines of a single cross maize hybrid, or in lines of a transgenic hybrid, may determine inter-plant variability of several traits. The objective of this work was to elucidate the effect of transgene introduction on plant growth, plant development and inter-plant variability of these traits. The conventional DK747 maize hybrid and three transgenic versions of this hybrid (DK747MG, DK747RR, DK747MGRR) were cultivated at two plant population densities (6 and 12 plants per square meter) during two growing seasons (experiments 1 and 2). Plant biomass and phenological stages were recorded along the cycle. Microsatellite variation around MG insertion was also studied, in order to describe genetic variability around the insertion. Tested genotypes exhibited differences in both plant growth and plant development. Some of them were sustained at both plant population densities. The DK747MGRR had the highest ear growth rate around the critical period (EGRCP), but a similar kernel number per plant (KNP) due to a lower reproductive efficiency (RE). On the other hand, the DK747RR showed the shortest thermal time to anthesis (TT anthesis) and to silking (TT silking), and this fact was not related either to the total leaf number, or leaf appearance rate. Inter-plant variability analysis of these traits revealed that DK747MGRR showed leptokurtic curves in most traits, with the exception of TT anthesis which had a platikurtic distribution of data associated to a bi-modal trend. This hybrid explored narrower ranges of EGRCP (1 to 3 g day⁻¹) and RE (100 to 300 day g⁻¹) than those of the other genotypes. At the highest plant density, however, the frequency distribution of RE of the most suppressed plants of DK747MGRR was displaced to lower RE values. No microsatellite variation between conventional and MG hybrids was found, suggesting that phenotypic differences between versions were not attributed to genetic variation due to linkage drag.



3274 - Crop Physiology and metabolism

Mércio Luiz Strieder

PLANT PHENOLOGY OF SOYBEAN GENOTYPES CULTIVATED FROM SEPTEMBER TO FEBRUARY IN SOUTH BRAZIL

Strieder,ML; Bertagnolli,PF; Pires,JLF; Cunha,GR;

EMBRAPA TRIGO;

The length of life cycle and the length of individual development phases of soybean are regulated by the environmental temperature and mainly by the photoperiod. The anticipation of the sowing season or deployment of a second harvest, a common practice in some regions of South Brazil in the recent years, alters the environmental conditions and may affect negatively the plant development. In order to evaluate plant phenology of glyphosate-resistant soybean genotypes suitable for cultivation in South Brazil, six trials were conducted at Embrapa Trigo, in Passo Fundo -Rio Grande do Sul. Thirty-eight genotypes were sown in two early seasons (September 22th and October 5th), in two indicated (November 5th and December 14th) and two late ones (January 24th and February 17th). The trials were carried out in field conditions during the 2011/12 growing season. The soybean developmental stages determined were: seedling emergence (VE), flowering initiation (R1), full flowering (R2), early grain filling (R5) and physiological maturity (R8). Subsequently, the duration of some phenological sub-periods between sowing date and R8 were estimated. The largest plant cycle occurred in September, and the lowest one in February, with a variation higher than 70 days. Relatively to November, in the September and October sowings, the plant cycle increased 32.1 and 23.2 days, while in December it was reduced in 25.2 days, in the average of genotypes. In this comparison, the vegetative stage increased 4.8 and 7.9 days in September and October and reduced in 8.8 days in December. In addition, the reproductive stage reduced in 27.3, 15.3 and 16.4 days, respectively in the September, October and December sowing dates. So, the reproductive stage is more affected by early or late sowing seasons than the vegetative stage. The anticipation of sowing to October might increase the plant height and the risk of lodging, especially on determinate growth type genotypes with maturity group six and seven. On late sowing times, there are strong reductions in plant cycle, in plant height and on the height of insertion of the firstlegume, regardless of the genotype. In these conditions, the length of reproductive stage, and also of vegetative stage is severely affected. These results may allow the prediction of growth and development of soybean genotypes during the final phase of breeding development. The authors declare no conflict of interest and agree with this submitted form



3199 - Crop Physiology and metabolism

Michio Kawasaki

MORPHOLOGICAL CHARACTERISTICS AND FUNCTIONAL DIFFERENTIATION OF AMYLOPLASTS IN TUBERS OF YAMS

Kawasaki,MICHIO; Yoshida,HAYURU; Takahashi,KYOKO;

Faculty of Agriculture and Life Science, Hirosaki University;

Previously we reported that a projection formed in part of an amyloplast in stele of Japanese yam tubers and that the projection plays a role of developing of starch granule. Additionally, we reported that amyloplasts formed in the part beneath the stele in the apexes of elongating tubers in Chinese yams and that they were settled down by gravity and would be concerned in the gravity perception and morphogenesis of tubers. In this study, morphological characteristics of amyloplasts in both the stele in tuber and the part beneath the stele in tuber apex were investigated with some yams, for understanding the mechanisms related with formation of Dioscorea tubers. Japanese yam (Jinenjo) and Chinese yam, cv. Nagaimo which elongate until their harvest times to form long tubers, cv. Iseimo which spherically thickens until harvest time and cv. Genkotsujirou which elongates in the initial stage and then spherically thickens, were used. Amyloplasts in developing and mature tubers were observed by scanning electron microscopy using freeze-cracked samples which were treated by A-O-D-O method. In Chinese yams also, the projections were observed in many developing amyloplasts in the stele of growing tubers. These projections contracted in many amyloplasts in mature tubers after harvest. In the part beneath the stele in apexes of growing tuber in all materials, amyloplasts were also formed but did not have the projections. Sedimentation of amyloplasts was also observed in the part beneath the stele, while amyloplasts in the stele arranged in random order. The number of amyloplasts which settled down at the apexes in elongating tubers of Nagaimo and Jinenjo were greater than it in thickening tubers of Genkotsujirou and Iseimo. The length of the major axis of amyloplast in the part beneath the stele in apexes of growing tuber was shorter than the length of mature amyloplast in stele in all materials significantly. In Iseimo, the length of the major axis of amyloplast in the part beneath the stele was shorter than the length in the part in the other materials statistically. When tubers of all materials matured, few amyloplasts were observed at the part beneath the stele in tuber apexes. Two different types of amyloplasts were identified in each tuber in all materials in this study and would have separate roles for formation of Dioscorea tubers.



2842 - Crop Physiology and metabolism

Onoriode Coast

NOCTURNAL HEAT STRESS IN RICE: PHYSIOLOGICAL MECHANISMS OF TOLERANCE

Coast,O; Murdoch,AJ; Ellis,RH; Jagadish,SVK;

University of Reading, UK;

Rapidly increasing nocturnal temperature in major rice growing regions could negatively impact grain yield and global food security. Physiological mechanisms that govern response to nocturnal heat stress (NHS) in rice are not clearly understood. Our objectives were to determine traits that enhance tolerance to NHS and the possible influence of silicon. In multiple studies with diverse cultivars, we investigated nocturnal leaf respiration, transpiration and conductance, changes in spikelet temperature and fertility, silicon content of leaves and spikelets (palea and lemma), and flowering behaviour of rice in response to NHS. Reduction in spikelet fertility varied between 5-90% across ten diverse cultivars exposed to nocturnal temperatures of 24, 30 and 35°C for 4-21 days, beginning at anthesis. Flag leaf silicon content was least in the susceptible cultivars (Moroberekan and WAB56-104) and 10-30% less than in the tolerant N22. Spikelet fertility was not correlated with palea ($r=0.18$; $P=0.37$) or lemma ($r=0.28$; $P=0.16$) silicon content but was negatively correlated with spikelet temperature ($r=-0.51$; P



2817 - Crop Physiology and metabolism

Rafael da Silva Messias

EFFECT OF FOLIAR APPLICATION OF A NATURAL BIOSTIMULANT IN MAIZE AMINO ACID COMPOSITION

Messias,RS; Galli,V; Silveira,CAP; Schirmer,MA; Rombaldi,CV;

Embrapa Clima Temperado;

In this study the effect of foliar application of formulations based on shale water (SW), the constituent water of shale pyrobituminous rock, on the accumulation of aminoacids in maize grains was evaluated. Maize hybrid (Zea mays) Pioneer 30F53 was grown on field at Pelotas, Rio Grande do Sul, Brazil. Block design was randomized with five replicates and five treatments: C (without foliar application); DW-M (Micronutrients diluted in Distilled Water); SW-M (Micronutrients diluted in SW); SW-1 (SW dose 1); SW-2 (SW dose 2). The applications of the formulations were performed with the use of a pressurised sprayer (CO₂). The first two applications occurred during the vegetative growth period and the third during the reproductive phase. The free amino acids were extracted from 50 mg of lyophilized maize grains samples with 25% acetonitrile in 0.1N chloridric acid solution, using the Ez:faast kit from Phenomenex®. After centrifugation at 18.890 g, the supernatant was filtered in a 0.45 µm PTFE syringe and 2 µl was injected and analyzed by gas chromatography (GC-FID, Shimadzu) with a capillary column ZB-AAA. The carrier gas used was N₂, with the flow of the column adjusted to 2 ml/min and pressure of 60 kPa. The flow rate valve was split 1:17 and the injection and detection temperature was 280 and 320°C, respectively. Foliar application with the highest dose of SW (SW-2) resulted in improvement of asparagines, valine, alanine and proline in maize grains. These last two amino acids together with glutamic acid (at levels significantly greater in SW-M2 treatment) are related to stress tolerance. SW-1 treatment induced the increase only of tyrosine and valine, indicating that the accumulation of some amino acids is dependent of the dose applied. It is also significant to note the decrease on the content of some amino acids, mainly lysine, a limiting aminoacid in maize, and phenilalanine, a key amino acid in the synthesis of proteins and phenolic compounds as a result of the application of SW-2. When SW was enriched with minerals on SW-M treatment, aspartic acid, treonine, alanine and glycine content was improved, compared to DW-M treatment, showing the influence of the interaction between SW and minerals supplied. The profile of aminoacids in maize grains are influenced by the application of formulations based on shale water. Among them, alanine and proline are of interest, because are associated with stress tolerance.



2806 - Crop Physiology and metabolism

Rattalino Edreira Juan Ignacio

HEAT STRESS IN TEMPERATE AND TROPICAL MAIZE HYBRIDS: KERNEL WEIGHT DETERMINATION

Rattalino-Edreira,JI; Otegui,ME;

IFEVA-CONICET;

Heat stress affects kernel growth as it influences both rate and duration of grain filling. The former has been linked with potential kernel weight and may be affected by heating around flowering. The latter depends on assimilate availability per kernel during effective grain filling (i.e. postflowering source-sink ratio), and may be affected by heating during this period. The magnitude of these effects has not been documented for heat stress. In this work we evaluated mentioned traits in field experiments (Exp1 and Exp2), including (i) two temperature regimes, control and heated during daytime hours (ca. 33-40 °C at ear level), (ii) three 15-d periods (GS1: presilking; GS2: from silking onwards; GS3: active grain filling), and (iii) three hybrids (Te: temperate; Tr: tropical; TeTr: Te×Tr) with contrasting tolerance to heat stress. We also assessed the dynamic of water-soluble carbohydrates (WSC) in stem. Heat stress reduced final kernel weight (KW) in most of heated plots, but the magnitude of this effect was larger for (i) the Te (-20%) hybrid than the TeTr (-11%) and Tr (-9%) hybrids, and (ii) GS3 (-22%) than GS1 (-6%) and GS2 (-11%). Negative effect of heating on final KW was mostly related to changes in the duration of grain filling ($r^2 = 0.49$)



3347 - Crop Physiology and metabolism

Román Augusto Serrago

GRAIN WEIGHT RESPONSE TO FOLIAR DISEASES CONTROL IN WHEAT CROPS WITH DIFFERENT SOURCE-SINK RATIO

Lo-Valvo,PJ; Serrago,RA; Miralles,DJ;

Departamento Producción Vegetal, Cátedra de Cerealicultura, UBA.;

Foliar diseases are the main biotic restrictions reducing yield of wheat crops in Argentina. Several researches have documented a large variability in the effect of foliar diseases control on the grain weight (increases between ca. 0% and ca. 25%). One of the main determinants of the magnitude of this variability is the source-sink ratio of the crop. However, no critical experiments were carried out to test the effect of foliar diseases on grain weight in relation to the source-sink ratio of the crop. The objective of this work was to evaluate if the grain weight variation is accounted for by source limitations during the grain filling or by differences in potential grain weight. For this purpose, two field experiments were conducted during 2009 and 2010 in the experimental field of the Faculty of Agronomy of the University of Buenos Aires. Experiments combined two disease treatments (healthy and diseased) and two source-sink ratio levels. The disease was induced by application of "leaf rust" spores (*Puccinia recondita* f. sp. *tritici*) before anthesis. Two different manipulative treatments were imposed in order to modify the source-sink ratio; (i) shaded treatments consisted on a reduction of 80% of the incident radiation along a 10 days period (from 20 to 10 days before anthesis) and (ii) trimmed treatments consisted on an extraction of 50% of the spikelet per spike 10 days after anthesis. In both experiments, foliar diseases affected diseased plots exclusively during the grain filling period. Shaded treatment applied before anthesis, reduced the grain number either for healthy or diseased plots in both years, increasing markedly the source-sink ratio at anthesis. Foliar diseases reduced significantly the grain weight in non-shaded treatments in both years. However, in shaded plots grain weight decrease, due to foliar diseases, only in 2009. The effect of trimmed was different depending on the shading treatment and year. Considering non-shaded plots, the trimmed treatment increased the grain weight in diseased plots in both years whereas no differences were observed in grain weight in healthy crops in 2010. In shaded plots, the behavior observed was different. The increases in the source-sink ratio due to trimming did not modify the grain weight (except on diseased plot in 2009).



3112 - Crop Physiology and metabolism

Román Augusto Serrago

PHYSIOLOGICAL TRAITS LINKED BY TOLERANCE TO FOLIAR DISEASES IN BREAD WHEAT (*TRITICUM AESTIVUM* L.)

Serrago,RA; Lo-Valvo,PJ; Miralles,DJ;

Departamento Producción Vegetal, Cátedra de Cerealicultura, UBA; Consejo Nacional de Investigaciones Científicas y Técnicas (CONICET);

Foliar diseases are the main biotic restriction reducing wheat yield in Argentina. The most important foliar diseases are: (i) leaf rust (*Puccinia striiformis* f.sp. *tritici*), (ii) Septoria leaf blotch (*Mycosphaerella graminicola*) and (iii) Tan spot (*Drechslera tritici-repentis*). The objective of this work is to explore and determine the potential useful of four different physiological traits linked by the tolerance to foliar diseases in wheat: (i) source-sink ratio, (ii) the canopy extinction coefficient (k), (iii) reserves mobilization to growing grains and (iv) the spike photosynthesis. Different experiments were carried out during 6 years (2005-2011) in Argentina and France. The treatments included different sowing dates, N fertilization and fungicide applications (healthy and diseased crops). Foliar diseases appeared mainly during the grain filling period reducing grain yield through reductions on grain weight. The decrease in grain weight due to foliar diseases ranged between 0 and 25% and were associated with changes in source-sink ratio during grain filling period ($r^2=0.80$). When diseases were mainly located in lower leaf layers (e.g. Tan spot), wheat cultivars with lower k values ($k=0.45$) had greater loss of absorbed radiations than those with higher k values ($k=0.75$). However, this behaviour was increased when the variations in k were accompanied with variations on the leaf area index. The reserves located in the stems were mobilized to growing grains both, on healthy and diseased crops. However, reserves mobilization were higher on diseased than on healthy crops. The spike photosynthesis was evaluated by indirect (grain weight of shaded spikes) and direct methods (spike photosynthesis measurements of healthy and diseased crops). No significant differences were founded on grain weight between control (non-shaded) and shaded spikes, neither healthy nor diseased crops; although, consistently the spike photosynthesis of diseased crops was higher than the healthy crops during the grain filling period. The foliar diseases tolerance could be increased enhancing the source-sink ratio and the reserves mobilization to growing grains. However, the relationship between this physiological trait and the potential grain yield needs to be established. In the same way, more efforts are needed to determine the contribution of the canopy architecture and the spike photosynthesis to foliar diseases tolerance.



2870 - Crop Physiology and metabolism

Sang Kuk KIM

INFLUENCES OF PROTON BEAM IRRADIATION ON EARLY GROWTH AND PASTING PROPERTIES OF STARCH IN RICE

Kim,SK; Kim,KR; Kim,HY;

Division of Crop Science, Gyeongsangbuk-do Provincial Agricultural Research and Extension Services;

In this study, two rice cultivars were treated by proton beam irradiation in order to investigate the responses of early growth and the pasting properties of rice starch. TwoRice [*Oryza sativa* L. cv. Ilpum (japonica type), Hanmaum (indica type)] seeds were exposed to proton beam accelerated to 45 MeV (LET 1.57 keV/m) with a dose of 0, 50, 100, 200, 300, 400, 500, 600, 700 and 800 Gy. Germination rate, plant height and root length were measured at 14 days after proton beam irradiation. The pasting properties of rice starch were determined by Rapid Visco Analyzer, Differential Scanning Calorimeter and X-ray Diffraction. Survival rates decreased at 300 Gy. Survival rate was much higher in Hanmaum than in Ilpum at 200Gy. Ilpum rice seeds at 300Gy had a survival rate of 38%, whereas the Hanmaum rice seeds had a lower survival rate of 30%. LD50 of survival rate in both Ilpum and Hanmaum was determined around 250Gy. Amylose content in Hanmaum rice seed was much more decreased at 300Gy than that of Ilpum rice seed. The pasting temperature and time was considerably decreased with increasing proton beam irradiation dose. Peak viscosity, hot peak viscosity, cool peak viscosity, breakdown, and setback were considerably decreased with increasing irradiation dose. Thermal properties of the proton beam-irradiated rice starch showed that proton beam irradiation caused a slight decrease in the peak temperature (Tp) and decrease in conclusion temperature (Tc) and enthalpy change. It was also found that the T_o, Tp and Tc of Ilpum rice starch was lower than that of Hanmaum rice starch. The Ilpum and Hanmaum rice starch in an increased proton beam irradiation had a slight increased crystallinity. The Ilpum rice starch had the greater crystallinity than the Hanmaum rice starch at 300 Gy.



3243 - Crop Physiology and metabolism

Susana R. Valle Toledo

NUTRIENT UPTAKE AND UPTAKE EFFICIENCY OF WHEAT AT DIFFERENT DEVELOPMENT STAGES UNDER SOIL ALUMINUM TOXICITY AT FIELD CONDITIONS

Valle,SR; Pinochet,D; Calderini,DF;

Universidad Austral de Chile;

Soil acidity is an important constraint for agriculture regarding that acidic soils account for a third of agricultural land in the world. The negative effect of soil Al toxicity on grain yield and biomass accumulation has been attributed to decreases of root growth, however, most of the evidences showing this has been carried out in short term experiments under controlled conditions. Few evidences have been made under field conditions. The objective of this study was to quantitatively evaluate the effect of different soil Al levels on shoot and root responses, nutrient uptake (N, P, K and Ca) and nutrient uptake efficiency at three different development stages. Two field experiments were conducted in a Duric Hapludand soil in Valdivia (39° 38' S, 73° 5' W) during the 2005/6 (S1) and 2006/7 (S2) growing seasons. In both experiments, treatments consisted of a factorial combination of 2 spring wheat cultivars (an Al-tolerant: Dalcahue. INIA, and an Al-sensitive: Domo.INIA cultivar) and 5 exchangeable Al levels in the soil (0.3-25.3% at S1 and 0.5-61.3% of soil Al saturation). Treatments were arranged in a randomized complete block design with 3 replicates. In both experiments, soil samples were taken for accounting P, K, Ca and Al soil content. At double ridge (DR), anthesis (An) and maturity, shoot and root biomass were sampled. Plant samples were weighted and chemical analysis carried out. Roots were sampled by a pinboard monolith up to 60 cm at DR and 130 cm at An and PM from each plot. Nutrient uptake efficiency (UPE) was calculated as the ratio between nutrient uptake by the crop to nutrient supply, which has been estimated as the element available. Biomass accumulation both in shoots and roots were significantly.



2868 - Crop Physiology and metabolism

Sylvia Morais de Sousa

PHENOTYPES AND GENES ASSOCIATED WITH ROOT TRAITS UNDERLYING PHOSPHORUS ACQUISITION EFFICIENCY IN MAIZE

Desousa,SM; Clark,RT; Mendes,FF; Oliveira,AC; Kochian,LV; Vasconcelos,MJV; Parentoni,SN; Guimarães,CT; Magalhães,JV;

Embrapa Maize and Sorghum;

Phosphorus (P) is an essential nutrient to plants and is acquired as inorganic phosphate from the rhizosphere solution. P is one of the least available nutrients particularly in highly weathered, tropical soils, limiting substantially plant growth. An interesting approach to circumvent P deficiency in tropical areas is to explore the genetic diversity available in plants to breed cultivars more efficient in P acquisition. It has been shown that root traits, such as root length and volume, are important to determine if a genotype is P efficient. This study aimed to study root traits that could be involved with P acquisition efficiency and to identify candidate genes with an expression profile consistent with a possible role in root morphology. Field phenotyping results under low and high P conditions enabled us to define two contrasting genotypes for P acquisition efficiency that were used for root traits studies. We standardized the nutrient solution conditions in order to find the best phenotyping parameters for root early screening. Root traits presented overall a high heritability and a low coefficient variation. Also, out of 24 root traits analyzed, 10 presented a correlation above 0.9. These results together with PCA allowed us identify four root traits which adequately represent the variation observed among genotypes. The information described in this study is important for designing early selection strategies for P efficiency in maize, which are needed to support advanced molecular and physiological studies. Supported by Embrapa, Fapemig, McKnight Foundation and Generation Challenge Program (GCP).



3103 - Crop Physiology and metabolism

Vívian Ebeling Viana

ANALYSIS OF THE PHYSIOLOGICAL QUALITY AND EVALUATION OF ENZYMATIC ACTIVITY OF CATALASE AND SUPEROXIDE DISMUTASE IN CASTOR BEAN SEEDS (*RICINUS COMMUNIS* L.) CV BRS ENERGY IRRADIATED WITH CO-60

Ebeling-Viana,V; Moreira-Lopes,A; Anjos-Silva,SD; Bobrowski,VL; Deuner,S;

Universidade Federal de Pelotas;

The castor bean (*Ricinus communis* L.) is an oilseed with great importance in Brazil and the world. Induced mutations have been used to improve major crops. In the M1 generation, physiological effects of the mutagenic treatment can be observed and therefore studies analysing the degree of injuries caused by these effects are necessary. In these work, the effects of gamma radiation on seed germination and antioxidant enzymes superoxide dismutase (SOD) and catalase (CAT) were studied in the root tissue of seedlings of castor bean BRS Energia. The experiments were conducted at the Laboratory of Genetics, IB / UFPel in Pelotas, in the first semester of 2011. Three hundred seeds without caruncle were pre-soaked for 24 hours and irradiated at doses of 0; 50; 100; 150 and 200 Gy. At the greenhouse, seeds were sown in trays with 72 cells containing soil, using 12 cells for each treatment. Sowing was performed by hand using a seed in each cell. The first count test was performed on the 7th day after the seeding (DAS) and the germination test was held on the 14th DAS. On the 21st DAS the seedlings were collected and the roots were analyzed for antioxidant enzyme activities. Five hundred milligrams of root tissue were crushed in 2 mL of extraction buffer and centrifuged at 13000 rpm. The supernatant was collected for analysis of enzyme activity. The SOD and CAT activity were evaluated. A randomized complete design was used, with five repetitions of twelve seeds or twelve seedlings depending on the experiment, and the means were compared by a Tukey test (p-0.05). The germination test only showed differences between the control and the dose of 200 Gy. In the first count test, only the doses 50 Gy and 200 Gy were different from each other (p-0.05). Irradiation accelerated seed germination at low doses (0 and 50Gy). As to the other doses, we observed a decrease in the germination percentage compared to the control. Enzymatic analyzes showed an increased activity of SOD when the radiation dose was increased, except for the dose of 150 Gy. For the enzyme CAT the same increase in activity was observed for doses above 100 Gy. Therefore, it can be concluded that low doses of gamma radiation, ca. 50 Gy, promote germination of seeds, therefore being indicated for mutation inducing projects. There was an increase in the activity of oxidative stress related enzymes when the mutagen dose was increased. Key words: Castor bean. Gamma radiation. Mutations.



3395 - Crop Physiology and metabolism

XU Ke-zhang

CHANGES OF ROOT ACTIVITY AND ITS CORRELATION WITH BIOMASS OF ABOVE-GROUND ORGANS OF SOYBEAN CULTIVARS RELEASED IN DIFFERENT YEARS

Ji,JP; Xu,XKZ; Yang,YCW; Xu,XC; Feng,FYD; Zhang,ZP;

Jilin Agricultural University of China;

Currently, with genetic improvement, physiological changes of roots and the reason for agronomic and physiological traits changes are not clear, the yield of soybean makes no big progress, whether it results from limitation of root? Therefore, we tested the changes of root activity (RA), root bleeding sap weight (BSW) and their relationship with biomass of above-ground in 2010 and 2011, aiming to explore the restrictive factors of root. The measuring stages were four leaves stage (V4), flowering stage (R2) pod setting (R4) and seed filling stage(R6), the varieties were 27 soybean cultivars bred in Jilin province from 1923 to 2009. The results showed as follows: 1.The differences of RA, BSW, biomass of above-ground and leaf area among different cultivars are remarkable, the results of the same cultivar in 2010 and 2011 showed the similarity. At all growth stages, the two year mean of RA, BSW and biomass of above-ground showed the positive correlation with year of release, even reached the significant positive level at R4 stage. 2. Biomass of above-ground and root were positive correlated with RA and BSW at whole growth stages and reached the significant positive or extremely significant level at R4. In conclusion, we made the further analysis at R4 stage. 3. At R4 stage, stem and leaf biomass showed the significant positive correlated with RA and BSW, the biomass of leaf stalk, pod and root also showed the positive correlation, but they did not reach the significant level; the biomass of upper and central layers had significantly positive correlation with RA and BSW, the lower layer did not show the significant level. 4. The ratio of the biomass of above-ground to RA or BSW was no big change among different cultivars. The test results illustrated: 1. with the genetic improvement, soybean cultivars have carried the stability characteristics among different years, meanwhile, there were apparent differentiation among different cultivars. 2.The genetic improvement of soybean increased RA, BSW and biomass of above-ground. 3. The correlation between RA, BSW and biomass of above-ground is closest at R4 stage. 4. The biomass of stem and leaf showed the closest correlation with RA and BSW. 5. The correlations of biomass of upper and central layers with RA, BSW were closest. 6. With the genetic improvement, root and parts of above-ground has the coordination evolution. Keywords: soybean; genetic improvement; root activity; bleeding sap weight; biomass



3350 - Crop Physiology and metabolism

XU Ke-zhang

PHYSIOLOGICAL RESPONSES OF SOYBEAN PLANTS AT DIFFERENT GROWTH STAGES UNDER DROUGHT STRESS

Xu,C; Yuan,Y; Xu,KZ; Zhang,P; Ji,P; Zhao,LP;

College of Chinese Herbal Medicine, Jilin Agriculture University;

Two drought-tolerant soybean varieties and two drought-sensitive soybean varieties were grown in pots at growth chamber. Drought stress was performed at seed germinate stage, vegetative stage (fourth leaf stage,V4), flowering stage (R2), pod setting stage (R4) and seed filling stage (R6). The soil water content in drought stress was 8%-11%. Physiological response mechanisms of the soybean varieties to drought stress at different growth stages. The main results are as follows. 1. The length of root, the stem diameter the number of fibrous root in drought-tolerant varieties are much greater than drought-sensitive varieties at seed germinate stage with petri dishes under water limitation. Under 8-11% soil water content in pot or under field conditions, drought-sensitive varieties could not finish their seeding stage. 2. The plant height, leaf area and stem diameter of drought-tolerant soybean varieties were significantly higher than drought-sensitive soybean varieties V4 stage. Roots and branches of the biomass accumulation of drought-tolerant soybean varieties were 32.59% and 14.29% higher than drought-sensitive varieties, respectively, 3. The MDA content, root vigor, the contents of soluble sugar and soluble protein in drought-tolerant soybean varieties were higher than the drought-sensitive soybean varieties at R2 and R4 stages under drought stress, But,it were only showed significantly difference R6 stage under drought stress.. 4. Net photosynthetic rate of drought-tolerant soybean varieties was 28.89% and 61.43% higher than drought-sensitive soybean varieties at R2 and R6 stage, respectively. 5. Under drought stress, maximum fluorescent light (Fm') and light chemical quantum efficiency (PhiPS2) of drought-tolerant soybean varieties were 8.26% and 12.78% higher than drought-sensitive varieties at R2 stage, but at R6 stage, drought-tolerant varieties were 13.26% and 17.88% higher than drought-sensitive varieties, respectively. The Fv/Fm of drought-tolerant soybean varieties was respectively 2.68% and 7.36%higher than the drought-sensitive soybean varieties at R2 and R6 stages, respectively. The electron transmission rate (ETR) of drought-tolerant varieties was 1.2% and 8.3% higher than drought-sensitive soybean varieties at R2 and R6 stages, respectively. Our results showed that seeding stage and R6 stage were the most sensitive stages to drought stress.Key Words : soybean, drought stress, photosynthesis, growth stage



3399 - Crop Physiology and metabolism

XU Ke-zhang

STUDY ON THE CHANGES OF SOYBEAN DIFFERENT NODE SOURCE-SINK RELATIONSHIP IN DIFFERENT YEAR

Feng,FYD; Xu, XKZ; Yang, YCW; Xu, XC; Ji, JP; Zhang, ZP;

Jilin Agriculture University;

Many studies showed that the limitation of soybean yield mainly is that the source is not harmonious with the sink, so it is coordinating soybean source-sink relations that has larger potential yield. In order to understand the changes of soybean different node source-sink relationship in genetic improvement, aiming at coordinating the ratio with source and sink, we studied 21 soybean cultivars representing genetic progress in Jilin Province from 1923 to 2004. They were tested at fourth leaves stage V₄, flowering stage R₂, pod setting R₄ and seed filling stage R₆. The results revealed that: 1 The source and sink of new and old varieties in the whole growth period presented a trend that they were first increased and then decreased along with the increase of the node. 2 Source-leaf area per plant. At V₄ stage, new and old varieties had no big distinction; At R₂ stage, old varieties reached to the maximum around the fourth node, and new varieties attained to the maximum in the eighth node or so; At R₆ stage, the leaves areas of old varieties at the bottom were became small, contrarily the leaves areas of new varieties were increased. Sink-the number and weight of seed per plant, which were intensively distributed in about the 8th node and 12th node, respectively old and new varieties. Source-sink ratio. The ratio of new varieties above the 12th node were increased. 3 As the increase of years, the leaves areas of the terminal and middle of soybean were increased by 1.36% and 0.39% in 82 years. The leaf areas of the basal were reduced by -0.28%; The numbers of seeds in the terminal and middle were increased by 0.79% and 0.37%. The basal were reduced by -0.54%; The weights of seeds of the terminal and middle were increased by 0.47% and 0.11%. The basal were reduced by -0.62%. The result of this paper indicated that in genetic improvement process, new soybean varieties still exist in which source-sink relations were not harmonious above the 12th node. If we increase unit leaf area, and it is too large, leaves shade each other, which are harmful for yield component. Therefore, it is improving the photosynthetic capacity of unit leaf area that is an important way to strength the source, especially the photosynthetic capacity of the terminal unit leaf area. High-yield soybean varieties breeding in the future should pay attention to improve the photosynthetic capability of unit leaf area.



Poster Session

Forage & Grazing Lands



3351 - Forage & Grazing Lands

ALCEU LUIZ ASSMANN

WHITE CLOVER ROOTS PRODUCTION AND NODULATION SUBMITTED TO BORON LEVELS

Assmann,AL; Rodrigues-Silva,M; Assmann,TS; Soares,AB;

IAPAR;

White clover production under different management and its answer to fertilizer levels have been tested, however just a few of these assays had evaluated the plant root development and nodulation when submitted to Boron levels. Due to it, the aim of this study was to evaluate the effect of boron levels over the white clover nodules and roots dry matter production cultivated in soil Oxisol. The experiment was carried out in a greenhouse of the Technological Federal University of Paraná, Campus of Pato Branco. The experimental units consisted of vases with a capacity of 3L. The experimental was laid out as a completely randomized design with five replications. Treatments consisted of five levels of B (0, 0.5, 1, 2 and 4 kg of B.ha⁻¹). The determination of the root was performed one year after the implementation of the experiment by counting the number of nodules and subsequent determination of dry matter of both (roots and nodules). Results The highest root dry matter production was obtained with 2.6 kg of B.ha⁻¹ resulting in a yield of 10.8 g.root.vase⁻¹ which was 83% higher than the control. This response of roots DM yield is consistent with data reported by Lenoble et al. (1996), who found that the use of 2.2 kg.ha⁻¹ B stimulated alfalfa roots growth up to 330% when compared with the plants that were not supplemented with boron. The highest nodules number was obtained with 2.8 kg B.ha⁻¹ and the highest nodules dry matter with 2.7 kg ha⁻¹ B, resulting in 281 nodules.vase⁻¹ and 0.222 g.vase⁻¹ nodules, respectively. Similar results were observed by Bonilla et al. (1997) who found that root nodulation of beans with boron deficiency was low in relation to nodulation with boron at levels sufficient. Conclusion Boron fertilization increased roots dry matter production, nodules number and its dry matter production up to 2.8 kg B.ha⁻¹. Higher rates, however, showed negative effects over the white clover production due to its toxicity. References Bonilla I.; Mergold-Villaseñor C; Campos M. E.; Sánchez N.; Pérez H., López, L.; Castrejón, L.; Sánchez, F.; Cassab, G. (1997). The aberrant cell walls of boron deficient bean root nodules have no covalently-bound hydroxyproline/proline-rich proteins. *Plant Physiol*, 115: 1329-1340. Lenoble, M.E., Blevins, D.G. And Miles, R.J. (1996). Prevention of aluminum toxicity with supplemental boron. II. Stimulation of root growth in an acidic, high-aluminium subsoil. *Plant, Cell and Environment*, 19: 1143-1148.



3280 - Forage & Grazing Lands

André Brugnara Soares

BEEF HEIFERS PERFORMANCE GRAZING WARM-SEASON GRASS PASTURES IN SOUTHERN BRAZIL

Glienke,CLG; Rocha,MGR; Potter,LP;

Federal Technological University of Paraná;

The better forage grasses options in southern Brazil to get heifers ready to mate up to 24 months old are Coast cross-1, as perennial, and Alexandergrass (known as weed and low cost forage) and pearl millet (most cultivated and high cost forage) as annual forage species. The aim of this trial was to evaluate the beef heifers performance and their relationship with forage quality of different warm-season pastures. An analysis was performed using a data set with 436 observations from six heifers grazing trial from 14 to 18 months of age on Pearl Millet, Alexandergrass, and Coastcross1 pastures. The experiments were carried out between 2001 and 2010, at Federal University of Santa Maria. Polled Hereford, Angus, Charolais and Nellore breed heifers were used. Continuous stocking and variable stocking rate to keep 3000 kg DM/ha of herbage mass was used. Forage chemical composition was obtained by hand-plucking method. The data were analyzed with software R version 2.12.2 (2011). Were utilized Kruskal-Wallis non-parametrics and Spearman correlation, with 5% significance level. Results: Average daily gain (ADG) was similar by the heifers grazing Pearl millet and Alexandregress ($P>0,05$), 0,864 kg. heifers grazing coastcross performed worse, 0,610 kg ($P=0.01003$) canopy strata. Similar animal performance was observed between heifers grazing the annual species. These ADG values allow heifers achieve 70% of mature body weight, at the end of grazing period, minimum recommended for mating 18-20 months old heifers (Souza et al., 2012). Conclusions: The green leaf: dead material ratio affect the heifers performance on warm-season pastures. Beef heifers grazing Alexandergrass and Pearl Millet from 14 to 18 months of age have similar performance. References SOUZA, A.N.M.; ROCHA, M.G.; ROSO, D. et al. Productivity and reproductive performance of grazing beef heifers bred at 18 months of age. Revista Brasileira de Zootecnia, v.41, n.2, p.306-313, 2012.



3215 - Forage & Grazing Lands

André Brugnara Soares

INFLUENCE OF CATTLE EXCRETA PATCHES ON SOIL ACIDITY IN RANGELAND OF SOUTHERN BRAZIL

Soares,ABS; Viccini,RV; Assmann,TSA;

Federal Technological University of Paraná;

Beef cattle production is extensively practiced over a rangeland region known as "Campos de Palmas" mainly in cow-calf system operations which preserve environmental conditions. Besides high organic matter content in the soil and high cation exchange capacity, forage production is often limited by chemical composition, specifically acidity (low pH and high Al concentration). Dung and urine deposition in grazing process may affect soil traits, particularly acidity index (Whalen et al., 2000). This work aimed to verify the effect of dung and urine deposition on soil acidification. Field experiment was carried out in the "Campos de Palmas" ecosystem, with the objective to verify possible effect of dung and urine patches on Haplumbrept soil acidification. Experimental plots were considered three concentric rings surrounding both dung and urine patches (0; 0.15 and 0.30 m). Soil samples (0-5 cm depth) were taken just after defecation event (0 day), 32 and 67 days after excreta deposition. Results It was observed dejection type influence on soil pH, H+Al and Al 32 days after deposition, but longer than 68 days no differences between excreta type were observed. Samples under urine influence, 32 days after deposition presented lower pH level, higher H+Al concentration and higher Al available concentration than samples taken under dung deposition. It can be explained because more than 75% of N in urine is N-urea form and it causes soil acidification during its hidrolisys process. Whalen, et al. (2000) concluded that in short-term (weeks), cattle manure can increase soil pH and to supply considerable quantities of plant-available nutrients. Urine deposition spot presented, 32 days later, lower pH value, higher H+Al concentration and higher availability of Al in relation to manure spots. However, this process did not remain longer than 68 days. References Whalen, J.K.; Chang, C.; Clayton, G.W.; Carefoot, J.P. 2000. Cattle manure amendments can increase the pH of acid soils. Soil Sci. Soc. Am. J., 64:962-966.



3240 - Forage & Grazing Lands

Lilian Elgalise Techio Pereira

STEM ELONGATION OF ELEPHANT GRASS SUBJECTED TO STRATEGIES OF ROTATIONAL STOCKING MANAGEMENT

Pereira,LET; Silva,SC; Paiva,AJ; Santos,TM; Geremia,EV; Vicente,SF; Oliveira,LP;

ESALQ/USP;

The objective of this experiment was to evaluate stem elongation on basal and aerial tillers during regrowth of elephant grass (*Pennisetum purpureum* Schum. cv. Napier) subjected to strategies of rotational stocking management characterised by combinations between two pre- and two post-grazing targets. The experiment was carried out from January to March 2011, in Piracicaba, SP, Brazil (22°43'S, 47°25'W and 580m a.s.l.), on elephant grass (*Pennisetum purpureum* Schum. cv. Napier) pasture. Treatments corresponded to combinations between two pre- (95% and maximum canopy light interception - LI95% and LIMax) and two post-grazing (sward height of 35 and 45 cm) targets, and were allocated to experimental units according to a 2x2 factorial arrangement and a complete randomised block design, with four replications. Monitoring of canopy light interception was performed using a canopy analyser LAI 2000 (LI-COR, Lincoln, Nebraska, USA) and of sward height using a sward stick (30 and 80 readings per paddock, respectively). Measurements of stem elongation rate (SER) were carried out every grazing cycle throughout the entire regrowth period, which was divided up into thirds (initial, intermediate and final). On each paddock, 30 tillers were tagged (six tussocks and five tillers per tussock, basal or aerial at random) and monitored every five days. Average pre-grazing height were 95 cm for LI95% and 137 cm for LIMax. Average grazing interval corresponded to 17.4, 20.0, 26.2 and 29.0 days for treatments LI95% /45, LI95%/35, LI 95%/45 e LI 95%/35, respectively. Data were analysed using the Mixed Procedure of SAS® (Statistical Analysis System), means estimated using the "LSMEANS" command, and comparisons made with Student t test with a 5% significance level. Except for swards managed with LI95% during the intermediate phase of regrowth, when there was no difference between tiller category, SER were consistently higher for basal relative to aerial tillers throughout regrowth for both LI targets. There was no difference between LI targets for SER on aerial tillers. For basal tillers, similar values were recorded for LI targets only during the initial phase of regrowth. During the intermediate and final phases, swards managed with LIMax showed higher SER relative to those managed with LI95%. Stem elongation is mainly determined by growth of basal tillers. Grazing at LI95% favours the control of stem elongation, ensuring leafness of elephant grass under rotational stocking.



3410 - Forage & Grazing Lands

Lucimara Chiari

CONTENT OF NUCLEAR DNA IN BRACHIARIA SPECIES ASSESSED BY FLOW CYTOMETRY

Chiari,L; Carvalho,CR; Valle,CB; Simeão,RM; Jank,L; Barrios,SCL; Alves,GF;

Embrapa Gado de Corte;

Brachiaria is the tropical forage grass with the greatest cultivated area in Brazil and has positively impacted animal production on pastures. Furthermore, it is responsible for the major part of the seed market both in Brazil and for export. In this study, flow cytometry was used to estimate the content of nuclear DNA of four Brachiaria species (*B. brizantha*, *B. decumbens*, *B. ruziziensis* and *B. humidicola*) from Embrapa Beef Cattle germplasm, with different ploidy levels and basic chromosome numbers. We evaluated one diploid accession each of *B. brizantha*, *B. decumbens* and *B. ruziziensis*, and the latter showed the lowest 2C-value (1.69pg) while the other two had the same value (2.00pg). The tetraploid accessions of these three species showed twice the 2C-value of diploids. Two pentaploid accessions were also analyzed: one of *B. brizantha* and one of *B. decumbens*, and the 2C-values were 4.90pg and 4.41, respectively. This pentaploid *B. decumbens* was specially selected for this study since previous cytogenetic analysis reported genome loss during meiosis, which was corroborated here. In *B. humidicola* we analyzed two accessions: one hexaploid and one heptaploid, with 2C-value equal to 4.20 and 5.22, respectively. These accessions of *B. humidicola* presented a smaller 2C-values than the hexaploid accession of *B. brizantha* (5.52pg). This probably occurred because *B. humidicola* has $x=6$ and *B. brizantha* has $x=9$, as *B. decumbens* and *B. ruziziensis*. So when the C-value (haploid genome) was considered *B. humidicola* presented the smallest genome (0.70pg), followed by *B. ruziziensis* (0.85pg), then *B. brizantha* and *B. decumbens* with the same C-value (1.00). Two interspecific hybrids from the cross between *B. brizantha* and *B. ruziziensis* were also evaluated in this work and the average 2C-value observed was intermediate to the 2C-value of the two species (3.77pg), indicating that flow cytometry technique can be used for this purpose when 2C-values are different. These results provided novel and relevant information for breeding programs, sequencing projects, and in research using molecular markers in these Brachiaria species.



3083 - Forage & Grazing Lands

Md Anowarul Islam

FENUGREEK: A POTENTIAL LEGUME FOR MULTIPURPOSE USE

Islam,MA; Krall,JM; Cecil,WK; Nachtman,JJ; Baumgartner,RE; Bandara,M; Acharya,S;

Department of Plant Sciences, Dept. 3354, University of Wyoming, Laramie, WY, USA;

Fenugreek (*Trigonella foenum-graecum* L.) is a specialty crop of the Fabaceae family and used both as herb and spice. Fenugreek can decrease cholesterol levels and is considered as a good breastmilk stimulator. Fenugreek has potential to be used as animal feed. The objective of this study is to evaluate most promising genotypes/accessions of fenugreek under varying environments for the phenotypic adaptability and stability for growth, seed yield, and quality. Thirteen genotypes/accessions were sown with four replicates during the spring of 2010 and 2011 at two locations of the University of Wyoming: Lingle (irrigated and dryland) and Laramie (irrigated). The seeding rate was 27 kg ha⁻¹. The plots were divided into two groups: forage production and seed production. Forage was mechanically harvested in mid-August to early September and seeds were harvested in early to mid-October of 2010 and 2011. At Lingle, line F80 produced the highest dry matter (DM) yield (2,380 kg ha⁻¹) while line IT produced the lowest DM (1,060 kg ha⁻¹) under irrigation in 2010. Line IT produced the highest DM (825 kg ha⁻¹) in dryland in 2010. In 2011, DM increased 3-7 folds under irrigated (range 5,830-10,700 kg ha⁻¹) and 2-7 folds under dryland (range 1,385-2,340 kg ha⁻¹) conditions, compared to DM of 2010. The highest yield was 10,700 kg ha⁻¹ (line F70) under irrigated and 2,340 kg ha⁻¹ (line L3068) under dryland conditions. In Laramie under irrigation, the highest yield was 1,550 kg ha⁻¹ from line F96 in 2010 and 3,000 kg ha⁻¹ from line LRC3708 in 2011. Large variations were also observed for seed yield under irrigated (range 820-2,250 kg ha⁻¹ in 2010; 545-1,990 kg ha⁻¹ in 2011) and dryland (range 62-390 kg ha⁻¹ in 2010; 64-530 kg ha⁻¹ in 2011) conditions at Lingle and under irrigation at Laramie (range 25-580 kg ha⁻¹ in 2010). The highest seed yield (2,250 kg ha⁻¹) was obtained from line F96 under irrigation at Lingle in 2010. Forage quality was in the acceptable range at both locations (e.g., 140-200 g kg⁻¹ crude protein). Conclusions It appears that line F96 is one of the best performers. Selection of well-adapted high performing fenugreek genotypes/accessions will result in development of superior cultivars.



3374 - Forage & Grazing Lands

Richard Sim

Growth and root:shoot dry matter partitioning in seedling lucerne (*Medicago sativa* L.) differ with sowing date and water availability

Sim,RE; Moot,DJ; Brown,HE; Teixeira,El;

Lincoln University;

Perennial reserves in lucerne (*Medicago sativa* L.) are important for both plant survival and growth. Taproot carbohydrate and nitrogen reserves have been shown to influence regrowth capacity after defoliation through increased photosynthesis from greater radiation interception and its efficiency of use. Lucerne growth during the seedling phase influences perennial reserves which are a key determinant of crop productivity. This study examined the effect of sowing date and water availability on root: shoot dry matter (DM) partitioning (Proot) of seedling lucerne. Lucerne was established on five dates, from early spring to late summer at Lincoln University, New Zealand (43°38S, 172°28E, 11 m.a.s.l) in two soils which differed in the plant available water content (PAWC). The high PAWC site is a silt loam soil with ~325 mm of water to 2.3 m. The low PAWC site had a very stony silt loam soil with only ~125 mm to 2.3 m. On the high PAWC site shoot yields significantly (PPKeywordsAlfalfa, leaf area index, lucerne, *Medicago sativa* L., root biomass



3338 - Forage & Grazing Lands

Sonia Santos

AVALIAÇÃO BROMATOLÓGICA DE GENÓTIPOS DE MILHO UTILIZADOS PARA SILAGEM

Sonia-Santos,SS; Newton-Martin,TN; Patricia-Bertoncelli,PB; Piran-Filho,FA; Luiz-Habitzreiter,TL; Grolli-Carvalho,AF;

UTFPR;

The objective of this study was to evaluate the characteristics of the nutritive value of corn genotypes for silage production in the Southwest region of Parana south of the test early-normal. The experiment was conducted at the experimental Federal Technological University of Parana (UTFPR, Capus Two Neighbors). We used 40 genotypes of maize, which were conducted: potential hydrogen silage, air dried sample, semple kiln dried, mineral matter, organic matter, crude protein, neutral detergent fiber, acid detergent fiber and ether extract. The maize genotypes evaluated showed no significant differences for the evaluates characteristics. Thua, all genotypes have similar quality and productive capacity.



3349 - Forage & Grazing Lands

Sonia Santos

AVALIAÇÃO MORFOLÓGICA, PRODUTIVA E PARTIÇÃO DE MATÉRIA SECA DE GENÓTIPOS DE MILHO UTILIZADOS PARA SILAGEM

Sonia-Santos, SS; Newton-Martin, TN; Patricia-Bertoncelli, PB; Piran-Filho, FA; Luiz-Habitzreiter, TL; Grolli-Carvalho, AF;

UTFPR;

The objective of this study was to evaluate the morphological characteristics, yield and dry matter partitioning of corn genotypes, the test early south-normal for silage production in the Southwest region of Parana. The experiment was conducted at the experimental Federal Technological University of Parana (UTFPR, Campus Two Neighbors). We evaluated 40 genotypes of maize supplied by EMBRAPA (Corn and Sorghum). Significant difference only for characteristic number of rows. As for the characteristics: plant height, ear height, stalk diameter, ear length, ear diameter, percentage of dry leaves, dry matter percentage of the spike and dry matter production per hectare, there was no difference significant. Thus, all genotypes have similar potential for the production of dry matter.



3342 - Forage & Grazing Lands
Sonia Santos

CARACTERIZAÇÃO MORFOLÓGICA E PARTIÇÃO DE MATÉRIA SECA DE GENÓTIPOS DE MILHO UTILIZADOS PARA SILAGEM

Sonia-Santos, SS; Newton-Martin, TN; Patricia-Bertoncelli, PB; Piran-Filho, FA; Luiz-Habitzreiter, TL; Grolli-Carvalho, AF

UTFPR;

The objective of this study was to evaluate the morphologic characteristics of dry matter partitioning and production of corn genotypes, South Super early test for silage production in the Southwestern region of Parana. The experiment was conducted at the experimental Federal Technological University of Parana (UTFPR, Campus Two Neighbors). Was used 30 maize genotypes, supplied by EMBRAPA (Corn and sorghum). Significant differences for: plant height, stem diameter, ear length, ear diameter and number of rows of grain in the ear. As for the percentage of stem dry matter, percentage of dry leaves, dry matter percentage of the spike and dry matter production per hectare is no significant difference. Therefore, all genotypes possess a similar potential for the production of dry matter.



3348 - Forage & Grazing Lands

Stéphanie Ferreira Vicente

DRYING METHODS AND THE CHEMICAL COMPOSITION OF CATTLE EXTRUSA SAMPLES

Vicente,SF; Da-Silva,SC; Paiva,AJ; Geremia,EV; Santos,TM; Pereira,LET; Oliveira,LP;

Escola Superior de Agricultura "Luiz de Queiróz" ESALQ - USP;

The objective of this experiment was to evaluate the effect of two methods for drying extrusa (forced draught oven and lyophilisation) on the contents of neutral and acid detergent fibre and in vitro dry matter digestibility of samples harvested from oesophageal fistulated cattle grazing marandu palisade grass (*Brachiaria brizantha* (Hochst ex A. Rich) Stapf. cv. Marandu). The experiment was carried out from January to March 2009 in Piracicaba, SP, Brazil (22°43'S, 47°25'W and 580m a.s.l.), on a continuously stocked marandu palisade grass pasture managed with variable stocking rate to maintain swards at 30 cm. Treatments corresponded to three rates of nitrogen fertilisation (150, 300 and 450 kg/ha of N) plus the control (non-fertilisation), and were allocated to experimental units (1200 m² paddocks) according to a complete randomised design, with four replications. Two oesophageal fistulated beef heifers were used to harvest extrusa samples in 15 minutes grazing trials. These were divided into two subsamples, one for determination of morphological composition and other for determination of chemical composition using two drying methods: lyophilisation and forced dry oven at 65°C. After drying samples were subjected to chemical analysis for estimates of neutral and acid detergent fibre (NDF and ADF - Van Soest et al., 1991) and in vitro dry matter digestibility (Tilley & Terry, 1963). Data were analysed using the Mixed Procedure of SAS® (Statistical Analysis System), means estimated using the "LSMEANS" command, and comparisons, when appropriate, made with Student t test with a 5% significance level. Drying method affected the NDF (P



3208 - Forage & Grazing Lands
Tangriani Simioni Assmann

INFLUENCE OF GRAZING AND NITROGEN LEVELS OVER BLACK OAT NITROGEN RELEASE ON CROP-LIVESTOCK SYSTEM

Assmann,TS; Caldas,TS; Assmann,AL; Adami,PF;

Universidade Tecnológica Federal do Paraná;

Litter maintains nutrient and energy flow at the soil-plant-animal interface and due to it plays an important role at the crop-livestock system. The objective of this study was to evaluate how nitrogen fertilization and grazing affect black oat biomass (litter) nitrogen release. The experiment was carried out at the Agronomic Institute of Paraná - IAPAR, experimental unit of Pato Branco, PR. Treatments were laid out as a random block design in a split-plot model with three replications. The main plots were formed by black oat cultivar IAPAR 61 with grazed and ungrazed treatments and the sub-plot by the use (150 kg of N.ha⁻¹ using urea) or not of nitrogen fertilizer, applied in sidedress. From these treatments, black oat biomass nitrogen decay constant was evaluated along 7 different field incubation periods (0, 15, 30, 45, 60, 90 and 120 days) by the litter bag technique. With these data, were determined the rates of nitrogen release. Single nonlinear model was used to fit the decay curves described by equation: $RN = A e^{-ka \cdot t} + (100-A)$, where, RN = proportion of remaining nitrogen at time t (days), ka = decay constant of the easily decomposable compartment (A). Results The percentage on nitrogen at the easily decomposable compartment was similar between the ungrazed treatments with higher rates of nitrogen release at the treatment with nitrogen fertilization. At the grazed treatments, nitrogen concentration at the easily decomposable compartment was higher at the fertilized plots due to the influence of the animal over the plants tissue turnover, although, it was followed by lower nitrogen decay constant. These data indicate that nitrogen accelerates the biomass decomposition rate and therefore the nitrogen release what leads to greater nutrient cycling and increases the supply of nutrients to plants. Conclusion Nitrogen fertilization increased the percentage of nitrogen at the easily decomposable compartment at the grazed plots and did not at the ungrazed plots. Nitrogen release rate increased by nitrogen fertilization at the ungrazed plots and decreased at the grazed plots. In general the addition the N, in both systems, grazing and no-grazing, are essential to ensure the efficiency of N cycling in intensive systems, mainly in crop-livestock systems.



Poster Session

**Genomics, Molecular Genetics and
Biotechnology**



3232 - Genomics, Molecular Genetics and Biotechnology

Alice Casassola

VALIDATION OF MOLECULAR MARKERS TO STEM RUST RESISTANCE GENES IN BRAZILIAN WHEAT GENOTYPES

Casassola,A; Brammer,SP; Chaves,MS; Fagundes,BS; Da-Silva,PR;

University of Passo Fundo, Passo Fundo, RS;

The wheat stem rust is not an epidemic disease in Brazil. However the fungus *Puccinia graminis tritici* is overcoming the resistance conferred by several resistance genes, representing a risk to Brazilian and world wheat production, because it increases the chances of spreading of the pathogen beyond East Africa, its point of concentration. Characterization of Sr resistance genes present in Brazilian wheat genotypes helps to predict resistance or susceptibility, constituting a strategy of prevention of wheat stem rust by using resistant cultivars. The identification of markers associated with genes for resistance to wheat stem rust and validation of existing markers is extremely important because they allow new strategies to overcome the inherent difficulties in the identification and use of disease resistance genes. The objective of this study was to validate microsatellite molecular markers previously developed for resistance genes to stem rust in Brazilian wheat genotypes. Thirty seven lines developed by the wheat breeding program of Embrapa Wheat, 19 highest grown cultivars in Brazil in recent years and 23 recommended cultivars are evaluated using 13 SSR molecular markers. Two positive controls for each gene were used. DNA was extracted by the CTAB protocol, the amplification was performed by PCR and the fragments were separated on 2% agarose gel. Of the 13 molecular markers used only six amplified fragments according to the literature: csSr2 (linked to Sr2 gene), Sr24#12 (linked to Sr24 gene), PSY-E1 (closely linked marker to Sr25), Seca2/3 (linked to ω -secalin gene/Sr31), O11B3/5 (linked to Glu-B3 gene/Sr31) and URIC/LN2 (linked to the cluster Lr37/Sr38/Yr17), indicating that they are promising molecular markers to be used in molecular marker assisted selection. Several factors may influence the accuracy and efficiency of the marker in detection of the gene, such as the distance from the marker to gene (linkage), mutations and gene silencing, which can result in false positives or negatives, making more difficult the selection process. Our results confirm the necessity of previous validation of molecular markers in regional populations before the routine use in assisted selection.



3212 - Genomics, Molecular Genetics and Biotechnology

Ana Paula Körbes

COMPREHENSIVE PREDICTION OF MIRNA TARGETS INVOLVED IN LIPID METABOLISM OF BRASSICA NAPUS

Machado, RD; Körbes, AP; Loss, G; Turchetto-Zolet, AC; Cagliari, A; Maraschin, FS; Margis-Pinheiro, M; Margis, R;

PPGBM, Departamento de Genética, Universidade Federal do Rio Grande do Sul;

Brassica napus is an important crop for oil production. The vast majority of the storage reserves are made up of lipids (40-50%), which are almost exclusively localized in the cotyledons of the maturing embryo. To the present, the regulatory network of lipid metabolism during embryogenesis of *B.napus* is not fully understood. MicroRNAs (miRNAs) are an important class of endogenous small RNAs which regulate plant development and seed formation, by cleavage of target mRNAs or by repressing their translation. Previous studies demonstrated that miRNAs regulate gene expression mainly by binding to perfect or near-perfect complementary sites of mRNA sequences. These binding characteristics indicate that plant miRNA targets can be predicted by simple sequence homology-based searches. To understand the regulatory functions of miRNAs in the lipid metabolism during seed development, this work focuses on a computational approach to predict candidate targets genes of *B. napus* miRNAs. Differentially expressed miRNAs during seed development were identified and their putative target genes were predicted by aligning the mature miRNAs to assembled contigs of *B. napus* mRNA-seq data using the web-based computer psRNATarget server with default parameters and maximum expectation value of 5 (number of mismatches allowed). Results: Several contigs matched with differentially expressed miRNAs from 25 *B. napus* miRNA families. All identified targets were subjected to BLASTX against protein databases followed by GO analysis to evaluate their potential functions. In total, 75 distinct potential targets were directly related to the lipid metabolism, from which 16 were transcription factors and 59 key enzymes in the acyl-lipid metabolism. This work provides an overview of potential targets of miRNAs differentially expressed during seed development and involved in the processes of accumulation and degradation of lipids. Supported by: CAPES, CNPq, FAPERGS-MCT



3084 - Genomics, Molecular Genetics and Biotechnology
Ana Paula Körbes

IDENTIFICATION OF CONSERVED AND NOVEL MIRNAS IN DEVELOPING BRASSICA NAPUS SEEDS BY DEEP SEQUENCING

Korbes, AP; Machado, RD; Guzman, F; Almerão, MP; De-Oliveira, LFV; Loss, G; Turchetto-Zolet, AC; Cagliari, A; Maraschin, FS; Margis-Pinheiro, M; Margis, R;

PPGBM, Departamento de Genética, Universidade Federal do Rio Grande do Sul;

Brassica napus is the third most important edible oil crop planted worldwide and the valuable lipids are synthesized and stored in specific seed tissues during embryogenesis. MicroRNAs (miRNAs) are important post-transcriptional regulators of plant development and seed formation. However, the miRNA transcriptome of *B. napus* is still not well understood, especially at different seed developmental stages. This work aims to describe the *B. napus* (Bna) miRNAome of developing seeds through the identification of plant conserved and novel miRNAs and the comparison of miRNAs abundance in mature versus developing seeds. Two small RNA and two RNA-seq libraries of (i) pooled immature developing stages and (ii) mature *B. napus* seeds were constructed and profiled by high throughput sequencing (HiSeq2000, Illumina). Conserved miRNAs were identified by alignments with known plant mature miRNAs and precursors (Viridiplantae) deposited at miRBase (Release 18). Pooled mRNA-seq data was assembled in contigs and used to search for putative precursors of novel miRNAs. MiRNA reads were normalized and differential expression between libraries was determined by statistical analysis. A large number of reads were obtained from each library and a total of 62 miRNA families were detected. From this number, 17 miRNA families were known in *B. napus* in miRBase, 32 were new in *B. napus* but conserved in other plants and 13 families were reported for the first time in plants. Expression analysis revealed that several miRNA and isomiRNAs were more abundant during developing stages. Furthermore, assembled contigs were used to identify putative targets of new miRNAs. This work presents a comprehensive study of miRNA transcriptome of *B. napus* seeds and will support future research on more targeted studies of individual Bna miRNAs and their function on embryogenesis, seed maturation and lipid accumulation. Supported by: CAPES, CNPq, FAPERGS-MCT



2886 - Genomics, Molecular Genetics and Biotechnology

Andreia Carina Turchetto Zolet

Diacylglycerol acetyltransferase (DGAT) enzymes: a phylogenetic analysis and comparative gene expression in soybean

Turchetto-Zolet, AC; Christoff, AP; Loss, G; Korbes, AP; Cagliari, A; Maraschin, FS; Margis-Pinheiro, M; Margis, R;

Universidade Federal do Rio Grande do Sul; Universidade Federal do Rio Grande do Sul;

Triacylglycerols (TAGs) are the most important seed storage lipids of plant species, which are responsible for carbon and energy reserves. Plant TAGs are primarily used as human food source but increasingly used for non-food applications. Diacylglycerol Acyltransferase (DGAT) genes encode the main enzymes needed for TAG biosynthesis. Different types of DGAT genes (DGAT1, DGAT2, DGAT3 and DAcT) have been identified, reinforcing its importance in the TAG formation. DGAT1 and DGAT2 are well characterized, but little is known about DGAT3 and DAcT genes in most plant species. The understanding of these enzymes is important to improve the content and composition of nutritional and industrial oils. Soybean [*Glycine max* (L) Merrill] is an oilseed crop and has long been one of the most important economical crops all over the world. We aim to perform a phylogenetic analysis of DGAT3 and DAcT proteins in plants and a comparative expression analysis in soybean. Homologs of the DAcT and DGAT3 genes were searched against 22 plants species using BLAST search in Phytozome database and phylogenetic analysis using Bayesian and Maximum-likelihood (ML) methods were performed. Subsequently, quantitative real time PCR (RT-qPCR) was performed in order to analyze the DGAT gene expression pattern throughout leaf and four seed development stages (R-stages: R5, R6, R7 and R8) in soybean. Homologs of DGAT3 and DAcT genes were identified in all plant genome searched. The phylogenetic analysis of both DGAT3 and DAcT sequences revealed the separation of eudicot and monocot species in different clade. For DAcT genes, we observed the presence of many duplication events. All genes evaluated were expressed within all analyzed tissues, though their expression levels were relatively higher in seeds than in leaves. In general, all DGAT members were more expressed at middle to last stage of soybean seed development (R6 to R8) when compared with leaf tissue and initial seed development stages. The four different types of DGAT are divergent in their exon/intron organization and in their expression patterns, as well as in their nucleotide and protein sequence composition, showing that they have different origins, evolution and functional patterns. The results suggest that the studied proteins are involved in different processes during TAGs biosynthesis. FINANCIAL SUPPORT: FAPERGS, CAPES, CNPq.



3072 - Genomics, Molecular Genetics and Biotechnology

Augusto Lima Diniz

A SEQUENCE DIVERSITY ANALYSIS OF ACCESSIONS OF COMMON BEAN (PHASEOLUS VULGARIS L.) BASED ON AN IRON REDUCTASE GENE (FRO1)

Diniz,AL; Zucchi,MI; Vieira,MLC;

Escola Superior de Agricultura "Luiz de Queiroz" - USP;

Bean seeds have an important role as a source of minerals, especially iron and zinc, in the human diet. Accessions of common bean are normally classified into two major gene pools - Mesoamerican and Andean. A range of results have been shown that Andean beans tend to have higher seed iron content than Mesoamerican beans, and the study of genes involved in iron uptake and its accumulation in seeds can reveal the source of this polymorphism. The iron content in seeds is directly related to the activity of an iron reductase, a plasma membrane enzyme of root cells. Investigate the frequency of polymorphic sites in coding and non-coding regions of an iron reductase gene (FRO1), and consider the usefulness of these polymorphisms in phylogenetic approaches. We used 31 accessions of *P. vulgaris* and one accession of *P. lunatus*, as an outgroup. The collection contains a representative sample from Mesoamerican and Andean cultivated beans. Three primers pairs, designed from the FRO1 cDNA sequence, and which generate fragments that correspond to approximately 40% of the gene sequence, were used to amplify the DNA from each sample. Then amplicons were purified and sequenced directly. Sequences were processed using the software CodonCode Aligner. Molecular diversity indices were calculated by Arlequin 3.5. Multiple Alignments and estimative of the phylogenetic relationships between the accessions were performed using MEGA 5.1. Results: A total of 215 variant sites were found among the accessions, including 96 SNPs, and 120 indels. All SNPs were bi-allelic, having only two alternative nucleotides, with 56.2% of them being transitions and 43.8% transversions. Of 2.115 base pairs evaluated, 43.3% were located in non-coding regions, which showed a frequency of 19% polymorphic sites. The frequency of SNPs was equal to 7% and the indels, 12%. On the other hand, the frequency of polymorphic sites in coding regions was 3.25%, with a frequency of SNPs equal to 2.5% and indels, 0.75%. The accessions were grouped into two clusters: cluster I includes Mesoamerican accessions and Brazilian cultivars, and cluster II contains Andean accessions. The analysis of the polymorphic sites in the FRO1 gene is consistent with the current system of hierarchical gene pools of common bean. The evaluation of the FRO1 complete sequence will possibly emphasize the differences between the Andean and Mesoamerican gene pools, and clarify the Brazilian cultivars cluster's position.



3150 - Genomics, Molecular Genetics and Biotechnology
Beatriz Wiebke Strohm

CHARACTERIZATION OF A NOVEL MEMBER OF THE SOYBEAN UREASE GENE FAMILY

Wiebke-Strohm,B; Ligabue-Braun,R; Homrich,MS; Pasquali,G; Bodanese-Zanettini,MH;

Universidade Federal do Rio Grande do Sul;

In plants, ureases have been related to urea degradation, as well as to defense against pathogenic fungi and phytophagous insects. Two urease isoforms have been described for soybean: the embryo-specific, encoded by Eu1 gene, and the ubiquitous, encoded by Eu4 gene. By searching the completed soybean genome sequence, a third urease-encoding locus was identified. The goal of the present study is the characterization of this novel urease member. The gene was designated Eu 5 and its product SBU-III. In silico analyses showed that SBU-III has a shorter amino acid sequence when compared to other ureases. Many gaps and mutations are found in SBU-III and a mutation in a highly conserved amino acid residue suggests absence of ureolytic activity. On the other hand, a 3D-structure analysis revealed the overall protein architecture remains very similar to the other ureases. Clustering analysis shows that the third urease is closely related to the soybean embryo-specific isoform. Expression profile of the soybean urease-encoding genes in different organs and developmental stages was determined by RT-qPCR. Eu5 transcripts were detected at low levels in seeds one day after dormancy break, roots of young plants and developing seeds. Eu1 and Eu4 transcripts were found in all analyzed organs, but Eu4 expression was more prominent in seeds one day after dormancy break and Eu1 in developing seeds. Our results showed that Eu5 is transcribed but its product may not be involved in nitrogen availability to plants. The isolation and cloning of the cDNA is now in progress and in vivo high expression levels will help to understand the biological role of this gene. Performed and means were compared using the least significant difference (LSD)



3203 - Genomics, Molecular Genetics and Biotechnology

Beatriz Wiebke Strohm

GERMINATION AND DEVELOPMENT OF SOYBEAN IS AFFECTED BY UREASE ABSENCE

Rechenmacher,C; Wiebke-Strohm,B; Bodanese-Zanettini,MH;

Universidade Federal do Rio Grande do Sul;

Urease, produced by plants, fungi and bacteria, is a nickel-dependent metalloenzyme that catalyzes the hydrolysis of urea to ammonia and carbon dioxide. However, it has been demonstrated that fewer ureases are involved in nitrogen availability to plants. In soybean three urease encoding genes have been described: ubiquitous urease encoded by Eu4 gene; embryo-specific urease encoded by Eu1 gene and a third urease, SBU-III, encoded by the recently detected Eu5 gene. Soybean transgenic plants with suppression of Eu4 expression were previously obtained by our team. These transgenic plants represent a powerful tool for functional genomics, because null mutants have never been obtained for the ubiquitous urease. The goals of the present study were to investigate soybean ureases role during seed germination and plant temporal developmental pattern. T1 and T2 seeds obtained from T0 and T1 transgenic plants, respectively, were screened for gfp-reporter gene expression. Presence of transgenes was also confirmed by PCR. Expression levels of the three urease isoforms were evaluated by RT-qPCR and ureolytic activity was measured by determining the ammonia released by enzymatic activity. Results confirmed that the transgenic progeny showed not only the expected suppression of Eu4, but also display silencing of Eu1 and Eu 5 genes. Decreased ureolytic activity in leaves, roots and seeds indicated absence of urease activity in all organs of transgenic plants. In order to investigate the role of individual urease encoding genes on germination and plant developmental processes, eu4 and eu1 single and eu4/eu1 double mutants were also evaluated. Lack of one or more ureases isoforms did not affect germination capacity of transgenic and mutants seeds, even after long seed store period. Regarding development, transgenic plants showed a significant delay in development, but mutant plants did not exhibit the same phenotype. The main difference between transgenic and mutant plants is the absence of SBU-III in the transgenic plants, which indicates that this protein may have a great contribution on plant development.



3261 - Genomics, Molecular Genetics and Biotechnology

Camila Maistro Patreze

DATA MINING OF GENES RESPONSIVE TO DROUGHT IN COFFEA ARABICA USING EST LIBRARIES

Silva,FSP; Azevedo,F; Nobres,P; Loh,R; Alves-Ferreira,M; Patreze,CM;

Universidade Federal do Estado do Rio de Janeiro;

Brazil responds for more than one third of the global coffee production and exports. Coffee has long been improved with important agronomic characteristics such as flowering, yield, bean size, cup quality, caffeine content, disease and drought resistance. Allied to the traditional methods, the applied technologies in plant genomics and bioinformatics have provided the potential identification of new genes related to important characteristics, as drought resistance. There are important data available at The Brazilian Coffee Genome Project database obtained from ESTs libraries of *C. canephora* and *C. arabica* species, the last one has the higher trade value. The objective of this work was the identification of candidate genes that may contribute to drought tolerance in *C. arabica* using bioinformatics tools. We selected eleven genes, including genes encoding for transcription factors, based on literature which are known by drought involvement in plants: RD22, RD29B, RD20A, ERD1, RD29A, AREB1, DREB1, CBF, DREB2A, MYC2 and NAC. Each gene has other close relatives or belong to families that also were used in our searching. All genes sequences were selected of *Arabidopsis thaliana*, a model plant, retrieved from The *Arabidopsis* Information Resource (TAIR) database and used as bait to retrieve coffee of *C. arabica* from ESTs libraries, by tBLASTn tool. For each gene of *Arabidopsis*, the coffee orthologs sequences with e-value lower than 10⁻⁵ were selected. The Early Responsive to Dehydration (ERD1) family was the major family, with 19 putative genes in *C. arabica* and 26 sequences in *Arabidopsis*. Also, a consensus sequence (cobbler) was generated for each gene family evaluated with three or more members of *Arabidopsis* to select coffee sequences by tBlastn tool. New phylogentic trees were obtained with improved bootstrap values, resulting in the identification of some coffee contigs related to different members of the same gene of *Arabidopsis*. We are employing the same cobbler strategy to retrieve orthologs of other two species genome sequenced, *Mimulus guttatus*, a monkeyflower (Phrymaceae), which is more related to *Coffea* genus and *Oryza sativa*, from PHYTOZOME database. Phylogentic trees are being reconstructed using sequences of four species above mentioned and the coffee genes identified will be validate by expression analysis during drought stress in *C. arabica* plants.



3123 - Genomics, Molecular Genetics and Biotechnology

Camila Pegoraro

CONSTRUCTION OF PLASMID FOR GENETIC TRANSFORMATION IN RICE AND TOMATO AIMING AT TOLERANCE TO DIFFERENT ABIOTIC STRESSES

Pegoraro,C; Kruger,MM; Santos,RS; Margis,MMANP; Maia,LC; Rombaldi,CV; Oliveira,AC;

Plant Genomics and Breeding Center at Federal University of Pelotas;

Biotic and abiotic stresses affect growth, development and the yield of crops. In plants, the response to these stresses involves mechanisms of perception networks of signal transduction and a set of stress response genes. Studies demonstrate the participation of Heat Shock Factors-HSFs in response to various environmental stresses. HSF transcription factors are central regulators of response of defense and bind to Heat Shock Elements-HSEs to regulate the transcription of Heat Shock Proteins-HSPs during the normal development of plants as well as under stress conditions. In addition to the control of stress response to heat, HSFs are involved in the defense response to attack by pathogens, oxidative stress, heavy metal, dehydration, salinity and in certain processes of development and differentiation. The co-expression of HSFs in response to different abiotic stresses in rice indicates that these transcription factors are able to regulate multiple mechanisms. The potential of HSFs to respond to different stresses can be utilized in obtaining transgenic plants tolerant to several environmental stresses. In this sense, this work had as objectives the construction of plasmid for the overexpression of the OsHSFA4d (Os05t0530400) gene in Rice and tomato plants. This study utilized the pENTR/D-TOPO® entry vector and the pH7WG2,0-Ubi and pH7WG2,D,1 destination vectors for rice and tomato. The coding sequence of the OsHSFA4d gene, containing 1390 pb was amplified by RT-PCR from cDNA in rice plants and, was cloned in the entry vector and inserted in *E. coli* cells. A PCR reaction utilizing primers for the OsHSFA4d gene was carried out and finally the plasmid along with the M13 primers was sent for sequencing. According to the identity results of 99% and e-value of 0, it can be stated that the cloned sequence corresponded to the gene of interest. The fragment was transferred to the pH7WG2,0-Ubi and pH7WG2,D,1 destination vectors through a recombination reaction, the recombination reaction was inserted in the *E. coli* cells. In order to verify whether the transference of the fragment occurred, a PCR was carried out with specific primers. From results obtained in agarose gel and sequencing, it is believed that the transfer of the fragment of the entry vector to the destination vector had occurred correctly. Constructions will be utilized in future studies to transform rice and tomato plants aiming at tolerance to adverse environmental conditions.



3365 - Genomics, Molecular Genetics and Biotechnology

Carla Andrea Delatorre

SEARCHING FOR ALUMINUM-TOLERANCE MECHANISMS IN *Avena sativa*

Delatorre,CA; Schneider,AB; Hervé,CB; Islamovic,E; Jackson,EW;

Universidade Federal do Rio Grande do Sul;

Aluminum (Al) toxicity is a limitation to yield in acid soils. Oats are considered one of the most Al tolerant small grains but the tolerance mechanism has not been elucidated yet. The mechanisms are commonly related to external chelation by exudation of organic acids or to internal detoxification. Al tolerance in oat has been considered monogenic. Several genes involved in Al tolerance have been isolated in other species. This study aimed to identify in oat ortholog genes related to Al in other species, compare their sequence and expression in contrasting genotypes, and evaluate the Al content and the ability to increase organic acid secretion under Al exposure. The sequences of nine Al-related genes were obtained from NCBI and compared to the USDA CORE Oat EST Database. The genotypes UFRGS17 (tolerant) and UFRGS930598 (sensitive) were used for isolation of the gene sequences. Expression analysis were conducted for UFRGS17, UFRGS930598, four RILs from their crossing, and the cultivars, Belle, Baker and Sesqui, considered, in the literature, tolerant, tolerant and sensitive, respectively. The Al content and organic acid secretion were measured for UFRGS17 and UFRGS930598. Only ALMT1 sequence has been isolated until now. The ALMT1-like gene was successfully cloned from UFRGS17 and has 2,496bp containing five exons and four introns. It showed high similarity to ALMT1 from *Aegilops tauschii*, rye and barley. Only a partial sequence was obtained from UFRGS930598. The difficulties in cloning the gene from UFRGS930598 suggest the existence of significant differences between the genotypes. Changes in sequence may render a gene nonfunctional. Expression data is currently being analyzed to verify if there are differences between the sensitive and tolerant genotypes. Smaller amounts of Al were found in UFRGS17 shoots compared to UFRGS930598, and malate secretion may be responsible for this reduction in uptake. Quantification of malate and citrate secretion is currently being performed. UFRGS17 accumulated less Al in the internal root tissue than UFRGS930598. The data obtained until now suggest that the difference in Al-tolerance between genotypes is at least partially due to differences in the ALMT1 gene, which causes Al-exclusion. However, it may not be the only mechanism. It has been shown that UFRGS17 and UPF91Al share one major gene as the responsible for Al tolerance and UPF91Al does not limit Al entrance. But both genotypes showed reduced oxidative stress



3104 - Genomics, Molecular Genetics and Biotechnology

Caroline Cabreira

IDENTIFICATION OF LESION MIMIC MUTANTS TYPE C₂H₂ IN SOYBEAN (GLYCINE MAX

Cabreira,C; Cagliari,A; Bucker-Neto,L; Pinheiro-Margis,M; Bodanese-Zanettini,MH;

UFRGS;

Legumes are one of the most important agricultural crops. In many regions, legume seeds are the only source of human food protein. Soybean plays an important role, providing oil and protein for animal and human food. However, many abiotic and biotic stresses could affect the crop, causing economical loss. So, biotechnology approaches is an important tool to better understand the mechanisms engaged in response and resistance against stresses. One of the well-characterized responses to biotic stress is called hypersensitive response. Many studies have been carried out to identify genes involved in this response, especially through analysis of mutants with the response mechanism altered. One of these mutant classes is known as Lesion Mimic Mutants and has been studied in *Arabidopsis thaliana*. The genes belonging to this class, featured by the presence of zinc finger domain C₂H₂, are involved in the control of cell death and detoxification of reactive oxygen species generated by stress. Thus, the aim of this study is to identify and analyze the genes belonging to the Lesion Mimic Mutants class type C₂H₂ in Soybean. For this, the identification of these genes in organisms with genome available has been performed, in order to study the phylogenetic relationship among the members. The search was carried out using the *Arabidopsis thaliana* complete nucleotide and protein sequences in the Phytozome (<http://www.phytozome.net/>) and NCBI database (<http://www.ncbi.nlm.nih.gov/>). Homologous sequences were aligned in MEGA5 for analysis of similarity. The presence of the characteristic zinc finger domain was analyzed in SMART (<http://smart.embl-heidelberg.de/>). The phylogenetic tree was made using MrBayes 3.1.2. The analysis of soybean genes promoter region was performed using Plant Care database (<http://bioinformatics.psb.ugent.be/webtools/plantcare/html/>). As a result, 94 genes were identified in the genome of the species analyzed, including green algae basal organism. Eight genes were found in the soybean genome. Therefore, the emergence of this family seems to have occurred before diversification between monocotyledon and dicotyledonous plants. The soybean genes promoter region showed many cis elements involved in response to abiotic and biotic stress, hormones and lesion. Analyses of expression profile from the soybean genes are being performed in different tissues and metabolic conditions, in order to better understand the role of this soybean gene family.



3260 - Genomics, Molecular Genetics and Biotechnology

Claudia Toniazzo

OCCURRENCE OF MICRONUCLEUS AND ANALYSIS OF GENETIC STABILITY IN SYNTHETIC WHEAT

Toniazzo,C; Brammer,SP; Wietholter,P; Bonow,S;

Embrapa Trigo;

Wild cereals species close to the cultivated plants are large reservoirs of genes, which can be transferred to the cultivated species if properly exploited. These species can be used for gene transfer, due to the large number of important genes. Therefore, it becomes possible to introduce genetic variability and transfer of desirable traits from wild species or known genome to cultivated plants. Wheat is one of the main species used for human food, because it represents an important nutrition source and is widely grown worldwide. The synthetic wheat that results from a cross between a tetraploid species, AABB genome and a diploid, DD genome, represents an excellent genetic resource for introgression of agronomically important genes to *Triticum aestivum* genetic improvement, in order to increase agricultural production. However, the manipulation of these genomes may lead to various genetic instabilities such as chromosomes laggards, chromosomal bridges, micronuclei and abnormal cytokinesis. The main consequence of the micronuclei occurrence is the loss of chromosomes and the formation of pollen genetically unbalanced and/or sterile. The objective of this study was to analyze the micronuclei occurrence in tetrads and/or microspores in the early stage of development, and infer on the instability of 67 synthetic wheat accessions. These accessions are from the International Center for Maize Improvement (CIMMYT) and kept in the Active Germplasm Bank of Embrapa Trigo. The plants was cultivated in a greenhouse at Embrapa Trigo (Passo Fundo, RS) in 2010 and the spikes were collected in the stage prior to anthesis, fixed with Carnoy solution for 24 hours, transferred to 70 % alcohol and stored at -20°C. For the slides preparation 1% acetic carmine dye was used. One hundred microspores per slide were analyzed, with three replicates per accession. There were significant differences (1%) in the analysis of variance among accessions on the presence of micronuclei in tetrads and/or in microspores. The lowest micronuclei average was CASW00GH00062S, representing 95% of normal cells, while the CIGM93.177 presented 46% of normal cells. The micronuclei presence in accessions may influence the genetic stability when used in backcrosses with *Triticum aestivum*, affecting thus the fertility of the hybrids.



3214 - Genomics, Molecular Genetics and Biotechnology

Daisy Leticia Ramirez Monzon

DIFFERENTIAL GENE EXPRESSION RELATED TO LIGNIN CONTENT AND THE TEGUMENT COLOR OF SOYBEAN SEEDS

Ramirez-Monzon,DL; Bevilacqua-Borges,C; Maia,LC; Zimmer,PD;

Universidade Federal de Pelotas;

The soybean (*Glycine max* L. Max) is one of the main crops grown in Brazil, the second largest world producer. Its evolution has been strongly supported by the development of technologies that allowed the increase in cultivate. Currently, the use of biotechnology tools aims to contribute to the development of new genotypes with characteristics that can continue increase the production. The identification of genes responsible for characters that can assist in developing varieties with improved seed quality, may constitute in something innovative. The seed tegument has an important function as for the seeds resistance to deterioration. In this sense, the partial characterization of the protein expression FLA 14 (Arabinogalactan), directly related to the cell wall synthesis in the seed tegument may contribute to the advancement of these studies. This work aimed to create and validate primers that are able to quantify the gene expression of the FLA 14 protein in four soybean genotypes, two with black tegument (TP and IAC 222) and higher lignin content and two with yellow tegument (CD 202 and Potência) and lower lignin content. The tegument was collected 50 days after the anthesis. In order to obtain the gene expression among genotypes, was used the qRT-PCR technique and tested four primer combination, constructed from sequence models of soybeans ESTs. With the validation results, the primers that were found within the standards were the FLA 14p1, FLA 14p2 and *B-Actina*. They were all used in expression studies. The results showed that in soybean genotypes with black tegument and higher lignin content, FLA 14 gene had higher expression to the genotypes with yellow tegument and lower lignin content. Keywords: qRT-PCR, black tegument, Arabinogalactan



3194 - Genomics, Molecular Genetics and Biotechnology

Daniel da Rosa Farias

THE SEQUENCING OF *ORYZA GLUMAEPATULA* STEUD.

Farias,DR; Chaparro,C; Maia,LC; Barbosa-Neto,JF; Panaud,O; Oliveira,AC;

Plant Genomics and Breeding Center - Federal University Of Pelotas;

Rice is one of the most important food crops in the world, being the staple food for almost half of the world population. The wild species *O. glumaepatula* is distributed in central and south America and the Caribbean and differs from cultivated rice, *Oryza sativa* in morphology, environmental adaptability and growth habit. Wild rices generally lack agriculturally important traits. However, they carry many desirable genes that have been lost in cultivated rice. This explains why the wild rice species are adapted to unfavorable environments and show resistance to many pests and diseases. *O. glumaepatula* is one of 21 wild species of the genus, of AgpAgp genome, found in various parts of Latin America, from 23°S in Brazil up to 23°N in Cuba. This study aims to present the sequencing of *O.glumaepatula* (GEN 1233). We used a whole-genome shotgun sequencing (WGS) approach. We generated 50Gb of raw sequence from the next-generation sequencing (NGS) Illumina HiSeq 2000. The sequencing produced three libraries, two short insert paired end (with 540b and 545b insert size) and a long insert paired end with 4,700b insert size. An alignment of these reads with *O.sativa* genome (IRGSP-1.0) was performed and showed an alignment rate of 67%, being 55% of the reads properly paired. This information is important to understand and analyze the differences between the two genomes. We also performed a preliminary assembly of the *O.glumaepatula* genome, the total of bases assembled were 465M in 84,052 scaffolds, the N50 scaffold size was 33,744 and 3,923 L50 scaffold length. We will improve the assembly with some future analysis such as the comparison between different assemblers, the anchoring of *O.glumaepatula* scaffolds in BAC-ends sequences and the alignment with *O.sativa* and *O.glaberrima* genomes. The *O. glumaepatula* genome will greatly enhance rice research since it is the only diploid wild American species. Its importance relies on its use in crosses with *O. sativa* in plant breeding programs, aiming at introgression of important traits from the wild species and amplifying the genetic basis of the cultivated crop.



3092 - Genomics, Molecular Genetics and Biotechnology

Dielli Aparecida Didoné

TEMPERATURE STRESS EFFECT DURING INFECTION OF MAIZE IMMATURE EMBRYO BY AGROBACTERIUM TUMEFACIENS EHA101:PTF102

Silva,MR; Didoné,DA; Almeida,VO; Torres,B; Ceccon,CC; Suzin,M; Grando,MF;

Universidade de Passo Fundo;

Genetic engineering offers new sources of genetic variability for corn improvement. Great effort has been made to improve the efficiency of gene transfer into cereal via *Agrobacterium tumefaciens* since this technology permit the integration of the transgene in transcriptionally active regions of the genome and low copy number transference. Maize, as other cereal crop, is very limited in relation to in vitro cultivation and presents limitations to infection by *A. tumefaciens*. Thus, adjustments are essential in genetic transformation protocols. This study evaluated the effect of maize genotype and temperature stress during the stage of infection of zygote embryos by *A. tumefaciens* in transient expression of the *gus* reporter gene. Immature embryos (1.2 to 2.0 mm) of the model hybrid Hi-II and Brazilian variety BRS 541 were infected for five minutes in suspension of *A. tumefaciens* strain EHA10:pTF102 (*gus* and *bar* genes). At this stage the maize embryos underwent three treatments:(a) infection without heat shock, (2) infection using heat shock of 40°C, (3) infection using heat shock of 40 °C for 5 minutes prior to infection. The infected embryos were transferred to the co-culture, remaining for three days in the dark at 20°C. After that, it was performed the GUS histochemical assay to verify the transiente expression of *gus* gene. The variables analyzed were number of embryos with blue spots and number of blue spots per embryo (NBS) *gus* positive. The frequency of embryos showing blue spots varied from 11.7 to 50% among the treatments. Comparing the genotypes, Hi-II hybrid presented a higher percentage of *gus* positive embryos (34.3%) compared to BR451 (12.7%). The same was observed for the NBS (9.2 for Hi-II and 2.2 for BR451). The temperature stress treatment did not enhance the percentage of blue embryos (12.7%) neither the NBS (2.2) for BR451 genotype. However, for Hi-II hybrid, 50% of embryos submitted to 40oC during infection showed blue sports, being this, the best results among the treatments. These embryos showed in average 15.2 NBS. The instability of the explants plasma membrane caused by heat shock, that can facilitate the infection.



3190 - Genomics, Molecular Genetics and Biotechnology

Eduardo André Roesler

PROTOCOL ADJUSTMENT FOR GENETIC TRANSFORMATION OF WHEAT BY AGROBACTERIUM TUMEFACIENS

Roesler,EA; Yamazaki-Lau,E;

Universidade de Passo Fundo;

Plant genetic transformation is a powerful tool that can assist the incorporation of desired traits hard to reach by conventional breeding. In Brazil, one of the features targeted for wheat transgenesis is drought tolerance, especially for planting under rainfed conditions in the Cerrado region. The transformation by *Agrobacterium tumefaciens* is particularly interesting for the good possibility of inserting few copies of the transgene in transcriptionally active sites of the genome. This technique is not yet established for wheat in Brazil. For such reasons, the objective of this study was to evaluate the effect of different factors, below described, in the process of wheat genetic transformation using *A. tumefaciens*. Two wheat genotypes were used, a Brazilian line developed by Embrapa for rainfed cultivation with good capacity of in vitro regeneration, and Bobwhite SH9826', which is widely known for its high regeneration and transformation capacity. The protocol used was based on Wu et al. (2009). The effects of pre-incubation of immature seeds collected 9 to 10 days after anthesis at 4°C for one, two, three and four days before placing the embryos in culture medium were tested. *A. tumefaciens* AGL1 containing p7UG-AB or pAL154/pAL156 plasmids were used with cell concentration ranging from 1.0 to 2.0 in OD600 for the inoculation step. The effect of rinsing explants with inoculation medium after inoculation step was also tested. Assays consisted of 100-133 transformed explants per treatment, plus 30-35 untransformed control explants. GUS histochemical staining was performed two to three days after the co-cultivation. The most promising treatment was rinsing explants after inoculation, in which 5% and 29% of the Brazilian wheat line explants showed blue spots when inoculated with *A. tumefaciens* AGL1 containing p7UG-AB and pAL154/pAL156, respectively. The average number of blue spots per explant was 1.0 and 3.1, respectively. This result indicates that the amount of bacteria used in cocultivation is decisive in the transformation efficiency. The fact that the plasmid pAL154 contains additional vir genes was probably responsible for the more efficient transient transformation. Other treatments showed no blue spots. Explants are being conducted in the subsequent culture medium to verify the stable transformation. Most promising experiments should be repeated, as well as other factors should be tested in order to improve the transformation efficiency.



3707 - Genomics, Molecular Genetics and Biotechnology

Estela Reis de Andrade

GENETIC TRANSFORMATION OF COWPEA WITH THE GENE OF METHIONINE-RICH DELTA-ZEIN FROM MAIZE

Citadin,CT; Andrade,ER; Aragão,FJL;

Embrapa Recursos Genéticos e Biotecnologia;

Cowpea (*Vigna unguiculata* L. Walp) is a legume of great importance in human nutrition, being a rich source of protein. Its great adaptability to different climates and environmental conditions, makes it an important culture in breeding programs. Although it is a rich source of protein, cowpea, like other legumes, is deficient in sulfur amino acids. The storage proteins of maize (*Zea mays*) of the δ -zein family, possess high levels of sulfur containing amino acids with methionine constituting about 26%. For this reason, the proteins are used as targets for heterologous expression in cultivars that are subjected to nutritional improvement. The objective of this study was to obtain cowpea plants carrying an expression cassette seed-specific to a gene of a protein rich in methionine residues. To achieve this, we constructed an expression vector bearing a methionine-rich delta-zein gene from maize under the control alpha chain of beta-conglycinin of soybean as a promoter linked to its signal peptide and 35S CaMV terminator. The vector also contains an expression cassette of Atahas gene conferring tolerance to herbicides from group of imidazolinones, for selection of transformed plants. Following transformation via the biolistic technique, embryos were selected on MS medium containing imazapyr. Out of the 3,052 embryos bombarded, 4 positive plants were recovered as confirmed by PCR and Southern blot. Subsequent acclimatization allowed for the recovery of only one plant with the transgene inherited by its progeny. However, when germinated PCR positive seeds of the progenies were analyzed by Western blot there was no evidence of the expression of delta-zein. These results led us to believe that delta-zein was not expressed or that its expression was not detectable possibly due to the lodging of the transgene at genome sites with low expression levels or physiological differences between the source of the transgene and cowpea. Attempts are still being made to obtain more transgenic events that may lead to in the level of methionine in cowpea seeds.



3359 - Genomics, Molecular Genetics and Biotechnology

Flávia Thiebaut

EPIGENETIC REGULATION IN DIFFERENT GENOTYPES OF SUGARCANE SUBMITTED TO DROUGHT STRESS

Thiebaut,F; Tanurdzic,M; Grativol,C; Vieira,T; Vincentini,R; Hemerly,AS; Martienssen,RA; Ferreira,PCG;

Laboratório de Biologia Molecular de Plantas, Instituto de Bioquímica Médica, Universidade Federal do Rio de Janeiro;

In order to increase our understanding on the epigenetic regulation in response to abiotic stresses in plants, we analyzed the sRNA regulation in sugarcane plants submitted to drought stress. A deep sequencing analysis was carried out to identify the sRNAs regulated in sugarcane cultivars with different drought sensitivities. For this analysis, sugarcane plants in a greenhouse for three months were exposed to drought stress (ceasing irrigation) during 24 hours. Leaves and roots were collected separately from treated and control plants, and total RNA from a pool of samples was extracted with Trizol reagent. Eight sRNA libraries for deep sequencing were prepared from RNA pool of leaves sensitive (S) and tolerant (T) sugarcane cultivars submitted to drought stress (24h) and controls (0h) for each tissue. The sRNA libraries were sequenced by Solexa/Illumina. The sequences were filtered to remove adaptors and contaminants rRNA and tRNAs, and sequences with 18-28 nt the length were selected. The pool of sRNAs selected allowed the analysis of different sRNA classes (miRNAs and siRNAs). To identify the miRNAs present in these libraries, the non-redundant sequences obtained were aligned to the conserved miRNAs using the miRBase database (release 13.0, <http://microrna.sanger.ac.uk>). The reads that match to those sequences, with 0-3 mismatch, were retained for further analyzes of differential expression analysis using the miRProf pipeline (<http://srna-tools.cmp.uea.ac.uk>). We identified 28 and 36 conserved miRNA families in leaf and root libraries, respectively. The bioinformatics analysis of four differentially expressed miRNAs (miR397, miR408, miR159 and miR164) was validated using stem-loop RT-PCR assay. The biological functional of miRNAs was accessed by analyzing their putative targets. Furthermore, a large scale investigation of sRNA in sugarcane using a computational approach has identified siRNAs candidates from targets of miRNAs with 22-nt in the length. The expression of five siRNAs was verified by stem-loop RT-PCR in plant submitted a drought stress. To characterized siRNAs, these were aligned in cluster of repeats and the T0h libraries shown a different distribution of siRNAs aligned. Our findings contribute to increase the knowledge of sRNA roles in epigenetic-regulatory pathways of response to drought stress in the complex, polyploidy sugarcane plant.



2893 - Genomics, Molecular Genetics and Biotechnology

Gabriela Guerra dos Santos

In silico search for cis regulatory elements in the promoter region of Agamous gene in *Oryza sativa*

Guerra,G; Silva,GJ; Maia,LC; Oliveira,AC;

Federal University of Pelotas;

Rice is one of the most studied cultures, since it is an important food source for much of the world population and increasing demands are projected for the next decades. This justifies its importance as an object of study, especially related to biotechnology and breeding challenges. MADS box are responsible for encoding transcription factors related to the development of yeast cells, plants and animals. Some MADS genes identified in floral organ can be divided into four classes (A, B, C and D). Gene promoters present specific DNA sequences, known as cis regulatory elements (CREs) that are recognized by specific transcription factors and RNA pol II in the formation of pre-initiation complex. The level of spatial and temporal expression of each gene is determined and regulated by the interaction of transcription factors with CREs, which constitutes the basic mechanism controlling the regulation of gene expression of organisms. The identification of these CREs is a major biological challenge of genome studies. This work aimed to search in silico CREs in the promoter region of Agamous gene in rice, and by Z test, electing the most significant for future studies, which may provide the necessary information to build models of genetic regulatory networks. AGAMOUS gene sequence is obtained from the stock data, referring to the rice genome (*Oryza sativa*), the National Center for Biotechnology Information (NCBI). On the basis of location information of the NCBI gene will be cut and defined sequence of 1000 bp of the promoter region of this gene. The abundance of CREs in the promoter region of the gene. For sequence analysis were using the Signal Scan Search portal Plant Cis-acting Regulatory DNA Elements (PLACE). Thus, in the promoter of the gene Agamous, 68 motifs were found, but only 19 showed a significance by the Z test, with $p < 0.05$, and potential for future studies of gene regulation.



2866 - Genomics, Molecular Genetics and Biotechnology

Glacy Jaqueline da Silva

STRATEGY FOR IDENTIFICATION OF CIS REGULATORY ELEMENTS RESPONSIBLE FOR EXPRESSION PATTERN IN DEVELOPMENT OF RICE WITH ESTRESS CONDITION

Silva,GJ; Pegoraro,C; Maia,LC; Costa-Oliveira,A;

Federal University of Pelotas;

The worldwide growth in population translates into higher demands for food such as cereals and fruits, requiring the search for new strategies to increase food production without increases in area. Most agricultural products are derived from the reproductive process of flowering plants. Therefore, a detailed understanding of gene regulation during the development of flowers and fruits under stress conditions is essential for increasing productivity. The regulation of gene expression in eukaryotes is mediated by recruitment of transcription factors that interact with elements present in promoter region of genes, forming signaling networks. Thus, the objective of this study was to investigate the presence of cis regulatory elements (CREs) in promoters of rice flowering genes, which could be associated with the expression under stress conditions. For this purpose, a search for homologues in rice, for genes that participate in the ABC model of flowering in *A.thaliana* were performed using the BLAST-X program. The cis elements present in the 1Kb promoter region of these 13 homologues and applied the Z test with p-0.015. A total of 77 CREs that showed significant results were found, with at least one copy each in the 13 promoters. Of these, 47 were present in a single gene, with a copy number ranging from 1 to 10 in each promoter. 19 CREs were significant in at least two promoters simultaneously with an average of 2.73 copies per promoter. In seven promoters, three CREs were significant, with an average of 4.3 copies per promoter. Only 4 CREs were significant in four promoters, with an average of one copy per promoter. Only one CRE was identified with a significance for six promoters in the same time, with an average of 1.16 copies per promoter. These data were compared with expression results of GENEVESTIGATOR platform to check for patterns of CREs found in the promoter, concerning the expression pattern of these genes. The CREs NAPINMOTIFBN and PROLAMINBOXOSGLUB1 showed significant values for the Soc1 and Shatterproof1 homolog genes which showed an unique expression pattern among the 13 genes. These results suggest a possible signaling function of these CREs in the expression pattern of these genes in Zeatin excess and root impedance. Work is being conducted in our group, to validate these results.



2865 - Genomics, Molecular Genetics and Biotechnology

Glacy Jaqueline da Silva

STRATEGY FOR IDENTIFICATION OF CIS REGULATORY ELEMENTS RESPONSIBLE FOR EXPRESSION PATTERNS IN RICE

Silva,GJ; Guerra,G; Maia,LC; Costa de Oliveira,A;

Federal University of Pelotas;

The increase of population and consequently demand for increased agricultural productivity, with the concern of avoiding environmental degradation, requires plant breeders to develop new technology strategies to ensure the food supply for the population without increases in area. The understanding of gene regulation in plants is of paramount importance in order to improve agronomic qualities and problems related to stress. The regulation of gene expression in eukaryotes is mediated by recruitment of transcription factors that interact with elements present in promoter regions of genes that act in signaling networks. Therefore, we aimed to perform this work in order to study gene expression in rice metal carriers, in order to look for an expression pattern of these genes with cis-acting elements (CREs) found in the promoter region under the anoxia germination condition. For these, we selected 29 genes identified as metal carriers and analysed in GENEVESTIGATOR database (www.genevestigator.com) against previously published microarray germination under anaerobic condition at 12, 24, 27 and 30 hours of stress. Of these, 13 genes showed overexpression in some period of stress. With these results, we analyzed the 1kb upstream promoter region of each this 13 genes in the (www.microsatellite.org) platform, identifying the CREs present in these promoter regions and applied the Z test with $p < 0.05$. A total of 177 CREs presented significant results, with at least one copy of the 13 promoter genes, were identified. Of these, 56 were identified in at least two promoters, with copies ranging from one to 17. Seventeen CREs were identified in at least three promoters, with a copy number ranging from one to seven. Three were found in at least four promoters in common with varying copies of one to six and one CRE had a significant value in at least five genes, with one copy in the promoter. These data were compared with expression results of GENEVESTIGATOR platform to look for a pattern of CREs found in the promoter, concerning the expression pattern of these genes. The CREs POLASIG3 and CARGCW8GAT showed significant values for the OsNramp2 and OsNramp3 genes which displayed an unique expression, suggesting a possible signaling function of these cis-acting elements in the activation the expression of these genes in anoxia condition in rice germination. Work is being conducted in our group, to validate these results.



3279 - Genomics, Molecular Genetics and Biotechnology

Graciela Castilhos

CHARACTERIZATION OF THE PPR₂ GENE IN RESPONSE TO THE PHAKOPSORA PACHYRHIZI INFECTION

Castilhos,G; Bucker-Neto,L; Campos,LL; Fonini,LS; Rechenmacher,C; Cabreira,C; Wiebke-Strohm,B; Bodanese-Zanettini,MH; Margis-Pinheiro,M;

UFRGS;

The identification of genes that respond to stress conditions can help the understanding of soybean's defense mechanisms against pathogens, such as *P. pachyrhizi*, the causal agent of Soybean Asian Rust. A large number of transcription factors (TF) are differentially expressed in response to stresses. The bHLH family of TF acts regulating several biological processes in plants, including the defense against phytopathogens. PPR₂ (*P. Pachyrhizi* Responsive₂) gene encodes a bHLH protein. The aim of this study is the functional characterization of the PPR₂. The gene expression pattern was *in silico* analyzed using the LGE-Soybean subtractive libraries database (<http://bioinfo03.ibi.unicamp.br/soja/>). This analysis showed that PPR₂ gene is induced after *P. pachyrhizi* inoculation. In addition, RT-qPCR analysis showed that the amount of transcripts of PPR₂ is higher in a susceptible than in a resistant cultivar under fungus infection, suggesting that this gene is involved in the soybean susceptibility to the pathogen. To assess the function of PPR₂ gene in the plant defense mechanisms we are currently obtaining transgenic soybean plants with altered PPR₂ expression (overexpression or silenced). The Gateway recombination cloning system was used to insert the fragments of 1669 pb and 157pb corresponding to the coding region of the PPR₂ gene into pH7WG2D and pH7GWIW2(II) vectors respectively. Soybean somatic embryos from cultivars Vencedora and Bragg were submitted to genetic transformation. Eight-month-old proliferating embryogenic tissues were submitted to transformation by particle bombardment using the particle inflow gun (PIG). After three months in selection medium, hygromycin-resistant embryogenic soybean tissues were visually selected, counted and separately cultured for the establishment of lines corresponding to putative independent transformation events. These experiments are currently in progress. PPR₂ overexpression is expected to reduce the resistance and PPR₂ silencing is expected to decrease the susceptibility of plants.



2848 - Genomics, Molecular Genetics and Biotechnology

Hak Soo Seo

OSPDI IS A CRITICAL FACTOR IN ENDOSPERM AND ALEURONE LAYER DEVELOPMENT

Kim,YJ; Choi,SH; Kim,SI; Koh,HJ; Seo,HK;

Department of Plant Science, Seoul National University;

Protein disulfide isomerase (PDI) is a chaperone protein that involves in oxidative protein folding by acting as catalysts and folding assistants in the endoplasmic reticulum (ER). Genome database showed that rice contains three PDI-like genes. But, their functions are not clearly identified. Here, we show possible functions of rice PDI (OsPDI) during seed development. Seeds of T-DNA insertion OsPDI mutant, OsPDIL1-1, identified by genomic DNA PCR and western blot display chalky phenotype. Electron microscope analysis revealed that endosperms of the OsPDIL1-1 mutant show imperfect packing of round starch granules, causing floury-white color. Abnormal form of protein body I (PB-I) containing prolamin and thick aleurone layer were also observed in the OsPDIL1-1 mutants. Protein content per seed was significantly low in the OsPDIL1-1 mutant. In addition, proteomic analysis of the OsPDIL1-1 mutant seed showed that OsPDI is post-translationally regulated and its loss causes accumulation of many types of seed proteins. Our results indicate that OsPDI plays a critical role in seed development through its regulatory activity for various proteins. This work was supported by a grant from the Next-Generation BioGreen 21 Program (Plant Molecular Breeding Center no. PJ008123), Rural Development Administration, Republic of Korea. This research was also supported by Technology Development Program for ('Agriculture and Forestry' or 'Food' or 'Fisheries'), Ministry for Food, Agriculture, Forestry and Fisheries, Republic of Korea.



3315 - Genomics, Molecular Genetics and Biotechnology

Insoo Choi

IDENTIFICATION OF GENES AND MOLECULAR MECHANISM FOR BACTERIAL PUSTULE IN SOYBEAN.

Choi,IS; Kim,SY; Kim,YC; Kim,ST;

Pusan National University;

Bacterial pustule, which caused by *X. c. pv. glycines* is one of the most serious diseases in soybean. This study has been conducted to find out genes resistant to Bacterial pustule and to identify molecular mechanisms. The ultimate goal is to do molecular breeding through direct selection of genes for the regeneration of soybean cultivars. F7 lines developed through pedigree method from the cross of Saturn x (Lee x Seonheuk) have been used as plant materials. The Agilent eArray platform was used to design a microarray based on sequences of 33,574 unigenes from Glycine max database. 42,564 probes were used and length of each probe was 60-mer. We've checked expression of genes in 3h, 12h, 24h, 3d, and 10d after inoculation. Genes showing high expression at each time interval have been selected as candidate genes. We identified 13 genes resistant to Bacterial pustule in soybean through comparing results of microarray analysis with that of real-time PCR. In molecular mechanism, we found out that these 13 genes were mapped at sugar metabolism, which suggest that these genes might be involved at the regulation of sugar metabolism. In in vivo bioassay with 'Taekwangkong', occurrence of Bacterial pustule has been significantly reduced as the concentration of sugar was increased to 0.5%, 1%, and 2%. Subsequent effort is required to minimize loss of soybean yield through the development of soybean cultivars using new technologies such as the selection of genes resistant to Bacterial pustule, elucidation of molecular mechanisms, and molecular breeding using map(gene) assisted selection.



3312 - Genomics, Molecular Genetics and Biotechnology

Jorge Fernando Pereira

ALLELIC VARIATION IN THE TAALMT1 PROMOTER REGION AND ALUMINIUM RESISTANCE IN A BRAZILIAN WHEAT COLLECTION

Pereira,JF; Barichello,D; Aguilera,JG; Consoli,L; Silva-Júnior,JP;

Embrapa Wheat;

The wheat TaALMT1 gene codes for an anion channel responsible for the malate efflux from the root. Once released into the apoplasm, the malate forms complex with aluminium (Al) present on acid soils protecting the plants from its harmful effects. There is a significant correlation between TaALMT1 expression and the amount of malate released by the wheat root tip. Usually, there is also an association between high levels of TaALMT1 expression and tandem repeats present at the TaALMT1 promoter. On the other hand, low level of TaALMT1 expression is normally correlated with promoter containing no tandem repeats. Previous studies reported two markers, named LPF and SPF, which are able to discriminate different TaALMT1 promoter alleles that are associated to different number of repeats at the region. In that context, the goals of this work were to (i) analyze the allelic variation in the TaALMT1 promoter and (ii) use hydroponics to access the Al resistance variation in a collection of 285 Brazilian wheat genotypes. To reach such goals, each genotype was grown for four days in a nutrient solution (pH 4.0) with or without AlCl₃ 2μM following the measurement of the longest root and determination of the relative root growth (RRG). Genotypes "IAC5 - Maringá" and "Anahuac" were used as resistant and sensitive controls in each experiment, respectively, and according to the obtained RRG, the wheat genotypes were classified as resistant (R), moderately resistant (MR), moderately sensitive (MS) and sensitive (S). The leaves of each genotype were used to DNA extraction and the LPF/SPF markers were used in amplification reactions. Of the 285 genotypes analyzed, 153 (53.7%) were classified as R, 88 (30.9%) MR, 20 (7.0%) MS and 24 (8.4%) S to Al. Considering the 241 R or MR genotypes, 222 (92.1%) presented the TaALMT1 promoters type V or VI, while, among the 44 MS or S genotypes, 31 (70.5%) showed promoters type I or II. Interestingly, 12 (54.5%) of the genotypes presenting promoters type II were MR or R. Once promoter type II is usually correlated with low TaALMT1 expression, the resistance presented by those genotypes could be related to other genes. Some genotypes presented better RRG than the positive control "IAC5 - Maringá" and could also be futurely analyzed for the mechanisms, besides malate efflux, implicated in their Al resistance. This is the first time that a large number of Brazilian wheat genotypes were screened using molecular markers related to Al resistance.



3138 - Genomics, Molecular Genetics and Biotechnology

Kyujung Van

DISCOVERY OF MUNGBEAN SINGLE NUCLEOTIDE POLYMORPHISMS USING NEXT-GENERATION SEQUENCING TECHNOLOGY

Van,K; Kang,Y; Han,KS; Jang,HJ; Lee,SH;

Seoul National University;

Mungbean (*Vigna radiata* (L.) Wilczek) is an important legume crop in Asia. Digestible protein (ca. 25%) with high quality amino acid profiles in mungbean seeds can complement to the Asian nutrition and mungbean sprouts are one of the popular vegetables for Asian cuisine. Mungbean, a self-pollinated diploid plant, has $2n = 22$ chromosomes and 579 Mb is the commonly accepted genome size of mungbean determined by flow cytometric analysis. Construction of mungbean genetic map with the recently developed molecular markers, such as single nucleotide polymorphisms (SNPs) including insertions/deletions (indels), is needed for mungbean cultivar improvement. Our study used whole-genomes of two mungbean cultivars, Sunhwa Nokdu and Gyeonggi Jaerae 5, for surveying sequence variations between two cultivars after these genomes were sequenced by Illumina HiSeq. More than 40,000 million reads from both mungbean cultivars were generated with 65x of sequencing depth. After Sunhwa Nokdu contigs were de novo assembled by ABySS1.3.2. ($N50=9,958$ bp), these Sunhwa Nokdu contigs longer than 10 kb were aligned with Gyeonggi Jaerae 5 reads using BWA. SAMTools was used for retrieving SNPs between Sunhwa Nokdu and Gyeonggi Jaerae 5 defining lowest/highest depth as 5 and 100, respectively, and sequence quality as 100. Of the 524,380 single-base changes we identified, 66.7% of the SNPs were of the CT (GA) variety (i.e., transitions), whereas transversions accounted for 33.3% (174,821 cases). In the mean time, Sunhwa Nokdu contigs longer than 10 kb were selected, if they showed 80% of similarity with common bean ESTs using est2genome. Among filtered SNPs, only SNPs positioned in the putative exon regions determined by est2genome were used for validation of putative mungbean SNPs. With seven mungbean cultivars from various origins addition to Sunhwa Nokdu and Gyeonggi Jaerae 5, most of SNPs called by bioinformatics tool were confirmed by Sanger sequencing. Thus, these SNP markers could be enriched the resource of EST-based genic markers and useful for constructing a transcript map of mungbean.



3139 - Genomics, Molecular Genetics and Biotechnology

Kyujung Van

DOMESTICATION OF SOYBEAN: INVESTIGATION OF GLYCINE MAX AND GLYCINE SOJA DIVERGENCE TIMES USING LOW COVERAGE NGS SEQUENCING

Kim,SK; Kang,Y; Yoon,MY; Kim,MY; Van,K; Lee,SH;

Seoul National University;

From hundreds of different edible crops around the world, soybean (*Glycine max*) has been playing an important crop because of its versatility. There are many soybean varieties with different phenotypes that may have been influenced by evolutionary events and gave rise to genetic diversity from the ancestors. Studies on domestication history in the relation to population divergence have yielded the molecular and genetic evidence for the origin of species. Based on the complete sequence of *Glycine max* and *Glycine soja*, the undomesticated ancestor of *G. max* (in particular, *G. soja* var. IT182932), we were able to perform an in-depth study of the time divergence in a total of 12 soybean genotypes (6 *G. max* and 6 *G. soja*), which were selected after conducting the genetic diversity analysis of SSR dendrogram using 104 wild and landrace soybeans from China, Korea and Japan. With the whole genome resequencing NGS technique of Illumina GA at lower depth of 6.5, 892.5 Mb and 903.3 MB consensus sequences were produced from these 12 soybean genotypes with the coverage of 91.54% and 92.65% for *G. max* and *G. soja*, respectively. We compared sequence variations and haplotype diversity among soybean populations. Single nucleotide polymorphisms identified as nonsynonymous change in protein coding regions from each genotype were used for calculating an approximate divergence time to look at the complexity of *G. max* and *G. soja* divergence, which can be very useful for the investigation of evolutionary events based on the molecular clock technique.



3295 - Genomics, Molecular Genetics and Biotechnology

Larissa Giroto

AGROBACTERIUM-MEDIATED TRANSFORMATION OF SOYBEAN VARIATED, BR16, GENE 35S:AREB1, ANALYSIS BY SOUTHERN BLOTTING

Giroto,L; Soldera,MCA; Marin,SRR; Kanamori,N; Fujita,Y; Yoshida,T; Marcelino-Guimaraes,FC; Yamaguchi-Shinozaki,K; Nepomuceno,AL;

Japan International Research Center for Agricultural Sciences (JIRCAS), Tsukuba, Japan;

Soybean is the most important source of vegetable oil and protein for human and animal diet in the world. The frequency of occurrence of drought has increased significantly over the last decade, probably associated with climate change occurred due to global warming. Researchers are looking for a long time to improve and optimize the characteristics of the culture. Several strategies can be used to reduce losses caused by drought, ranging from adequate soil management and agriculture, to the use of irrigation. Another possibility is the development of cultivars adapted to drought conditions and in this respect, Biotechnology has become an important tool in the development of varieties adapted to different conditions of biotic and abiotic stress. The genetically modified plants can be transformed by direct gene transfer using particle bombardment (biolistics), which inserts a high number of copies of the transgene into the host genome, resulting many times in deactivation of the transgene by gene silencing. Moreover, the transformed plants via *Agrobacterium tumefaciens* generally have a low number of copies of the transgene. The use of this method allowed a stable expression and insertion of the interest gene in transgenic plants. The AREB is an important transcription factor signaled by the ABA, which acts in response to regulate the expression of other genes that are involved in tolerance to drought and high salinity stress. This study aimed to analyze the T1 plants transformed *Agrobacterium* by Southern blotting technique to detect the number of copies of the gene 35S:AREB1. The experiment was conducted at the Laboratory of Plant Biotechnology at Embrapa Soja, Londrina - PR. The process was performed according Kanamori et al., 2011. The Southern blotting was performed on 22 plants T1, AREB positive from two independent events. Of the 22 samples, 20 T1 plants had only one copy number and two plants had two copy numbers. Considering the complexity of the mechanism response to water deficit caused by drought, which can vary depending on the intensity and duration of stress, analysis on the molecular level, physiological and agronomic are needed later to assess the efficiency of the presence of the gene in transformed plants.



3354 - Genomics, Molecular Genetics and Biotechnology

Leomar Guilherme Woyann

REGULATION OF RECEPTOR-LIKE KINASE (RLK GENE FAMILY RESPONSIVE TO IRON EXCESS IN RICE

Woyann,LG; Finatto,T; Tessmann,EW; Maia,LC; Costa-Oliveira,A;

Universidade Federal de Pelotas;

Receptor-like kinases (RLKs) plays a critical role in the communication between the plant cell wall and the cytoplasm, they are involved in diverse functions in plants including heavy-metal tolerance (Kanneganti & Gupta, 2011). This work aimed to identify cis-regulatory elements (CRE) in promoters of RLK genes responsive to iron excess. The list of RLK genes up-regulated in rice (*Oryza sativa* L. ssp. japonica cv. Nipponbare) leaves of seedlings grown in iron excess (7mM $\text{FeSO}_4 \cdot \text{H}_2\text{O}$) was obtained by Finatto (2012) using a microarray approach. The promoters (1.0 Kbp upstream portions of start site of transcription) of 10 RLK genes were obtained in RAP-DB (Rice Annotation Project Database). We obtained a consensus sequence of 469 plant CREs in PLACE database and calculate the Z score for each CRE considering their occurrence in all genes of rice genome. We found 101 different CREs with significant occurrence (P-0.05). Ten CREs are present from five to three gene promoters each one. The average of incidence of CREs per gene promoter was 14.4 and the standard deviation (SD) was 3.02. The maximum number of different CREs in the promoter was 21 and the minimum was 10. Among the 10 studied promoters the average of significantly occurrence of binding sites (considering the number of different CREs and the number of times that each CRE is repeated in each gene promoter) was 30.8 per promoter and the SD was 12.45. The CRE ASF1MOTIFCAMV is present in 5 promoters, and the CREs HEXMOTIFTAH3H4, MYBPZM, PRECONSCRHSP70A are present in three promoters each one, these CREs are recognized by transcription factors families of bZIP and MYB that are responsive to iron excess. Kanneganti, V. & Gupta, A.K. (2011). RNAi mediated silencing of a wall associated kinase, OsiWAK1 in *Oryza sativa* results in impaired root development and sterility due to anther indehiscence Wall Associated Kinases from *Oryza sativa*. *Physiology and Molecular Biology of Plants*. v.17, n.1, p.65-77. Finatto, Taciane (2012). Transcriptomic analysis of genes and LTR-retrotransposons in rice (*Oryza sativa* ssp. japonica) in response to iron toxicity. PhD. Thesis.



3224 - Genomics, Molecular Genetics and Biotechnology

Liane Balvedi Poersch

THE EFFECT OF COLD AND 2-HNA (2 HYDROXY-NICOTINIC ACID TREATMENTS ON ISOLATED MICROSPORE CULTURE AND ANDROGENIC RESPONSE OF DIFFERENT BRAZILIAN WHEAT GENOTYPES

Poersch, LB; Scagliusi, SM; Lau, EY; Bodanese-Zanettini, MH;

Universidade Federal do Rio Grande do Sul;

Microspores are gametic cells with an extraordinary capacity of giving rise into a new plant via in vitro embryogenesis. Doubled haploids generated by isolated microspore culture are completely homozygous, and represent an important tool for research in plant genetics and breeding. Stress treatments act as a trigger and are employed to switch microspores from gametophytic development to a sporophytic pathway. The most utilized stress treatments in cereals are cold, heat and starvation. With the aim to determine the best type of stress treatment and to evaluate in vitro culture response, five different Brazilian wheat genotypes were tested, and two stress treatments were applied: cold (4°C) and a combination of heat (32°C) and 2-hydroxynicotinic acid (2-HNA, 100 mg/L). Wheat cultivar Pavon 76 was used as androgenic positive control. Microspore purification was carried out using ten spikes per genotype. Spikes were sampled when microspores were in the early to mid uninucleate stages. Microspores were purified by gradient centrifugation. With the exception of the positive control (showing no differences between treatments), our results demonstrated that cold treatment was the most efficient type of stress, producing green plants in four out five tested genotypes. Only two genotypes treated with the combination of heat and 2-HNA produced plants, and one of them produced one single albino plant. One genotype did not produce green plants, just albinos, in both stress treatments. Albino plants are the bottleneck for the production of doubled haploids by androgenesis, and to minimize their occurrence is a great challenge. Although albinism is a major genetic characteristic, also influenced by environmental conditions, some level could be avoided with appropriated stress treatment and culture medium optimization. In this study, a Brazilian wheat genotype was identified as highly androgenic, showing significant genotype interaction. In addition to the production of doubled haploids for breeding or for genetic studies, the present results may be interesting for transgenic purposes. Microspores are considered promising targets for genetic transformation. As an immediate product of meiosis, the microspore represents the haploid chromosome set, where the transgene will be inserted. With embryogenic competence and genome duplication, the desired trait is fixed in T0 homozygous plants. Testing a protocol using microspore for transformation is our next step.



3343 - Genomics, Molecular Genetics and Biotechnology

Lívia Vargas dos Santos Ferreira

EXPRESSION PROFILE OF SUGARCANE ETHYLENE SIGNALING GENES DURING DROUGHT STRESS IN RESPONSE TO INOCULATION WITH BENEFICIAL DIAZOTROPHIC BACTERIA

Vargas,L; Rojas,C; Ferreira,PCG; Hemerly,AS;

Universidade Federal do Rio de Janeiro;

Studies to increase drought tolerance in sugarcane are needed to lower production costs of sugarcane industry in northeastern of Brazil. Sugarcane established long time ago an efficient interaction with particular types of plant growth promoting bacteria (PGPB). They can offer several benefits to host plants such as production of plant growth hormones (eg. auxins and gibberellins), increase in biomass, promotion of plant development, pathogen defense and tolerance to abiotic stress. Our group's effort to understand at the molecular level the relationship between plant and beneficial endophytic bacteria led to the identification of sugarcane members of the ethylene signaling pathway. Ethylene becomes an interesting model in studies of water deficit since it participates in various stages of plant life cycle, including responses to drought. Here we aim to study the effects of association between diazotrophic bacteria with sugarcane in drought conditions by characterizing gene expression profile of ethylene response pathway genes. Micropropagated sugarcane plants (cv. SP70-1143) were co-cultivated with the diazotrophic bacteria *Gluconacetobacter diazotrophicus* PAL5 in hydroponic conditions for 7 days, and transferred to substrate with vermiculite and sand. Inoculated and non-inoculated control plants were subjected or not to lack of water. No difference was found between the plants in the four experimental conditions after 3 days of water deficit. Nevertheless, 1 month after water deficit, only inoculated plants survived, albeit with a decrease in shoot development compared to inoculated plants growing without drought stress. Remarkably, inoculated root samples showed higher levels of *G. diazotrophicus* colonization 3 days after water deficit than roots of non-inoculated plants. Differential expression profiles are being generated by Illumina RNAseq. The first results indicate differential responses of members of the ethylene signaling pathway in the four experimental conditions analyzed. The ethylene receptor ScER1, previously reported as responsive to the interaction of sugarcane with diazotrophic bacteria, showed higher expression in inoculated shoots 3 days after water deficit than in inoculated samples without stress. The data suggests that ethylene signaling might be one of the key signals for an efficient communication between sugarcane and beneficial diazotrophic bacteria during drought stress conditions.



2835 - Genomics, Molecular Genetics and Biotechnology

Magda Laiara Bezerra de Lima

INFLUENCE OF DIFFERENT GROWTH REGULATORS ON SHOOT REGENERATION OF JATROPHA CURCAS L.

Lima,MLB; Lima,VSF; Carvalho,CPS; Campos,FAP;

Universidade Federal do Ceará;

The present study aimed to establish a protocol for regeneration of *Jatropha curcas* L., through organogenesis, using shoot apex as explants in culture media containing different growth regulators. Mature seeds of *Jatropha* were germinated in greenhouse, receiving daily irrigation. After twenty days, shoots of *J. curcas* were disinfected with sodium hypochlorite solution (1% of active chloride, 5 minutes) and rinsed three times with sterile distilled water. Shoot tips were isolated and incubated in MS medium containing different types of cytokinins: BAP (6-benzylaminopurine), KIN (kinetin) and 2-iP (2-isopentenyladenine) at a concentration of 2.0 mg.L⁻¹. For the rooting, the obtained shoots were transferred to MS medium supplemented with 1.0 mg.L⁻¹ of IBA (indole-3-butyric acid). The culture media were supplemented with 3% sucrose and 0.7% agar with pH adjusted to 5.8 before autoclaving at 121°C for 20 min. Cultures were maintained at 25 ± 2°C with a 16h photoperiod. A completely randomized experimental design was applied, consisting of five replicates with six plants each. Statistical analysis was performed using the ANOVA followed by Tukey test at 5% probability. In the first week, the growing shoots showed visible signs of swelling in all treatments. At the end of the fourth week, explants were evaluated for the development of the aerial parts. The medium supplemented with KIN showed an average of four leaves per shoot, being superior to other treatments i.e. BAP and 2-iP, which showed an average of 2.2 and 2 leaves. Chlorosis and vitrification (32 and 20%, respectively) were identified in the shoots obtained in medium with kinetin (KIN), while in the medium supplemented with 2-iP the values for the same characteristics were of 26 and 35%. In the medium supplemented with BAP, vitrification was 36% and showed no chlorotic leaves. The aerial parts showed no significant signs of rooting while using the IBA. Thus our study showed satisfactory results while using kinetin (KIN) in the culture medium, however new experiment should be conducted to establish the rooting medium for the aerial parts.



3250 - Genomics, Molecular Genetics and Biotechnology

María Rosa Simón

LOCATION OF THE RESISTANCE TO TAN SPOT IN WHEAT

Simón,MR;

Cereals. Facultad de Ciencias Agrarias y Forestales;

Tan spot, caused by *Pyrenophora tritici-repentis*, is an important foliar disease in the major wheat growing areas of the world. Isolates of the pathogen are classified into at least eight races based on their ability to cause necrosis and/or chlorosis in differential wheat lines, however new races can arise. Genes or QTLs effective against races 1; 2; 3 and 5 have been identified in different populations. No genes have been identified effective against races 4; 6; 7 and 8. Studies on races determination are recent in Argentina. In this study, a selection of RILs from the International Triticeae Mapping Initiative mapping population created by crossing the synthetic hexaploid wheat 'W7984'; with the spring wheat cultivar 'Opata 85'; was examined to identify genomic regions harboring QTLs for resistance to two isolates (H0019 and H0120) of the pathogen obtained at the Faculty of Agricultural and Forestry Sciences, La Plata. Experiments were conducted at seedling and adult stages in three environments. A locus coming from 'W7984' was discovered on the short arm of chromosome 6A linked to Xksuh4c conferring resistance in seedlings with LOD scores between 1.90 and 3.76 when considering isolate H0019 for two of the environments, and on the same chromosome linked to the same marker for isolate H0120 with LOD scores between 2.25 and 4.29 for the three environments. In addition, for the average of the three environments for each isolate the same locus was detected on chromosome 6A with LOD scores of 3.76 and 5.87 for isolates H0019 and H0120 respectively. The isolate H0120 considered as race 4, based on the absence of symptoms on the cultivars and lines selected, did not amplify for the *Ptr-tox b*, however amplified for the *Tox A* gene. If we consider that we need the *Ptr-tox b* amplification to assign an isolate to race 4, we can consider isolate H0120 as a potential new race. Isolate H0019 was considered phenotypically as race 1, because it produced necrosis on the differential lines 'Glenlea' and 'Katepwa', and chlorosis on '6B365'. Chlorosis on '6B365' can be attributed to the production of *Ptr Tox C*. However the gene(s) has not been characterized and it is not possible to confirm this result by PCR at the moment. As chromosomal location for the resistance to this race in this population has been established by other researchers mainly on chromosome 1AS, we speculated that it could also belong to a new race of the pathogen.



3119 - Genomics, Molecular Genetics and Biotechnology

Mariana Madruga Krüger

Accumulation of transcripts of genes of the TIM/TOM and TIC/TOC complexes in rice plants under stress by anoxia

Kruger,MM; Pegoraro,C; Santos,RS; Mertz,LM; Rombaldi,CV; Oliveira,AC;

Federal University of Pelotas;

The total or partial absence of oxygen results in energy deficiency affecting the growth, development and yield of plants. The depletion of energy increases the production of reactive oxygen species which affect the integrity of the membranes of cells, mainly of the membranes of organelles such as chloroplasts and mitochondria. The main proteins of chloroplasts and mitochondria are coded by nuclear genes and their importation up to these organelles involves protein complexes located in the membranes. In mitochondria, these complexes are called translocases of the inner membrane - TIM and translocases of the outer membrane - TOM, while in the chloroplasts they are called translocon at the inner envelope membrane of chloroplasts - TIC and translocon at the outer envelope membrane of chloroplasts - TOC. Damage in the membrane of mitochondria and of chloroplasts caused by stress hampers the import of proteins coded by the nuclear genome, through the TIM/TOM and TIC/TOC complexes, respectively, leading the plants to death. In this context, the study aimed to evaluate the expression of genes belonging to the TIM/TOM and TIC/TOC complexes in rice plants under conditions of stress by anoxia as well as under conditions of other abiotic stress, attempting to relate the genic expression of these genes with the integrity of the membranes and consequent importation of proteins to mitochondria and chloroplasts under conditions of stress. Based on the expression data obtained by the Genevestigator program, it was possible to verify that the majority of the genes of the TIM/TOM and TIC/TOC evaluated presented an increase in the level of transcripts when the rice plants were subjected to different abiotic stress. Data obtained by qRT-PCR showed that the genes TIM17/22-Os02g0672500, TIM17/22 - Os03g0296300, TIM17/22-Os12g0514900 e TIC62-Os10g100300 presented high levels of expression 24 hours after anoxia, suggesting the participation of these genes in the response to stress by anoxia. However, after 72 hours under conditions of anoxia, there occurs the inhibition of expression in the majority of genes belonging to the TIM/TOM and TIC/TOC, suggesting that there is an interruption in the transport of proteins to the mitochondria and chloroplast during this period of stress, possibility due to the damage of the membranes of these organelles.



3121 - Genomics, Molecular Genetics and Biotechnology

Mariana Madruga Krüger

Effects of hypoxia storage on gene transcript accumulation during tomato fruit ripening

Kruger, MM; Pegoraro, C; Santos, RS; Mandabula, F; Tiecher, A; Maia, LC; Rombaldi, CV; Oliveira, AC;

Federal University of Pelotas;

Tomato (*Solanum lycopersicon* L.) is a model plant species and is the second most important vegetable crop, given its importance for studies on fruit molecular pathways, development and ripening. Also, it is a frequent component of the human diet due to its high antioxidant and vitamin contents and its versatile culinary use. Moreover, tomato is a climacteric fruit, i.e., during its ripening a high rate of respiration and increase in ethylene synthesis is observed. Low oxygen levels might inhibit or block ethylene biosynthesis and therefore retard the ripening process. Despite commercial applications of low-oxygen treatments, the precise mode of action of low oxygen in fruit tissues and ripening is not well understood. In order to delineate the molecular responses to low-oxygen stress in fruits, hypoxia-responsive tomato genes encoding HSFs (Heat shock factors), HSPs (Heat shock proteins), and enzymes involved in fermentation and ethylene synthesis pathways were analyzed. In this study, tomato fruit stored under hypoxia conditions showed that HSP17.7 and HSP21 genes were highly induced by low oxygen level, indicating their primary role in maintaining cellular homeostasis after this stress.



3117 - Genomics, Molecular Genetics and Biotechnology

Mariana Madruga Krüger

STUDY ON THE ROLE OF 15 ERFs SUBMITTED TO IRON TOXICITY STRESS

Kruger,MM; Pegoraro,C; Santos,RS; Maia,LC; Oliveira,AC;

Federal University of Pelotas;

Rice (*Oryza sativa* L.) is a very important staple food for more than half of the world's population and plays a fundamental role in the social, economic and cultural spheres. However, biotic and abiotic stresses affect the development and production of this crop. Among the abiotic stresses, those caused by the excess of nutrients, such as iron and aluminum, stand out. The process of flooding results in an increase of Fe^{2+} availability on the soil at levels that may be toxic to plants grown under these conditions. Iron toxicity is one of the major abiotic stresses which drastically affect the flooded rice crop worldwide, leading to considerable production losses. Some works have demonstrated that under iron stress situations, rice plants unchain several response mechanisms to stress, among them, production of ethylene. Members of ERF gene family (Ethylene Responsive Factors) encode transcriptional regulators with diverse functions which are involved in the development and physiological processes of plants. Thus, 15 ERFs were selected in this study with the objective of evaluating their expression profiles in rice under iron stress. Data obtained by qRT-PCR showed that all ERFs analyzed suffered significant regulation under stress condition by toxicity due to iron excess. In general, it was observed that only four ERFs had their expression decreased by iron stress (AK067313, AK072749, AK109390 e AK241281) in both stress periods tested. The ERFs AK067313 e AK241281, however, maintained their expression levels during the first 6h after stress and shortly afterwards presented the same behavior as the ERFs AK072749 and AK109390. The 11 remaining ERFs were induced by iron stress although with significant changes among the tested periods. The ERFs AK1059991 and AK108830 presented high expression levels up to 24 hours after the stress, whereas the ERFs AK241243, AK068312 and AK099221 had their expression levels increased up to 18h after stress. The ERFs AK101949, AK241246 and AK109226 were induced up to 12h after stress, and the ERFs AK109360, AK069833 and AK104576 had an early induction only after 6h of stress. The results obtained demonstrate that the majority of genes responsive to ethylene were induced when subjected to iron stress and may take part on the response mechanisms used by rice plants.



3185 - Genomics, Molecular Genetics and Biotechnology

Marta Bencke

SOYBEAN WRKY FAMILY ANNOTATION AND FUNCTIONAL CHARACTERIZATION OF GENES INVOLVED IN THE RESPONSE TO PHAKOPSORA PACHYRHIZI

Bencke,M; Wiebke-Strohm,B; Bucker-Neto,L; Mancini,E; Osorio,MB; Homrich,MS; Carvalho,MCCG; Stolf,R; Margis-Pinheiro,M; Weber,RLM; Cabreira,C; Westergaard,G; Marcelino-Guimarães,FC; Abdelnoor,RV; Bodanese-Zanettini,MH;

Universidade Federal do Rio Grande do Sul;

Soybean productivity is frequently threatened by environmental stresses. At the present one of the major diseases affecting soybean production is Asian Soybean Rust (ASR), caused by *Phakopsora pachyrhizi*, an obligate biotrophic plant-pathogenic fungus which colonizes primarily leaf tissue. Many global gene-expression studies have reported the involvement of soybean WRKY transcription factors in response to *P. pachyrhizi* infection. Besides, soybean WRKY family was underrepresented in previous studies since the whole soybean genome sequence was unavailable. In the present study a genome-wide annotation of soybean WRKY family and the functional analyzes of genes involved in response to *P. pachyrhizi* were performed. Following a search in different public soybean databases, WRKY-encoding genes were annotated and those involved in response to *P. pachyrhizi* were identified using global gene-expression experiments. In some cases, gene expression pattern was validated by real time RT-qPCR. Over hundred-seventy WRKY genes were annotated and over seventy identified as differentially expressed during fungus infection. Furthermore, soybean somatic embryos were transformed aiming WRKY overexpression and silencing, and transgenic plants were challenged with *P. pachyrhizi*. By comparing data mining in response to *P. pachyrhizi* infection with the clustering result, similar expression pattern could be observed in closely related genes. The participation of four homologous genes in response to pathogen was demonstrated using RNAi approach. When infected by *P. pachyrhizi*, leaves of silenced transgenic line showed higher number of lesions than wild-type plants. In conclusion, the complete soybean WRKY family was annotated and the participation of some members in response to *P. pachyrhizi* was demonstrated.



3148 - Genomics, Molecular Genetics and Biotechnology

Mauricio Wolf Wilwerth

HIGH-RESOLUTION TEMPORAL PROFILING OF TRANSCRIPTS DURING ARABIDOPSIS EXPOSITION TO TO HYDROCARBONS MIXTURE REVEALS A DISTINCT CHRONOLOGY OF PROCESSES AND REGULATION

Saad,CF; Nardeli,SM; Wilwerth,MW; Caetano,VS; Alves,MR; Reinert,F; Oliveira,AC; Paes,JES; Peixoto,R; Ferreira,MA;

UFRJ;

The growing demand of energy sources promotes the increasing of oil pollution worldwide. Despite that mangrove flora is one of the major biosystems affected by petroleum spills there is lack of studies in the literature analyzing the impacts of these exposition. In order to elucidate the molecular effects of complex mixture of hydrocarbon on plants, global gene expression analysis of 10 days-old *Arabidopsis thaliana* exposed to water soluble fraction of the marine oil MF-380 (WSF-380) was evaluated by a high resolution time-course DNA microarray experiment. The microarray results revealed 340 genes modulated by the stress condition. These genes were distributed in 12 clusters according to expression profile and different classes of biological processes were over-represented, such as the response to heat, response to oxidative stress, response to osmotic stress and response to hypoxia. The expression of the genes involved in different stresses can be the evidence of the complex chemical composition of the oil. The transcriptional factors and effector genes related to these pathways were selected for validation by q-PCR. The plant pathways involved in the response to exposure of oil were clarified by using software tools that allow visualizing and interpreting the results of high-throughput experiments. The Exploratory Gene Association (EGAN) displays biological processes and functions that are enriched in the experiment as also the genes involved in those processes or functions. For example, EGAN exhibited 28 genes that responded to inorganic substances over the 340 genes modulated in microarray. The data analysis will help to elucidate the role of those genes in the physiological and molecular response to hydrocarbon derived mixtures stress, such as oil and its derivatives.



3081 - Genomics, Molecular Genetics and Biotechnology
Paula Wietholter

GENETIC SIMILARITY AMONG RACES OF PUCCINIA TRITICINA, CAUSAL AGENT OF WHEAT LEAF RUST, OCCURRING IN SOUTHERN BRAZIL

Wietholter,P; Brammer,SP; Moras,A; Chaves,MS;

Embrapa Trigo / Faculdade Meridional - IMED;

Leaf rust is a major disease of wheat, occurring in all regions of the world where it is grown. The disease is caused by the fungus *Puccinia triticina* Erikss and has a major impact on world agriculture. In South America about nine million hectares of wheat are grown annually. The fungus has a great ability to evolve rapidly and overcome the resistance of resistant cultivars. In Brazil, between one and three new races of *P. triticina* are identified each year, although the reproduction of the pathogen is only asexual. The development of microsatellite markers (SSR) for *P. triticina* has facilitated the biological studies of races, allowing a better understanding of the evolution of these populations, which are often associated with mutations of avirulent to virulent forms, which possibly are due to single mutations. Therefore, the objective of this study was to determine the genetic similarity between races of the *P. triticina* fungus. Ten races identified in southern Brazil between 1982 and 2007 were analyzed, belonging to the germplasm bank of the pathogen maintained at Embrapa Trigo. As control, *P. coronata* f. sp. *avenae* species, the causal agent of leaf rust in oat and *P. hordei*, the causal agent of leaf rust in barley were used as control. Eleven microsatellite loci were tested. DNA was extracted from spores using the extraction methodologies of Brammer et al.(2010) and the PCR (Polymerase Chain Reaction) products were separated on 3% agarose gel. Genetic similarity between races was estimated from SSR data with the Jaccard Coefficient. The mean number of alleles per locus was 2 with a mean similarity of 68% among every *P. triticina* race. Analysis of the 10 races revealed the existence of two distinct groups. The first group consisted of five *P. triticina* races identified between 1982 and 1995, with an average similarity of 62%. The second group consisted also of five *P. triticina* races identified between 2003 and 2007, with an average similarity of 76%. *P. coronata* f. sp. *avenae* presented a genetic similarity of 14% with the *P. triticina* races, and *P. hordei* presented 0%. These data suggest that the appearance of new races occurs from the existing genetic background, with the occurrence of a variable number of mutations each year, turning avirulent races into virulent and with a high genetic similarity between races.



3393 - Genomics, Molecular Genetics and Biotechnology

Priscilla Nobres dos Santos

DATA MINING OF CO₂ RESPONSIVE GENES IN *A. THALIANA* AND COFFEE SPECIES

Nobres,P; Azevedo,F; Loh,R; Patreze,CM; Alves-Ferreira,M;

Universidade Federal do Rio de Janeiro;

The enrichment of the CO₂ concentration [CO₂] in the atmosphere is reflecting on the rise of global temperature which probably will also result in changes in precipitation levels. The positive effects of the increased photosynthetic rate can be neutralized by the reduction in water availability resulting from [CO₂]. Coffee is one of the main commodities in Brazil and its growth is severely affected by high temperatures and water deficit. Therefore, understanding the combined effects of drought stress (DS) and [CO₂] are essential to predict and mitigate the forthcoming effects of global climate changes. A general survey in a gene expression database from *A. thaliana* was performed in order to identify putative transcription factors (TFs) modulated by the [CO₂]. All known TFs of *A. thaliana* were evaluated in the Genevestigator database and select according to their expression profiles in both CO₂ and DS assays. A total of 280 TFs modulated by CO₂ in *A. thaliana* were identified (135 induced and 70 repressed in all experiments; 75 were variable-induced in some experiments and repressed in others). An intersection with genes responsive to DS was made using the CO₂ responsive TFs. From the 135 CO₂ induced TFs, 90 were also induced by DS, six were repressed, 18 were variable and 11 had no response. From the 70 CO₂ repressed TFs, 24 were induced by DS, 23 were also repressed, 10 were variable and six had no response. Considering the 75 TFs that showed a variable response, 44 were induced by DS, seven were repressed, 20 were also variable and one had no response. Therefore, our analysis was focused in the group of six TFs that simultaneously induced by CO₂ and suppressed by DS since it represents genes that are affected in opposite ways by the two abiotic factors which could possibly disrupt normal stress response routes. The gene family of basic-loop-helix (bHLH) transcriptional factors (TFs) was over-represented among select group of genes. This TF family is involved in the control of variety of biological processes. After the gene selection, COBBLER sequences were generated and a BLAST was performed in the Coffea genome database using *C. arabica* and *C. canephora* clusters in order to identify the coffee genes belonging to this family. A number of candidate genes were recovered to further analyses. The next step will be the validation of the expression of these genes during DS and under [CO₂] in coffee plants.



3127 - Genomics, Molecular Genetics and Biotechnology

Railson Schreinert dos Santos

ETHYLENE RESPONSE FACTORS A STUDY ABOUT SIMILARITIES OF TRANSCRIPTIONAL RESPONSE OF RICE UNDER OXYGEN DEPLETION AND IRON TOXICITY STRESS

Santos,RS; Kruger,MM; Pegoraro,C; Madabula,FP; Maia,LC; Rombaldi,CV; Oliveira,AC;

Plant Genomics and Breeding Center at Federal University of Pelotas;

The Ethylene Response Factors (ERFs) gene family encode transcriptional regulators for a wide variety of genes with important roles in physiological processes, like fruit ripening, flower and leaves senescence and for biotic and abiotic stresses. In rice the ERFs have been extensively studied for oxygen depletion. Another important environmental stress in rice is the iron toxicity, which is one of the most important abiotic stresses limiting rice production worldwide. The objective of this study was to evaluate, in different stresses, through qPCR, the transcriptional response of seven previously selected ERFs which showed interesting pattern of regulation for oxygen depletion in Genevestigator (a software based in publicly available microarray databases) meta-analysis. In order to test two different forms of oxygen depletion, rice (Nipponbare) seedlings were submerged in ultra-pure water (hypoxia) and treated with high purity nitrogen (anoxia), 15 days after their germination, for 24 and 72 hours. To test iron toxicity stress rice seedlings (15 days age) were grown in nutrient solution for more 15 days (16 hours of photoperiod) and then subjected to iron stress (2,000 mg.L⁻¹ of FeSO_{4.7}H₂O). Iron stressed samples were collected at 0 (Control), 6, 12, 18 and 24 hours. Differential regulation was observed through qPCR for all the different stresses. qPCR analysis for oxygen depletion showed some similar pattern of regulation to the previous results shown by Genevestigator but a much different regulation when compared to iron toxicity stress results. The function elucidation of these ERFs is still necessary and the possible redundancy of these difficult the study of this gene group. Although it is known that ethylene is an important hormone in plant stress response, and the fact that ERFs are an important part in this response, many ERFs have similar responses for hypoxia, a ethylene inductive condition, and anoxia, a condition where the ethylene production is not possible. We believe that these results indicate that the response of some ERF genes in conditions of complete or partial lack of oxygen may be due to other hormones or signals.



3125 - Genomics, Molecular Genetics and Biotechnology

Railson Schreinert dos Santos

PROSPECTING EPIGENETIC MARKERS FOR STRESS ANALYSIS USING SIMPLE SEQUENCE REPEATS PRESENT IN RICE GENOME

Santos,RS; Kruger,MM; Pegoraro,C; Groli,EL; Maia,LC; Rombaldi,CV; Oliveira,AC;

Plant Genomics and Breeding Center at Federal University of Pelotas;

When plants are exposed to stressful conditions, they resort to various strategies to minimize the stress effects with physiological alterations in metabolic pathways and modifications in gene expression states, which can be inherited. When under oxygen depletion, rice responds with the regulation of gene expression at different levels and the understanding of this regulation is of great interest to compare flooding tolerant and intolerant species. Modifications that alter DNA activity without altering its basic nucleotide structure are referred to as epigenetic changes. In this context, methylation is gaining interest because it may regulate the expression of genes that have a key role in acclimation responses. In order to obtain further information about gene regulation under flooding and the role of DNA methylation in this regulation we sought for eleven genes in different rice chromosomes, which showed interesting expression profiles in oxygen deficiency stress. The expression profiles of these genes were analyzed through Genevestigator for different oxygen depletion conditions. Subsequently the presence of CpG/CpNpG islands was analyzed in the promoter region of these genes, considering 1.5 Kb before to 100bp after the transcription start site using PlantPAN. We found CpG/CpNpG islands in seven of the eleven analyzed promoters. As an initial analysis of the possible relationship between methylation and expression of these genes we sought to project the analysis of methylation in regions near the genes which presented CpG/CpNpG islands seeking for CCGG Simple Sequence Repeats through the use of SSR Locator, selecting the nearest repeats to each gene. Primers to amplify these regions were designed using the Primer 3 software. Analyzing three different stresses in different cultivars, organs, and rates of oxygen it could be seen that ERF#67 and ERF#68, both upregulated in all analyzed stresses presented CpG/CpNpG islands in its promoter regions, however the EXPA7, P450#02, ERF#042 and ERF#063 genes did not show CpG/CpNpG islands. The CCGG regions are recognized by the enzymes MspI (methylation insensitive) and its isoschizomer HpaII (methylation sensitive). It is estimated that the analysis using Digestion with methylation-sensitive enzymes Followed by PCR could be a cheap and quick way to search regions that are possibly differentially methylated in response to different environmental stimuli. This study still needs validation.



3126 - Genomics, Molecular Genetics and Biotechnology

Railson Schreinert dos Santos

TRANSCRIPTIONAL REGULATION OF 15 ETHYLENE RESPONSE FACTORS IN RICE SHOOTS SUBJECTED TO OXYGEN DEPLETION STRESS

Santos,RS; Kruger,MM; Pegoraro,C; Figueiredo,R; Maia,LC; Rombaldi,CV; Oliveira,AC;

Plant Genomics and Breeding Center at Federal University of Pelotas;

To understand and manipulate plant responses against adverse conditions caused by environmental stresses is a major challenge currently faced by crop scientists. The Ethylene Response Factors (ERFs) encode transcriptional regulators for a wide variety of genes which have important roles in the physiological processes. Studies on gene expression have been giving special attention to this family regarding oxygen depletion response in rice (*Oryza sativa* L.). The lack of oxygen due to conditions such as submergence is a major abiotic stress to which plants are subjected. The limited availability of oxygen for oxidative phosphorylation caused by this poor aeration tends to decrease the amount of ATP produced in the cell and then reducing crop yields due to other several consequences in cellular metabolism. Studies have shown the importance of some genes under oxygen depletion conditions. In any event, the molecular response to hypoxia, are poorly understood. Some varieties such as FR13A can survive up to two weeks submerged, in large part due to the locus known as Submergence1 (Sub1), located on chromosome 9 which encode three ERFs. Some other studies have given special attention to the ERFs gene family when discussing oxygen depletion response. A computational analysis study aided by TIGR database (Rice Genome Project Annotation), found 139 rice ERFs, and of these, 77 showed complete sequence (full-length). Considering what was exposed this study aimed to characterize the expression of 15 ERFs in shoots of rice subjected to 24 and 72 hours of hypoxia (submergence) and anoxia (N₂) through quantitative polymerase chain reaction (qPCR). Most of the genes analyzed in this study show similar behavior when comparing the two tested oxygen depletion conditions. It was also noticed that most ERFs were induced when rice seedlings were stressed by oxygen depletion. Possibly these upregulated ERFs have important roles in the activation of genes that are part of essential metabolic processes in plants under low oxygen conditions.



3376 - Genomics, Molecular Genetics and Biotechnology

RAQUEL DALLA LANA CARDOSO

EVALUATION OF VIRUS-INDUCED GENE SILENCING (VIGS METHODOLOGY IN GERBERA

Cardoso,RDL; Jiang,CZ; Donnelly,L; Milach,SCK; Grando,MF;

IFRS Campus Ibirubá;

The aim this study was to evaluate the feasibility of the virus-induced gene silencing (VIGS) methodology in gerbera using the viral vector TRV to study the gene function. The present experiment was carried out at Louis Mann Laboratory in the University of California in Davis/USA. Two gerbera varieties were used in two experiments. The aim of the first experiment was to evaluate the effectiveness of three inoculation methods, vacuum application, rhizome injection and petiole and leaf vein injection. The second one was to test two different concentrations (optical density, O.D 2.0 and 3.0) of *Agrobacterium* in the infiltration medium using the petiole and leaf vein injection method for inoculation. In this test, the inoculation was carried out one time, and one month later repeated five times, at weekly intervals. The viral constructions pTRV1, pTRV2, and pTRV2 with Phytoene desaturase (pTRV2+PDS) were transformed independently into *Agrobacterium tumefaciens* strain GV3101 by electroporation. The infiltration solutions were prepared mixing the *Agrobacterium* pellet with the infiltration buffer. One of the infiltration solution was prepare mixing the *Agrobacterium* carrying the pTRV1 and the *Agrobacterium* carrying the pTRV2 (empty vector serving as control), and the other, mixing the *Agrobacterium* carrying the pTRV1 and the *Agrobacterium* carrying the pTRV2 +PDS. The infiltration with only the water was also used as control. The evaluations consisted of viewing of photobleaching phenotype in leaves caused by silencing of PDS gene, which is involved in the carotenoids biosynthesis. The photobleaching phenotype was not observed in the different methods of inoculation tested. The variegated photobleaching phenotypes were observed from both gerbera varieties when the inoculation was repeated multiple time for five weeks with the concentration of 3.0 O.D in the infiltration medium. Our results from this initial testing suggest the possibility for gene functional analysis using the TRV-based VIGS methodology in gerbera. However more studies should be carried out to evaluate the genotype, temperature, inoculation time and number, or even the use of other viral vectors to improve the efficiency of the VIGS technique for more effective gene silencing in gerbera.



3375 - Genomics, Molecular Genetics and Biotechnology

RAQUEL DALLA LANA CARDOSO

TRANSCRIPT EXPRESSION EVALUATE FROM EXPRESSED SEQUENCE TAG AND GENES ASSOCIATED TO FLORAL SENESCENCE IN GERBERA

Cardoso,RDL; Jiang,CZ; Donnelly,L; Milach,SCK; Grando,MF;

IFRS Campus Ibirubá;

This study was carried out to identify expressed sequence and genes involved in gerbera floral senescence. The experiment was conducted at the Louis Mann Laboratory in UC Davis. Four corolla ray flowers of gerbera were collected in ten different stages of capitulum senescence. The stage 0 was determined as the time the gerbera capitulum is at the commercial stage. Four stages (stage -4, -3, -2, -1) prior to the stage 0 as pre-senescence stages, and five after the stage 0, corresponding to 3, 6, 9, 12 and 15 after the commercial stage were chosen for this study. Total of 22 genes were evaluated including sixteen expressed sequence tags (ESTs) selected from the microarray data (Laitanen et al., 2007), and six genes associated with floral senescence (SAG Daylily, SAG Daylily (2), SA4 Daylily, Cyp Ipomea, MT Petunia e SAG Gerb). The gene specific primers were designed using the Primer3 software. Total RNA was extracted from corolla ray of gerbera using the Trizol reagent methodology. To synthesize the cDNA the Super Script® III First Strand Synthesis System for RT-PCR were used. The cDNA obtained was used as template for real time PCR and semi-quantitative PCR. The cDNA was normalized by the 26s rRNA. The PCR reaction was done to the 22 genes evaluated in each of the ten capitulum senescence stage determined in this experiment. It was analyzed the presence and absence, and band intensity obtained by PCR amplification to the different senescence stage for each one of the candidate gene. Out of the 22 genes evaluated, five did not demonstrate to be specifically related to senescence of gerbera corolla, thirteen showed to be up-regulated and four down-regulated as flowers enter in senescence. Five genes, namely Ger protease, Ger B-gal, Ger Cys prot, Ger WD, SAG gene Cyp Ipomea, showed to be promising for future studies since they already have been reported in other species as related to senescence. Transcripts of the SAG SA4 gene were accumulated only at two stages prior to the stage 0 and can be involved in the regulation that may trigger the corolla senescence process in gerbera.



2899 - Genomics, Molecular Genetics and Biotechnology

Roberta Kuan Tchien de Mello Loh

GLOBAL EXPRESSION ANALYSIS OF A. THALIANA TRANSGENIC LINES OVEREXPRESSING THE COFFEE HOMEBOX GENE CAHB7 RELATED TO INCREASED DROUGHT STRESS TOLERANCE.

Loh,R; Alves-Ferreira,M;

Universidade Federal do Rio de Janeiro;

Coffee is one of the main agricultural products in Brazil being amongst the 10 most valuable commodities in the country which is also the current number one coffee producer in the world (> two million hectares of cultivated area). A main issue concerning coffee growth efficiency is drought stress, which may reduce up to 80% in crop yield. The general mechanisms of drought stress response in plants involve complex strategies which include specific molecular responses. Recently, a number of studies have related homeobox (HB) transcription factors (TFs) to the modulation of drought stress response and ABA signaling, controlling plant development in such conditions. In a previous study of our research group, a coffee HB gene (CAHB7) was isolated and characterized. Ectopic expression of this TF in *A. thaliana* resulted in an increase in drought and salt stress tolerance during different developmental stages, revealing its biotechnological potential. In the present study, a global expression analysis of *A. thaliana* transgenic lines overexpressing CAHB7 was performed in order to reveal the molecular mechanisms involved in drought-stress response in relation to this gene. A whole transcriptome shotgun sequencing (RNAseq) was performed in two transgenic and two wild type lines and differential expression analysis revealed a total of 353 genes (123 induced and 230 repressed) modulated by the constitutive expression of CAHB7. GO processes including responses to several types of abiotic stress such as heat, drought and osmotic, as well as biotic stimulus, defense response and hormone stimulus are significantly enriched in transgenic lines overexpressing CAHB7. Several ethylene-related genes were repressed by the overexpression of CAHB7, in agreement with what was reported for the overexpression of the sunflower HB gene HAHB4, a putative orthologue of CAHB7. Overall, the main mechanism involved in the higher drought tolerance conferred by both HAHB4 and CAHB7 seems to be following a similar trend, pointing to a functional conservation of a signaling pathway in plants. Alternatively, in *Arabidopsis*, the putative orthologues to HAHB4 and CAHB7 (AtHB-7 and 12) may have acquired a divergent function in the course of evolution. Additionally, several genes related to defense response and programmed cell death were modulated by the overexpression of CAHB7, unlike what was reported for HAHB4 suggesting the existence of a tolerance mechanism that is unique to CAHB7.



3504 - Genomics, Molecular Genetics and Biotechnology

ROBERTO TUBEROSA

ASSOCIATION MAPPING FOR NOVEL SOURCES OF RESISTANCE TO UG99 AND OTHER ETHIOPIAN STEM RUST RACES IN DURUM WHEAT

Letta,TD; Maccaferri,M; Badebo,A; Ammar,K; Sanguineti,MC; Salvi,S; Crossa,J; Tuberosa,R;

DISTA, University of Bologna;

Puccinia graminis f. sp. *tritici*, the causative agent of stem rust in wheat, is known to rapidly evolve new virulence to resistance genes. While more than 50 stem rust resistance (Sr) loci have been identified in wheat, only a few remain effective, particularly against the highly virulent race Ug99 (TTKSK race) and a mixture of durum-specific races. Association mapping (AM) was deployed on 183 elite durum wheat accessions tested in four seasons under artificial inoculation in order to identify quantitative trait loci (QTLs) for resistance to Ug99 and durum specific races under field conditions. The panel was genotyped with 1,250 SSR and DArT markers (Mantovani et al., 2008, Mol. Breed. 22:629-648). Twelve QTL-tagging markers with R² values up to 11.3% were significantly associated with stem rust resistance across three to four seasons. While some markers were linked to known Sr genes (e.g. Sr9, Sr13 and Sr14), other significant markers were located in chromosome regions where no Sr genes have been previously reported. The allelic variation identified at these novel QTLs provides additional opportunities to deploy marker-assisted selection to improve resistance to stem rust in durum wheat grown under field conditions.



3506 - Genomics, Molecular Genetics and Biotechnology

ROBERTO TUBEROSA

DROPS: AN EU-FUNDED PROJECT TO IMPROVE DROUGHT TOLERANCE IN MAIZE AND WHEAT

Tardieu,F; Charcosset,A; Draye,X; Hammer,G; Usadel,B; Tuberosa,R;

INRA, Montpellier;

DROPS (DROught-tolerant yielding PlantS; www.drops-project.eu) is an EU-funded project that will develop novel methods and strategies to improve crop performance under water-limited conditions. An interdisciplinary approach based on high-throughput phenotyping under controlled and field conditions will generate data that will be used for ecophysiological modeling to predict the performance of maize and wheat under fluctuating water regimes. The identification of Quantitative Trait Loci (QTLs) for morpho-physiological traits that influence yield under drought conditions will produce additional data for modeling crop performance based on QTL effects. The project will target root architecture, transpiration efficiency, vegetative growth maintenance and seed abortion. In particular, DROPS will: - Develop new screens that will consider indicators which are (i) highly heritable and measurable in a high-throughput fashion in phenotyping platforms; (ii) based on metabolite concentration, sensitivity parameters of models or hormonal balance; (iii) genetically related to target traits and able to predict genotype performance in the field via simulation and/or statistical models; - Explore the natural variation of the target traits by (i) linking the target traits to physiological pathways, genes or genomic regions (ii) assessing the effects of a large allelic diversity for the four target traits via association genetics; - Support crop improvement strategies by developing methods for estimating the comparative advantages of relevant alleles and traits in fields with contrasting drought scenarios. This will be achieved via field experiments and by developing new crop models able to estimate the effects of alleles on crop growth, yield and water-use efficiency.



3505 - Genomics, Molecular Genetics and Biotechnology

ROBERTO TUBEROSA

PROGRESS IN THE POSITIONAL CLONING OF QYLD.IDW-3B, A MAJOR QTL FOR GRAIN YIELD IN DURUM WHEAT

Graziani,M; Maccaferri,M; Salvi,S; Paux,E; Feuillet,C; Sanguineti,MC; Massi,A; Tuberosa,R;

DISTA, University of Bologna;

In durum wheat, a major QTL (QYld.idw-3B) for plant height, peduncle length, stay-green, leaf greenness, thousand kernel weight and grain yield per se (i.e. not due to difference in flowering time) across a broad range of soil moisture regimes was identified in a RIL population derived from Kofa and Svevo (Maccaferri et al. 2008, Genetics 178:489-511) two high quality, elite cultivars well adapted to Mediterranean environments. The fine mapping of QYld.idw-3B is underway in the framework of the FP7 TriticeaeGenome project (<http://www.triticeaegenome.eu>). In this regard, three pairs of NILs with contrasted parental haplotypes at the target region were crossed to produce approximately 7,500 F2 plants that were screened for the identification of recombinants within the 11 cM interval between Xgwm389 and Xgwm493 that flanked the QYld.idw-3B peak. In 2011, 233 informative, homozygous F4:5 segmental isolines were evaluated in the field and profiled molecularly. To increase the map resolution in the target region, new polymorphic markers were identified by exploiting the sequence information produced from the assembly of the chr. 3B physical map of bread wheat. A total of 50 new markers (BAC ends-derived SSR, ISBP and SNP markers) have been added to the target interval. All markers were anchored to the Chinese Spring physical map of chr. 3B, thus allowing us to identify the BAC contigs that span the QTL region. A high-resolution map has been obtained with an average marker distance of approximately 0.25 cM. QYld.idw-3B has been confined to a 1 cM interval spanned by contig 954 of Chinese Spring which contains 10 genes. The functional characterization via transcriptomics of these genes is underway. The haplotype at this target region is being investigated in a collection of 189 elite genotypes suitable for association mapping studies (Maccaferri et al. 2011, J. Exp. Bot. 62:409-438).



3187 - Genomics, Molecular Genetics and Biotechnology

SANDRA PATUSSI BRAMMER

IDENTIFICATION OF CHROMOSOMAL 1BL.1RS TRANSLOCATION IN WHEAT GENOTYPES BY GENOMIC IN SITU HYBRIDIZATION

Brammer,SP; Casassola,A; Volpato,V; Morás,A; Cargnin,A; Almeida,N; Chaves,MS;

Embrapa Trigo;

The 1BL.1RS translocation between the chromosome 1B of wheat and the chromosome 1R of rye, presents several agronomically important genes, being used in breeding programs to confer genetic resistance to several diseases. Currently, more than 300 cultivars of wheat have this translocation, aiming the transfer genes of interest from rye to wheat. However, this translocation affects the breadmaking quality by the loss of Glu-1B gene, responsible for coding of glutenin which is present in the gluten formation. The aim of this study was the identification of 1BL.1RS translocation in different wheat genotypes. From this identification is possible to infer the presence of the Sr31, Lr26 and Yr9 genes which confer resistance to stem, leaf and yellow rust, respectively, and to characterize genotypes associated with the end-use quality. The identification was determined by Genomic In Situ Hybridization (GISH) technique. In the study we evaluated 159 cultivars, 85 lines and 16 synthetic wheat which are being maintained at Embrapa Wheat (Passo Fundo, RS). Roots of germinated seeds were collected, pre-treated at 4 °C on ice for 24 hours and fixed in Carnoy. The cytology slides were prepared with pectinase-cellulase and macerated with 45% acetic acid. The wheat cultivar "BR 35" DNA was used as blocking and the rye cultivar "BR 1" DNA was used as a probe. This probe was labeled with digoxigenin 12dUTP by Nick Translation technique. The denaturation of the chromosomes and probe, the hybridization and detection were performed according to Heslop-Harrison et al. (1991), with 77% of the stringency. The hybridization mixtures were: 100% formamide, 50% dextran sulfate, 0.5 ng/ul of probe and 0.5 ng/ul of blocking. The slides were denatured at 73 °C for seven minutes and the fluorochrome used was FITC. Slides were sealed with 2 ug/ml DAPI in Vectashield, 1:1. Ten cells were evaluated for each genotype, with three repetitions each, employing a fluorescence microscope Zeiss 40-AxioScop. The results indicated that 31 (19,5 %) of the cultivars and 37 (43,5 %) of the lines were positive for the 1BL.1RS translocation. Regarding synthetic wheat this translocation was not identified. These evaluations and characterizations are essential to define subsequent breeding methods as well as for phytopathological studies and analysis of end-use quality of wheat. Heslop-Harrison, J. S. et al., In situ hybridization with automated chromosome desnaturation. Technique, v. 3, p. 109-115, 1991.



2907 - Genomics, Molecular Genetics and Biotechnology

Sang-Soo Kwak

DEVELOPMENT OF ECO-FRIENDLY TRANSGENIC CROPS FOR SUSTAINABLE DEVELOPMENT ON MARGINAL LANDS

Kim,YH; Kim,MD; Kim,SH; Jeong,JC; Lee,HS; Kwak,SS;

Environmental Biotechnology Research Center, Korea Research Institute of Bioscience and Biotechnoloigy (KRIBB);

Who will support the world population of more than 9 billion people in 2050? The dramatic increase in population accompanied by rapid industrialization in developing countries has caused imbalances in the supply of food and energy. To cope with these global crises over food and energy supplies as well as environmental problems, it is urgently required to develop new crop varieties to be grown on marginal lands including desertification areas for sustainable development. Environmental stress conditions, such as drought, high salinity, and extreme temperatures, are major factors affecting plant growth and productivity. These environmental stressors cause oxidative stress by rapid and excessive accumulation of reactive oxygen species in plant cells. Many attempts have been made to confer tolerance to stresses in plants. The use of a stress-inducible promoter which provides a more precise regulation of expression might be useful for the development of stress-tolerant plants. To develop various transgenic plants with an enhanced tolerance to multiple environmental stresses, we are focusing on the manipulation of antioxidant genes in plant cells under the control of an oxidative stress-inducible peroxidase (SWPA2) promoter. Recently we developed several transgenic industrial food crops (sweetpotato and potato) and forage crops (tall fescue and alfalfa) expressing genes involved in multiple stress tolerance. Sweetpotato (*Ipomoea batatas* (L.) Lam) ranks seventh in annual production among food crops in the world. It is also an alternative source of industrial materials such as starch, ethanol and antioxidants including carotenoids. Moreover, it does not require large amounts of fertilizer and pesticides for cultivation and is rather tolerant to some environmental stresses. Its wide adaptability on marginal land ranging from tropical to temperature zones and rich nutritional content provide a high potential for preventing malnutrition and enhancing food security in the developing countries. In the presentation, the results and prospects of our studies on several industrial transgenic crops such as sweetpotato, potato (*Solanum tuberosum*), alfalfa (*Medicago sativa*) with enhanced tolerance to multiple environmental stresses will be introduced in terms of blue ocean strategy.



3195 - Genomics, Molecular Genetics and Biotechnology

Stéfanie Menezes de Moura

FUNCTIONAL CHARACTERIZATION OF MADS-BOX GENES OF GOSSYPIUM HIRSUTUM INVOLVED IN THE OVULE AND FRUIT DEVELOPMENT

Moura,SM; Nardeli,SM; Artico,S; Lambret Frotte,JS; Brilhante,O; Grossi-de-Sá,MF; Alves-Ferreira,M;

Universidade Federal do Rio de Janeiro - UFRJ;

Brazil is one of the major producers, exporters and consumers of cotton (*Gossypium hirsutum*) in the world. The importance of cotton production in Brazil and the world is mainly targeted to the production of textile fiber, thus, many researchers have been developed to maximize productivity by increasing the quantity and size of fiber cells that develop from the epidermis of the ovule in cotton. It is known that hormones such as gibberellin, auxins and brassinosteroids are required for normal development of these cells. In addition, genes encoding for hormone biosynthesis pathway (HBP), such as GA20-oxidases, when overexpressed can lead to greater size and quantity of fibers per ovule in *G. hirsutum*. An important strategy to improve productivity would be to control the expression of genes encoding for HBP directly into the ovule in specific stages of development of fiber. The family of transcription factors MADS-box includes genes important in determining the identity of floral organs and fruit in plants. In silico analysis of the *G. hirsutum* transcriptome allowed us to identify and classify phylogenetically 20 putative genes that show high identity with MADS-box genes already characterized in the model plant *Arabidopsis thaliana*. Among the identified genes, we decided to focus on a putative homologue of *Arabidopsis* SEEDSTICK, named GhAGL- like2. qPCR analysis revealed that GhAGL- like2 has a high expression throughout the different stages of cotton bud flower and fruit development. We isolated 1677 pb promoter region of GhAGL- like2 by Genome Walker strategy. In silico analysis of the promoter region identified putative cis elements involved in flower and seed specific expression, as well as putative cis elements involved in hormones response such as auxin and gibberellins. These two hormones are important regulators of cotton fiber initiation and elongation. Constructs with distinct fragments of the promoter regions will be fused to the UidA reporter gene to study the expression promoter activity in *Arabidopsis thaliana*. Our results will bring light to the regulation of GhAGL- like2 in cotton and also can be an important biotechnological tool for driven gene expression in cotton reproductive tissue to improve productivity.



3159 - Genomics, Molecular Genetics and Biotechnology

Tae Heon Kim

FINE MAPPING OF THE LOW-AMYLOSE CHARACTERISTICS OF RICE CULTIVAR BAEGJINJU

Lee,JHL; Shim,JHS; Lee,JYL; Cho,JHC; Song,YCS; Yeo,USY; Oh,MGO; Sohn,JKS;
Nam,MHN;

National Institute of Crop Sciences, Rural Development Administration;

Control of the amylose content is a major strategy for breeding rice with improved eating quality. To identify the low-amylose gene of the low-amylose rice cultivar Baegjinju 1 derived from MNU treatment, Genetic analysis was conducted on 200 F₂ individual plants derived from a cross between the japonica cultivars Milyang244 and Baegjinju1. Individual F₂ plants of Milyang244/Baegjinju1 were classified as wild type or mutant type (opaque grain) based on the grain appearance of brown rice. A total of 200 F₂ plants from Milyang244/Baegjinju segregated into 155 wild type, and 45 mutant type, which fit to a 3 :1 ratio and ($\chi^2 = 0.667$, $df = 1$, $p = 0.414$), suggesting the inheritance of a recessive gene for amylose content. The low amylose gene locus *du1(t)* was finely mapped within an approximately 800kb region between 17.5 to 18.8Mb on the short arm of chromosome 10, and simple sequence repeat(SSR) markers. This DNA marker developed in the candidate region of the *du1(t)* locus are useful tools for low amylose gene.



3353 - Genomics, Molecular Genetics and Biotechnology

Tatiane Medeiros Souza

MOLECULAR MARKER FOR IRON TOXICITY BASED IN THE POLYMORPHISM OF PROMOTERS AND GENES OF METALLOTHIONEIN FAMILY IN RICE

Souza,TM; Finatto,T; Silva,GJ; Guerra,G; Oliveira,AC;

Universidade Federal de Pelotas;

Rice, a cereal of great economic and social importance, can suffer with iron toxicity stress when is cultivated in waterlogged conditions, leading to high yield losses. Rice breeding programs of rice seek combinations of crosses aimed at obtaining genotypes tolerant to this stress. Among the genes that are related to this stress in plants are the members of metallothionein family. The metallothioneins (MTs) are a large and diverse superfamily of proteins of low molecular weight, rich in the amino acid cysteine, that are capable of binding via metal thiol groups present in their residues. The study of metallothionein genes can help to understand iron homeostasis and genotype differences in rice. Thus, the objective of this study was to design primer pairs that would amplify the region comprising the conserved cis-element in the promoter and the conserved coding regions of the MT gene family. Searches of promoter sequences (1kbp upstream of start site of transcription) of 15 genes of MT family were carried out in the RAP-DB database. In MEME (Multiple Em for Motif Elicitation) the occurrence of cis-elements motifs were searched in the upstream of genes. To design the primers, the motif that appeared more frequently among the 15 promoters was chosen. ClustalW was used to perform the search for conserved regions among the DNA sequence of MT genes. The size and position of the region were taken into account. The primers were designed in the program Vector NTI version 9.0.0. Ten pairs of primers were designed and tested in eight rice genotypes, as follows: two sensitive to iron toxicity (BRS Atalanta and Irga 409), one with intermediate tolerance (BRS Firmeza) and five genotypes tolerant to iron toxicity (BRS Agrisul, Epagri 107, Epagri 108, BRS Bojuru and Nipponbare). From 10 pairs of primers tested, one pair showed polymorphism. However, this polymorphism did not show a pattern of occurrence among tolerant and sensitive genotypes. This may be due to small sample of genotypes used in this work, which did not represent the variability necessary to distinguish the genotypes. However, the primers showed ability to uniquely amplify gene members. Further investigations are underway to better assess these genes.



3369 - Genomics, Molecular Genetics and Biotechnology

Thais Louise Gurjão de Carvalho

AUXIN SIGNALING IN SUGARCANE ROOT GROWTH PROMOTION BY DIAZOTROPHIC BACTERIA

Carvalho,TLG; Bomfim,ACJS; Pragana,MLF; Vicentini,R; Baldani,JI; Hemerly,AS;

Universidade Federal do Rio de Janeiro;

Root development and architecture are processes controlled by genetic program and modulated by a variety of endogenous and environmental signals. Several studies have demonstrated the positive effects of inoculation with diazotrophic bacteria on sugarcane root growth promotion. The aim of this work is to conduct a comprehensive analysis of the mechanisms involved in root development of sugarcane as well as in root growth promotion induced by association with diazotrophic bacteria. Root architecture was analyzed in germinated stalks and in diazotrophic bacteria free plants, grown in hydroponics, of two genotypes SP70-1143 (high Biological Nitrogen Fixation - BNF) and Chuneé (low BNF). In germinated stalks, it was observed that SP70-1143 presents greater root development when compared with Chuneé, this same phenotype difference was also observed in diazotrophic bacteria-free plants. Inoculation with diazotrophic bacteria promoted root growth in both genotypes, but it was more remarkable in SP70-1143. RNA samples from the two contrasting genotypes were used to construct the Illumina RNA-Seq database. The transcriptome data shows that plant colonization by diazotrophic bacteria regulates more processes in high BNF genotype than in low BNF. Moreover, we could identify mechanisms involved in genetic control and the efficiency of the association, which may be related to differences in root development between the two genotypes. Among the pathways differentially regulated between the genotypes and during association with diazotrophic bacteria is auxin response signaling, a key phytohormone in the regulation of root development. The use of model plants, such as rice and *Arabidopsis thaliana*, showed that both the levels of auxin and its distribution are modified during the interaction with the diazotrophic bacteria. Our data suggests that the molecular and phenotypic differences observed between genotypes may explain, at least in part, the differences in response to association between the contrasting genotypes. Furthermore, the auxin signaling is regulated during association with diazotrophic bacteria and root growth promotion might be, at least in part, a result of modulation of this phytohormone pathway. Financial support: FAPERJ, CNPq, INCT, CAPES



3213 - Genomics, Molecular Genetics and Biotechnology

Vítor da Silveira Falavigna

TRANSCRIPTIONAL AND METABOLIC PROFILING OF TWO APPLE TREE CULTIVARS CONTRASTING IN CHILLING REQUIREMENT

Falavigna,VS; Porto,DD; Anzanello,R; Buffon,V; Souza,DA; Margis-Pinheiro,M; Pasquali,G; Oliveira,PR; Centeno,DC; Santos,HP; Revers,LF;

PPGBCM - UFRGS;

Considering the limited information about bud dormancy control, this work aimed to investigate the differential gene expression and metabolic profile between Gala and its derived bud sport Castel Gala, which are apple tree cultivars displaying respectively medium and low chilling requirement. In a previous work, a suppressive subtractive hybridization (SSH) assay yielded 28 candidate genes associated to dormancy cycling. We performed RT-qPCR in order to validate differential expression on buds from 2007, 2008 and 2009. Samples from 2007 and 2008 were harvested with approximately the same phenological patterns of the ones used for SSH libraries construction. In 2009, sampling was performed on six dates at a commercial orchard with both Castel Gala and Royal Gala trees. Total RNA was isolated by LiCl precipitation, and cDNA synthesis was carried out using the GeneAmp kit (Applied Biosystems). RT-qPCR was performed on a StepOne Plus thermal cycler (Applied Biosystems) with SYBR Green chemistry (Ambion). In parallel, the first two of the six dates from 2009 sampling were screened for a range of metabolites, mainly carbohydrates and organic acids. Frozen tissues were ground in liquid nitrogen and extracted in methanol:chloroform:water (12:5:1) with 20 mg/ml adonitol as internal standard. Derivatized samples were analyzed in a GC-MS system (Agilent). Of the 28 candidate genes identified by SSH, 18 showed differential expression at the predicted dates in 2007 and 2008 samples. The expression of the 18 genes was tested in buds from 2009 sampling, and 12 of them were differentially regulated between cultivars as expected. The final 12 genes were annotated as ARP6, CONSTANS-LIKE, Dormancy-associated MADS box, GAST-like, two histones H2A variant H2A.Z, NAC transcription factor, galactinol synthase, ESKIMO and three dehydrins. In the GC-MS analysis, raffinose, galactinol, pinitol and quinic acid showed the overall most contrasting results, mainly between dormant and non dormant samples of Royal Gala. The results displayed major differences in gene expression between cultivars through the winter, along with metabolic contrasts associated to cell water metabolism. The 12 genes selected are strong candidates to play key roles on dormancy process in apple trees, and further studies are underway to better understand their functions. Financial support: CAPES, CNPq, FINEP, ABPM.



3325 - Genomics, Molecular Genetics and Biotechnology

Yong Gu Cho

CBL-INTERACTING PROTEIN KINASE 1 FROM BRASSICA RAPA ENHANCED MULTIPLE ABIOTIC STRESS TOLERANCE IN RICE

Abdula,SE; Lee,HJ; Jee,MG; Jang,DW; Kang,KK; Cho,YG;

Chungbuk National University;

Calcium plays a vital role as a second messenger of several signaling pathways in plants. The calcineurin B-like proteins (CBLs) constitute a family of plant calcium-binding proteins that function in calcium signaling by interacting with their interacting protein kinases (CIPKs). Discovery and functional analysis of gene tolerant to abiotic stresses are important steps in increasing rice production, and mitigate the impact of climate change. In this study, we cloned BrCIPK1 gene from Brassica rapa and developed transgenic rice overexpressing lines. The gene named BrCIPK1 had a total length of 1982 bps, containing an open reading frame (ORF) of 1509 bps. It is highly conserved in the N-terminal region with the catalytic domain of AGC family protein serine/threonine kinases. Southern Blot analysis showed the presence of a single copy gene. The transgenic plants, which were 2-week old seedlings, showed elevated tolerance to cold, salinity, and drought compared to wild type, Gopumbyeo. The enhanced tolerance was further supported by the increasing mRNA transcript, increasing proline and free sugars overtime. Furthermore, to explain the involvement of proline in the enhanced tolerance, the P5CS1 (Delta1-pyrroline-5-carboxylase synthetase-1) gene that regulates proline biosynthesis showed several fold higher expression on the BrCIPK1 rice lines. Additionally, yeast two hybrid analysis showed that BrCIPK1 interacts with CBL5 indicating its involvement in the signaling pathways during stresses. The proposed mechanism of BrCIPK1 in abiotic tolerance will be presented.

*This work was supported by a grant from the Next-Generation BioGreen 21 Program (Plant Molecular Breeding Center No. PJ008129), Rural Development Administration, Republic of Korea.

*Corresponding author: Tel. 043-261-2514, E-mail: ygcho@cbnu.ac.kr



3330 - Genomics, Molecular Genetics and Biotechnology

Yong Gu Cho

OVEREXPRESSION OF GLUTAMINE SYNTHETASE (GS) IN RICE ENHANCES TOLERANCE TO CADMIUM AND ABIOTIC STRESSES

Lee,HJ; Abdula,SE; Jee,MK; Jang,DW; Park,SH; Yoon,UH; Kim,TH; Cho,YG;

Chungbuk National University;

Glutamine synthetase (GS) (EC 6.3.1.2) is enzyme that plays an essential role in the metabolism of nitrogen by catalyzing the condensation of glutamate and ammonia to form glutamine. Exposure of plants to cadmium (Cd) has been reported to decrease the GS activity of maize, pea, bean, and rice. To understand better the function of GS gene under cadmium stress in rice, we constructed a recombinant vector with GS under the control of CaMV 35S promoter and OCS terminator in pART vector and transformed using *Agrobacterium tumefaciens*. The expression patterns and physiological effect both in GS overexpressing plants and wild type under cadmium stress and abiotic stress conditions were then investigated. Although a decline in GS enzyme activity and mRNA expression were observed for both plants under cadmium solution, the decrease, however, is significantly higher in the wild type compared to the transgenic. Similarly, under low nitrogen treatment, GS-OX lines demonstrated a relatively higher expression level compared to the WT. This was further validated by the higher mRNA expression and GS enzyme activity in most transformed lines. Moreover, glutamine reductase (GR) enzyme showed lower or no malondialdehyde (MDA) activity after 10 days of Cd stress. With these results, it can be inferred that overexpression of GS in rice modulated the expression of enzymes responsible for membrane peroxidation that may result to death in plants.

*This research was supported by iPET, Ministry for Food, Agriculture, Forestry and Fisheries, Republic of Korea.

*Corresponding author: Tel. 82-43-261-2514, E-mail: ygcho@cbnu.ac.kr



3332 - Genomics, Molecular Genetics and Biotechnology

Yong Gu Cho

OVEREXPRESSION OF UDP-GLUCOSE-4-EPIMERASE 1 (UGE1) INCREASES YIELD AND ENHANCED DROUGHT TOLERANCE IN RICE

Abdula,SE; Lee,HJ; Jee,MG; Jang,DW; Cho,YG;

Chungbuk National University;

UDP-glucose-4-epimerase (GALE), also known as UDP-galactose-4-epimerase (UGE), is an NAD dependent enzyme that is responsible for reversibly inverting the UDP-galactose to form UDP-glucose in a wide variety of species. UDP-galactose and UDP-glucose are precursors for many biosyntheses of numerous carbohydrates, glycolipids and glycosides. In this study, the full-length cDNA of UGE1 was cloned from *Brassica rapa* and overexpressed in rice. The gene named BrUGE1 had a total length of 1328 bps that contains an open reading frame (ORF) of 1056 bps. It has a highly conserved catalytic domain and is highly expressed in stem, young shoot and leaf in rice. Southern blot analysis showed the presence of a single copy gene number. Over-expression analysis in rice showed enhanced tolerance to drought stress with increased mRNA transcript overtime using two-week old seedlings. The tolerance was partially explained by the activation and increased in osmolyte sugars. Further studies showed that BrUGE1 overexpressing lines produced significantly more yield than the wild type, Gopumbyeo. This can be accounted to an increase in the number of spikelets per panicle and filled grains. Interestingly, these lines were less affected by sugar toxicity compared to Gopumbyeo and might act in the direction of UDP-Galactose to UDP-Glucose.

*This work was supported by a grant from the Next-Generation BioGreen 21 Program (Plant Molecular Breeding Center No. PJ008129), Rural Development Administration, Republic of Korea.

*Corresponding author: Tel. 043-261-2514, E-mail: ygcho@cbnu.ac.kr



3420 - Genomics, Molecular Genetics and Biotechnology

Yutaka Ogura

GENERATION AND ANALYSIS OF EXPRESSED SEQUENCE TAGS IN RYE

Ogura,Y; Murata,M;

Institute of Plant Science and Resources, Okayama University;

Rye is an important crop, which shows high tolerance against abiotic stresses like draught, frost, low soil fertility and is also a source of alien chromosome segment containing genes for agronomically useful traits in wheat breeding. The objective of this study was to get more information on gene sequences in rye by generating expressed sequence tags (ESTs). Two libraries were constructed from seedling and young spike of rye (*Secale cereale* L. cv. Petkus). Double-stranded cDNAs synthesized from polyA RNA were ligated to plasmid vector and used for transformation of *E. coli*. Plasmid DNAs were extracted from randomly selected colonies of the libraries and sequenced from the 3'-end by Sanger method. The chromatogram files were base called by phred and then trimmed with SeqTrim. Trimmed ESTs were assembled into contigs using EGAssembler. The sequences of the contigs and the singletons were searched against databases (NCBI's dbest, DFCI Gene Indices and Sce_Assembly03 in GABI primary database). Over 1000 clones from seedling cDNA library and over 3000 clones from young spike cDNA library were sequenced. After removing vector and adaptor sequences and trimming of low quality sequences, a total of 3193 ESTs with average length of 480 bp were obtained. The ESTs were assembled into 1768 unigenes, including 402 contigs and 1366 singletons using the CAP3 program. In BLAST search, 976 unigenes showed "no hit" against 9,298 rye ESTs available in NCBI's dbest. And 147 and 142 unigenes did not hit against Sce_Assembly03 and DFCI Wheat Gene Index release 12.0, containing 115,400 contigs created from NGS reads and 221,925 unique sequences, respectively. We generated 3193 rye ESTs, including candidates for new genes, from seedling and young spike cDNA libraries. Accumulation of sequence data by Sanger method can be a help to better understand genes and genome of rye.



Poster Session

Plant Genetic Resources



2879 - Plant Genetic Resources

Adeliano Cargnin

GENETIC VARIABILITY IN BRAZILIAN BARLEY FOR GRAIN PRODUCTION

Cargnin,A; Minella,E; Santana,F;

Embrapa;

The main goal of a breeding program is to provide new varieties genetically higher, specially for grain production. The choice of the parental genotypes, considering the genetic variability, can be carried out by the breeders based only in their knowledge acquired from their fieldwork. However, the studies on the genetic variability could contribute as an auxiliary strategy for the breeders in order to choose parents with higher genetic potential. The goal of this study was to estimate the genetic variability of some Brazilian barley genotypes considering grain production. Fifty genotypes were evaluated, which represent the main barley cultivars usually grown in Brazil. The experiment was carried out on field conditions at Embrapa Trigo, Passo Fundo, RS, in 2011. Two randomized blocks experiments were conducted. Each plot was made of 6 rows with 0,20cm apart and 5m long. Grain yield (kg/ha) was estimated from the production plots. Data were submitted to variance analysis. It was also estimated the genetic dissimilarity among the genotypes and their groups. There was statistic difference for the grain yield, which demonstrates that there is genetic variability among the 50 Brazilian barley genotypes. Grain yield ranged from 1883kg/ha to 4616 kg/ha. The genotypes Embrapa 127 and BRS Suábia showed the highest yield, 4462 kg/ha and 4404 kg/ha, respectively. The genetic distances estimated among the 50 genotypes resulted in 12 distinct groups. Similarly, based on the dissimilarity dendogram, several groups were made, which support the genetic variability hypothesis. According to this grouping, the genotypes Embrapa 127 and BRS Suábia belong to one group which is the most genetically distant from the others. So, those genotypes if chosen as parental in crossing blocks could provide a segregating offspring with high yield potential. In conclusion, there is genetic variability among the Brazilian barley genotypes which can be exploited in order to generate segregating populations.



3299 - Plant Genetic Resources

Dr Awnindra Kumar Singh

ASSESSMENT AND UTILIZATION OF GENETIC DIVERSITY IN LOCAL LANDRACES OF MUNGBEAN (*VIGNA RADIATA* L. WILCZEK) OF ANDAMAN & NICOBAR ISLANDS, INDIA

Singh,AK; Gautam,RK; Sigh,PK; Kumar,N; Kumar,K; Singh,DR;

Central Agricultural Research Institute, Port Blair;

In order to evaluate and utilize mungbean germplasm effectively for the development of new varieties, an exhaustive characterization of the various landraces of Bay Islands and some promising genotypes that constitute the gene pools for the crop need to be fully characterized to identify the useful genetic diversity. With this aim, an experiment was laid down in augmented design comprising of 56 germplasm lines at two locations during November, 2011 to February, 2012 at CARI, Port Blair, India. Analysis of variance (ANOVA) was done to know the variations among the germplasm based on the 19 morphological and metric traits using SAS 4.1 enterprise and linkage distance was measured for 56 genotypes was also calculated on various traits. Cluster analysis using unweighted pair group method with arithmetic mean (UPGMA) (between group linkages) was used to investigate distance, similarity and relatedness of genotypes, so that similar genotypes can be classified into one group and dissimilar ones into other distinct groups. The analysis of variance showed significant differences among the genotypes for most of the traits. Using cluster analysis all genotypes were grouped into 2 main groups and 4 sub clusters. A dendrogram based on average linkage distance for 56 mungbean genotypes was also calculated. Cluster I consisted of 30 genotypes and cluster II had 26 genotypes. Sub clusters I consisted of 10 genotypes, II of 20, III of 24 and IV of 2 genotypes. Principal Component analysis was done to evaluate diversity and morphological traits which had more effects on diversity. The results showed that four principal components and factors with Eigen values more than one explained 75.59% of total variability. On the basis of results it has been revealed that, the local landraces of the Bay Islands were in all major clusters, while those from and main lands of India were mainly grouped into one cluster and having wider genetic base for most of the traits. Hence, it has been recommended that the germplasm from Bay Islands can be exploited more in cultivar development to enrich the breeding gene pool. High genetic variability was also found in yield components. Phenology traits such as plant height, days to flowering, and days to maturity also showed high genetic variability. These results of cluster and principal component analysis can be applied in a breeding program of mungbean aimed at yield improvement for location specific conditions.



3130 - Plant Genetic Resources

João Dimas Garcia Maia

EVALUATION OF GRAPEVINE GERMLASM UNDER TROPICAL CONDITIONS IN BRAZIL

Maia,JDG; Camargo,UA; Machado,CAE; Ritschel,P;

Embrapa Grape and Wine, Experimental Station of Tropical Viticulture - EVT;

In the last years, a great expansion of grape production towards tropical regions has occurred in Brazil and the influence of the climate conditions on agronomical and berry quality traits and features of grape-derived products is well-known. The objective of the current work is to evaluate agronomical traits of accessions from the Grapevine Germplasm Bank under tropical conditions. In 2010, a vineyard with 200 accessions from BAG-Uva was installed at the Experimental Station of Tropical Viticulture, Embrapa Grape and Wine (latitude 20° 09' S, and longitude 50° 35' W), employing 'IAC 572' as rootstock and in a pergola configuration. The group consisted mainly of *Vitis labrusca*, *V. bourquina*, hybrids and other wild *Vitis* species accessions. The genetic material is currently being characterized by phenological observations, flower typing and berry and cluster features. During harvesting, productive components are evaluated and samples are collected for must evaluation. Besides investigation of the incidence of main grapevine diseases, the occurrence of grapevine rust and leaf blight, two important diseases that increased their importance from the 1990s, causing losses for tropical viticulture, will also be studied. The evaluations will be carried out during a five-year period in order to define the accessions displaying the best agronomical and quality traits to be incorporated into the breeding program for tropical grape cultivars. The first evaluation was performed between October and November, 2011. Genetic variation among the accessions was observed for the considered traits, important in the development of novel grapevine cultivars for tropical regions, including berry color, flavor, sugar content, texture, adherence to cluster, berry and cluster size. From the investigated accessions, 8% exhibited high fertility and 76% displayed resistance to berry skin cracking. During that growth season, it was not possible to evaluate rust and leaf blight incidence due to unfavorable climate conditions to disease occurrence. Among the investigated accessions, it will be possible to identify progenitors with interesting attributes for the development of novel table grape cultivars for tropical regions, such as high fertility and resistance to berry skin cracking.



3305 - Plant Genetic Resources

José Guillermo Seijo

DIVERSITY AND CHROMOSOMAL DISTRIBUTION OF LONG INTERSPERSED NON- LTR ELEMENTS (LINES) IN THE A GENOME OF ARACHIS SPECIES

Samoluk,S; Carisimo,D; Robledo,G; Seijo,JG;

Instituto de Botánica del Nordeste;

Retroelements constitute part of the repetitive DNA and play an important role in both the evolution and structure of plant genomes. Section *Arachis* has 31 species grouped in five genomes (A,B,D,F and K), 29 are wild diploids and two are allotetraploids. Even though there is a conserved colinearity of different molecular markers among *Arachis* species with different genomes, GISH analysis suggested a large divergence at the sequence level. On these bases, it has been hypothesized that the repetitive fraction may have driven or participated in the genome differentiation of *Arachis*. Considering that, and as a first step to test this hypothesis, the diversity of a group of LINEs retroelements in *Arachis* species belonging to the A genome (*A. duranensis*, *A. cardenasii* and *A. helodes*) was analyzed. For this purpose, 20 sequences of the conserved region of the reverse transcriptase gene were amplified from genomic DNA of the three species using degenerate primers. The amplified sequences showed 81% of variable sites and stop codons in 40% of them. However, they had high homology at the amino acid level. These sequences also showed high homology with the amino acid motifs of the reverse transcriptase of LINEs present in other angiosperms and in gymnosperms. Despite the wide distribution of these elements in different groups of plants, the N-J dendrogram revealed that the *Arachis* sequences form a unique cluster, although nonspecific subclusters were observed for each species. This clustering suggests that the diversification of the elements present in *Arachis* took place before the origin of the A genome. The fluorescent in situ hybridization revealed a dispersed pattern of weak signals over most of the chromosomes of the three species, suggesting that even though these elements are ubiquitous, they have a low representation in the A genome.



3278 - Plant Genetic Resources

Laura Cortese

BIOENERGY CHARACTERISTICS IN FIFTY SWITCHGRASS CLONES GROWN ON MARGINAL AND PRIME LAND

Cortese,LM; Bonos,SA;

Rutgers, The State University of New Jersey;

Switchgrass (*Panicum virgatum* L.), a perennial C4 grass native to the US, is currently being grown as a bioenergy crop in the US. Although perennial grasses are expected to be used as biofuel crops on marginal land, there has been little to no research evaluating their performance on marginal land. The objective of this study was to examine the influence of soil type on bioenergy characteristics in switchgrass including tiller number, plant height, lodging, anthracnose (*Colletotrichum navitas*) and rust (*Puccinia* sp) diseases, and biomass yield to determine optimum selection procedures and broad-sense heritability. Five clones from 10 different switchgrass populations were vegetatively propagated into 18 clonal replicates. Clones were transplanted in a randomized complete block design with six vegetative replications at each of three locations in New Jersey in June of 2009. The three sites included two marginal sites - Somerset, NJ (class IV Kleinsville shale) and Jackson, NJ (class V Evesboro sand), and a prime farmland site in Freehold, NJ (class II Freehold sandy loam). Clones received 60 kg N ha⁻¹ in spring of 2009, 2010, and 2011. In 2010 and 2011, clones were evaluated for biomass traits including tiller number, plant height, lodging, anthracnose and rust resistance, and biomass yield. A significant location by clone interaction was observed for all traits evaluated. Overall, clones at the prime site (Freehold) showed the highest number of tillers while clones at Jackson had the lowest tiller numbers. Clones exhibited less lodging at the two marginal sites which could be due to the shorter plant heights observed at the marginal sites. Similar relative levels of anthracnose and rust resistance among clones were seen across all three locations. As expected, biomass yields were highest at the prime site. Broad-sense heritability estimates ranged from 0.64 for rust resistance to 0.98 for plant height. Significant location by year interactions observed indicate that plant height, lodging, anthracnose resistance and rust resistance, and biomass yield are affected by environmental conditions. Data for several traits evaluated seems to show that while soil types may affect plant performance, relative levels of performance tend to be similar across all three soil types included in this study indicating that selection for biomass traits can be made on prime soil with the expectation that selected individuals will also perform well on marginal land.



3128 - Plant Genetic Resources

Patricia Ritschel

GENETIC ANALYSIS OF 'MOSCATO BRANCO' AND OTHER MUSCAT GRAPES HELD BY THE GRAPE GERMPLASM BANK IN BRAZIL

Ritschel,P; Gomes,FGG; Ceriotti,I; Longhi,P; Maia,JDG; Zanús,MC; Tonietto,J; Ferreira,ME;

Embrapa Grape and Wine;

Among muscat grapes grown in Brazil, stands out the cultivar 'Moscato Branco', also called 'Moscato Italiano'. The origin of this grape is not known. Preliminary ampelographic studies indicate that there is no definition of its identity with any of the aromatic grape varieties described in Italian viticulture. The objective of this study was to estimate the genetic diversity of muscat grape accessions maintained by Brazilian Grape Germplasm Bank (GGB) with the use of microsatellite markers, focusing on the differentiation of 'Moscato Branco' from the other muscat grapes. A sample of 44 muscat grapes was selected for this study, including cultivars for fresh consumption and processing worldwide, in addition to 'Moscato Branco'. Seventeen polymorphic SSR markers were selected for DNA polymorphism analysis. DNA fragments were amplified by PCR, separated and visualized by silver stained polyacrylamide gel electrophoresis. Genetic parameters such as allelic variation, heterozygosity (H_o) and Polymorphic Information Content (PIC) were estimated, as well as the probability of Genetic Identity (PID) between samples presenting the same genetic profile in this group of muscat grapes. Pairwise genetic similarity was estimated by the 'band' coefficient. Cluster analysis (UPGMA) resulted in a dendrogram, which allowed the observation of the genetic relationships among accessions. Results The markers selected have high levels of PIC and H_o , with a few exceptions. The average H_o of the 44 muscat grapevine was 0.57. The accessions 'Italia', 'Ruby' and 'Ruby Okuyama' presented the same genetic profile and could not be distinguished from each other with the set the molecular markers selected for analysis ($PID=1.31 \times 10^{-14}$). The accession 'Ruby' is a known somatic mutation of 'Italy', differing from it by the color of the berry, while 'Ruby' and 'Ruby Okuyama' are duplicates of the same accession with different common name. Most interestingly, 'Moscato Branco' presented an unique genetic profile, and could be differentiated from all muscat accession tested, including cultivars such as 'Italy' and its mutations, 'Moscato Branco R2', 'Moscato Giallo', 'Moscato de Hamburgo', 'Moscato de Alexandria' and the 'Malvasia' accessions. Conclusions DNA polymorphism analysis at microsatellite loci allowed the identification of duplicates in the grape collection and indicated that 'Moscato Branco' can be readily differentiated from the other muscat grapes conserved by GGB.



2694 - Plant Genetic Resources

sun-jianchang

Analysis of Genetic Diversity within Populations of Rice Landraces from Yunnan using Microsatellite Markers

Sun-Jianchang, SUNJIANCHANG; Tengqiong, Y; Cuifeng, T; Guilan, C; Furong, X; Longzhi, H;

Institute of Crop Sciences, Chinese Academy of Agricultural Sciences;

Institution of Crop Research, Ningxia Academy of Agricultural Sciences, Yongning, Ningxia 750105, China;

Crop Genetic Resources Institute, Yunnan Academy of Agricultural Sciences, Kunming, Yunnan 650205, China;

Genetic diversity within populations of 16 rice landraces and 2 advanced cultivars from Yunnan were analyzed using 20 SSR markers. The results showed that the SSR marker polymorphism within populations for 87.5% of rice landraces was higher than that of advanced cultivars, while the SSR marker polymorphism within populations for 12.5% of landraces was similar with that of advanced cultivars. The number of alleles (N_a) and Nei's genetic diversity index (H_e) were showed that 81.2% of rice landraces were higher than those of advanced cultivars, and 18.8% of landraces were same or slightly smaller than advanced cultivars. The H_e within populations of rice landraces were significantly different, ranged from 0.0146 to 0.5117, while Huangbansuo-1, Huangbansuo-2, Maxiang-1 and Maxiang-2 were the highest with 0.4214, 0.5117 and 0.4489, respectively. Compared heterozygosity within rice varieties, 87.5% of rice landraces were significantly higher than improved cultivars. AMOVA showed that 1/4 genetic difference among rice landraces were from within populations of rice landraces (P).



3096 - Plant Genetic Resources

Vera Quecini

IN VITRO ESTABLISHMENT AND CONSERVATION OF GRAPEVINE GERMPLASM

Dalbosco,D; Sinski,I; Comachio,V; Maia,JDG; Fajardo,TVF; Ritschel,PS; Quecini,V;

Embrapa Uva e Vinho;

Plant genetic resources are characterized by the presence of significant phenotypic variation, due to the occurrence of allelic diversity, maintained by evolutionary processes or by artificial selection. Thus, plant germplasm comprise the huge genotypic diversity found in wild and cultivated species, which has been used as source of traits of interest. Although extremely valuable, biodiversity conservation has high demands for funding, physical space and work-power. In vitro conservation is an interesting alternative for the conservation of highly-heterozygous, vegetatively propagated, perennial species, such as grapevine. It also helps to improve the plants phytosanitary conditions. The current work aimed to develop effective and feasible means to in vitro establishment and conservation of grapevine germplasm. Woody stakes of ~ 30 cm were obtained from the field collection of the Grapevine Germplasm Bank, at Embrapa. Stakes were surface disinfected, planted in a mixture of autoclaved soil and vermiculite (1:1), and kept under controlled temperature ($23^{\circ}\text{C} \pm 5^{\circ}\text{C}$) and relative humidity (70%). Young apical shoots (~ 10 cm) were excised and superficially disinfected in 70% (v/v) ethanol followed by immersion in 1% (v/v) bleach with 1%(w/v) polyvinylpyrrolidone. Explants were transferred to tubes with 15 mL of medium with 0.25% (w/v) active charcoal, under aseptic conditions. Established plants were propagated and maintained in vitro as duplicates. For long-term conservation, the effectiveness of two cryopreservation techniques; vitrification and encapsulation-dehydration, was compared for 11 grapevine genotypes, including *Vitis vinifera*, *V. labrusca*, *V. berlandieri* x *V. rupestris*, and *V. riparia* x *V. berlandieri* hybrids. Shoot induction from treated stakes under protected greenhouse conditions significantly reduced environmental contamination and, along with the use anti-oxidant agents, allowed in vitro establishment of approximately 1000 (80%) grapevine accessions. The establishment of the remaining accessions is underway. Plants free of ectophytes were produced for 610 (41%) accessions. Cryogenic protocols require further modifications to achieve acceptable recovery rates. High-scale in vitro conservation of grapevine germplasm is feasible and may safeguard valuable biodiversity. Although promising, cryopreservation requires further studies for protocol optimization.



Poster Session

Seed Physiology, Production & Technology



3357 - Seed Physiology, Production & Technology

Camila Fátima Carvalho

ELECTRICAL CONDUCTIVITY IN SOYBEAN SEEDS WITH DIFFERENT OSMOTIC POTENTIALS

Carvalho,CF; Coelho,CMM; Gmach,JR;

Universidade do Estado de Santa Catarina;

The degradation of cell membranes is one of the main events related to the process of deterioration, with the determination of conductivity is possible to estimate the seed vigor, however during the fast hydration seeds can be easily damaged. The study objective was to evaluate the efficiency of the electrical conductivity with different osmotic potentials targeting the more gradual conditions during the seed priming process and thus discriminate more accurately the soybean cultivars regarding the integrity of their membranes. The cultivar seeds: BMX Turbo RR, BMX 3358RR, SYN 1059RR, FUNDACEP 66RR, FUNDACEP 60RR e BMX Power RR, were subjected to two osmotic potential concentrations (0.0; -0.2 MPa) obtained from polyethylene glycol (PEG 6000). The experimental design was completely randomized in a factorial 6x2 (6 cultivars and 2 osmotic potentials), that evaluated the electrical conductivity, expressed in $\mu\text{S} \cdot \text{cm}^{-1} \cdot \text{g}^{-1}$ seed. The results were submitted to variance analysis and comparison of means by Tukey test (P). The data of electrical conductivity in water (0.0 MPa) demonstrated that the FUNDACEP 66RR cultivar presented higher conductivity ($90.1 \mu\text{S} \cdot \text{cm}^{-1} \cdot \text{g}^{-1}$), that is, less vigor due to greater exudates release and lower integrity of their membranes, and the cultivars with higher vigor were FUNDACEP 60RR ($53.0 \mu\text{S} \cdot \text{cm}^{-1} \cdot \text{g}^{-1}$) and SYN 1059RR ($54.7 \mu\text{S} \cdot \text{cm}^{-1} \cdot \text{g}^{-1}$). The conductivity at a -0.2 MPa PEG concentration also presented the FUNDACEP 66RR cultivar with less vigor ($22.6 \mu\text{S} \cdot \text{cm}^{-1} \cdot \text{g}^{-1}$) compared to the other cultivars that did not differ significantly ($P < 0.05$). The priming condition avoids damage by imbibition, limiting the cellular content leaching, allowing better performance for seed germination. The paper concludes that, in water, FUNDACEP 60RR and SYN 1059RR cultivars had the highest vigor, and FUNDACEP 66RR cultivar presented the lowest vigor, in both osmotic potential concentrations. The osmoconditioning promotes the slowest seed hydration, preventing damage by imbibition, contributed to increasing the seed vigor in relation to non osmoconditioned seeds.



3356 - Seed Physiology, Production & Technology

Camila Fátima Carvalho

TOLERANTE CULTIVARS TO WATER STRESS BY POLYETHYLENE GLYCOL

Carvalho,CF; Coelho,CMM; Delgado,CML;

Universidade do Estado de Santa Catarina;

In the quality seeds higher is essential to stablishment and development of viable seedling under adverse field conditions. This work aimed to evaluate the physiological changes of soybean seeds of different cycles and maturity groups (MG), when subjected to water stress by polyethylene glycol (PEG). The seeds of the BMX RR Turbo (GM very early 5.8), BMX 3358RR (very early GM 5.8), 1059RR SYN (early GM 5.9) FUND.66 (early GM 6.2), FUND.60RR (early GM 6.4) Power and BMX RR (early GM 6.7), were subjected to different concentrations of osmotic potential (0.0, -0.2, -0.4 and -0.6 MPa) obtained from PEG 6000. The experimental design was completely randomized in a factorial 6x4 (four cultivars and osmotic potentials). Where evaluated the percentage of germination and seedling length (SD). The results were subjected to analysis of variance and regression. In the condition without stress (0.0 MPa) cultivars showed different percentages of germination, which three cultivars germinated above 90% (BMX 3358RR, 1059RR and FUND.60RR SYN), and another three cultivars with less than 78% germination (RR Turbo BMX, BMX and Power FUND.66RR RR). The SD was high germination ranged from 17.85 cm (BMX 3358RR) to 20.9 cm (SYN 1059RR), since the cultivars with low germination had lower seedling length (11.0 to 13.0 cm). At the concentration of -0.2 MPa, cultivars BMX 3358RR, 1059RR and SYN FUND.60RR remained with germination above 80%, according to market requirements as certified seed. The SD was reduced more in cultivars that had high germination (7.0 to 7.9 cm) compared with other cultivars (6.8 to 11.5 cm) due to decreased metabolism of the seeds due to lower water availability. With use of the concentration of -0.4 MPa cultivars differed more efficiently, the BMX 3358RR had sprouted seeds (57.5%). At the concentration of -0.6 MPa damage by stress was high and prevented the process of germination for all cultivars. The conclusion is that a concentration of -0.4 MPa was more efficient to detect vigor among cultivars, with the BMX 3358RR more tolerant to water stress imposed by PEG.



3367 - Seed Physiology, Production & Technology

Cileide Maria Medeiros Coelho Arruda de Souza

COMMON BEAN LANDRACES UNDER COLD STRESS

Prezzi,HA; Coelho,CMM; Polli,RG; Heberle,I; Souza,CA;

Universidade do Estado de Santa Catarina, Centro de Ciências Agroveterinárias (UDESC-CAV);

The use of genetic variability is essential for the improvement of common bean in areas such as increased yield and tolerance to abiotic factors such as cold condition. In Santa Catarina State the seed production occur in heat conditions and growing season is delay and harvest coincidence with rainier periods. An alternative to anticipate growing season would be the use landrace common bean with genetic variability to tolerance an adverse conditions. The objective this work was to evaluate to landrace cultivars of beans and to indicate the most tolerant to the cold condition. Ten beans accesses previously characterized as promising for production in the Campos Novos, SC, Brazil, the BAFs: 102, 112, 121, 13, 42, 46, 55, 57, 75 and 84 were evaluated. Each sample was composited by eight repetitions with 50 seeds each. The experimental design was in completely randomly, and germination test was germitest paper. Four replications were submitted it for cold in BOD to 10°C during three days and after this remained in camera germinate during 5 days (25°C). The others four replications were submitted directly to the temperature at 25°C during five days. The percentage of germination was evaluated, considerate normal seedling, abnormal seedling and die seed. The dates were submitted variance analysis and main between genotypes was compared Tukey test ($P>0.05$). The diversity genetic was observed in both treatments, with or without cold stresses. The genotypes with better adaptation in cold treatment were BAFs 75 and 42, with seedling normal percentage of 89 and 85%, and while germination was typically decreased in 7 and 3% respectively in both genotypes in relation the condition without stresses. Considering that the viability of 80% will be higher seed vigor, the BAFs: 42, 13 and 55 were promisor too. In conclusion, observed genetic diversity to cold stress and accesses 75 and 42 showed higher seed vigor and stability of yield under adverse conditions.



3398 - Seed Physiology, Production & Technology

Clovis Arruda de Souza

EFFECT OF PLANT SENESCENCE INDUCTORS ON ELECTRICAL CONDUCTIVITY OF COMMON BEAN SEEDS

Ataide,RCN; Souza,CA; Correa,C; Sponchiado,JC; Cechinel,MH; Werner,F; Zanesco,PR;

Santa Catarina State University (UDESC);

The objective of this work was to evaluate the effect of plant senescence inductors applied at plant physiologic maturity on common bean seed vigor. The seeds were produced at field conditions in research area of UDESC, Lages-SC under a completely randomized design with three replications and an useful area of 10.5m² per plots. The genotypes used were BRS-Campeiro, IPR-Uirapurú, Pérola, SCS-Guará, IPR-Tangará, BAF13, BAF50 and BAF55. When 50% of pods reach physiological maturity, the plants were treated with flumioxazin (30 g a.i. ha⁻¹), paraquat (400 g a.i. ha⁻¹), ethephon (120 g a.i. ha⁻¹) and prohexadione-Ca (55g a.i. ha⁻¹). The electrical conductivity test was conducted in seed laboratory from UDESC, Lages-SC, following the Brazilian Rules for Seeds Testing, under randomized block design with four replications of 50 seeds, physically pure. The 50 seeds were weighed and exposed to 75 ml distilled water and maintained into BOD (Biochemical Oxygen Demand) at 25 °C by 24 hours, after this time the EC was measured. The data were submitted to analysis of variance and the means compared by Tukey test (P). The electrical conductivity test grouped the genotypes into three groups: IPR-Uirapurú (first group; higher EC); Pérola, BRS-Campeiro, BAF55 and BAF13 (2nd group); IPR-Tangará and BAF50 (third group; lower EC), considering only isolated effects of maturing substances. For the genotypes BRS-Campeiro, BAF50, BAF55 and IPR-Uirapurú did not observed effects different products on the seeds EC. The genotypes with differential response to the maturing substances were: Pérola, SCS-Guará, BAF13 and IPR-Tangará. The prohexadione-Ca and ethephon reduced the EC for Pérola and SCS-Guará. On BAF13, the flumioxazin decreased EC and paraquat provided slight increase of EC. In IPR-Tangará flumioxazin and ethephon decrease EC. These results indicate that the application plant senescence inductors (prohexadione-Ca, ethephon and flumioxazine) in common bean plants positively affected seed vigor, however the reaction was differential according to genotype.



3708 - Seed Physiology, Production & Technology

Estela Reis de Andrade

COMPARATIVE ANALYSIS OF RESISTANCE TO MECHANICAL DAMAGE IN SOYBEANS WITH DIFFERENT COLORS OF TEGUMENT

Andrade,ER; Fagioli,M; Pereira,EA;

Universidade de Brasília;

The seed is a vehicle for transmission of technology and a genetic gain resulting from a breeding program. The soybean seed consists of three parts: embryo, cotyledons and seed coat. The coat has a role similar to coverage and acts as a modulator of the interactions between inside of the seed and the external environment, also to protect vital parts. There, the lignin content is important because provides resistance to mechanical damage also maintain the integrity of the cell walls. Thus, there has been particular attention in breeding programs for lignin content in the coat in order to indirect improves of physical and physiological quality. However, to achieve an improvement program is necessary that genotypes with the desired characteristic and which are donors of the gene of interest. The objective of this study was to evaluate the lineage of black soybean UnB 1125 for resistance to mechanical damage compared with six yellow commercial cultivars. The experiment was conducted at the Seed Analysis Laboratory of the Universidade de Brasília. The UnB 1125 was analyzed in comparison with the commercial cultivars, produced and harvested under the same conditions: P98Y51, P98N71, P98C81, Anhanguera, Conquista and TMG 801. The seeds were submitted to the pendulum test, with a kinetic energy of 0.267 joules and then classified into three categories of visual damage (I - seeds without any apparent damage; II - seeds with slight damage in the tegument and III - seeds with severe damage). The completely randomized design with four replications was adopted. The means were analyzed by Tukey test.



3352 - Seed Physiology, Production & Technology

Fábio Andrade Padilha

Comparison of germination of Seeds of Sorghum bicolor in different locations of Multiplication in Minas Gerais

Padilha,FA; Magalhães,KS; Netto,DAM;

UFSJ/Embrapa Maize and Sorghum;

Sorghum [*Sorghum bicolor* (L.) Moench] is a plant originally from Africa that has been considered an important crop, due to its use for food and feed. This crop has high protein, starch and nutrient content. It grows well in tropical climates, and tolerates drought as well as saline and waterlogged stresses. The present study aimed to determine the best location to multiply sorghum seeds. We analyzed the germination of 50 sorghum genotypes seeds which were chosen randomly from the Active Germplasm Bank (BAG) of Embrapa Maize and Sorghum. These genotypes were multiplied in two experimental areas, Sete Lagoas and Janaúba, MG and their seeds were stored for periods ranging from 25 to 29 years. The seeds were kept at 10°C and relative humidity of 30%. After this period of time, we performed a viability test with four replications of 50 seeds in a completely randomized design. A seed physiological analysis was performed in soaked paper rolls that were kept for seven days in a germination chamber with temperatures of 20-30 ° C. We used the softwares Bioestart and R to perform comparison of means by Student's t test (p Supported by Embrapa, CNPq, Fapemig.



3366 - Seed Physiology, Production & Technology

Flávia Regina Palhares Gonfio

GROWTH REGULATORS AND PHYSIOLOGICAL QUALITY OF CRAMBE SEEDS

Gonfio,FRP; Toledo,MZ; Zucareli,V;

Universidade Estadual de Maringá;

Crambe (*Crambe abyssinica* Hoechst) is an important crop to be included in programs to produce biodiesel. However, few studies have been conducted on production of high quality seeds. This species is known to produce dormant seeds, once it is not still part of any breeding programs. Therefore, one way to improve seed quality is to use growth regulators to enhance germination and seedling development. This study had as objective to evaluate the effects of increasing doses of growth regulators on physiological quality of crambe seeds. The experimental design was the completely randomized with five replications. Treatments consisted of soaking crambe seeds for five hours into solutions of gibberellin (GA) and gibberellin+cytokinin (GA4+7+CK) at doses 0, 50, 100, 200 and 400 mL L⁻¹. After this period, seeds were evaluated by germination, viability and vigor tests. Data was submitted to variance analysis. Growth regulators were compared by the Tukey test (p<0.05) and doses by regression analysis. Splitting was carried out whenever significant interaction was found and equations with higher significant determination coefficient were applied. According to the results, speed of germination and shoot length were influenced isolately by growth regulator doses. speed of germination was linearly increased by higher doses. On the other hand, shoot length was higher up to the dose of 200 mL L⁻¹, followed by an accentuated decrease. Seedling dry matter significantly varied depending on the regulator applied; higher value was observed for GA4+7+CK. All other evaluations showed positive interaction between products and doses. Possibly due to high initial quality of crambe seeds, GA doses did not influence germination. Nevertheless, higher doses of GA4+7+CK increased the number of abnormal seedling, consequently reducing germination percentage and first count. In general, doses higher than 200 mL L⁻¹ accentuate differences between both regulators. The application of increasing doses of GA and GA4+7+CK reduced speed of germination-index; this behavior was also observed in root length and seedling total length after GA4+7+CK application. Positive effects of GA were found as root development was increased in higher doses. In conclusion, GA application did not significantly affect seed quality, but increased root development in seedlings. Increasing doses of GA4+7+CK were detrimental to seed germination and seedling growth.



3364 - Seed Physiology, Production & Technology

Flávia Regina Palhares Gonfio

PHYSIOLOGICAL QUALITY OF SAFFLOWER AND CRAMBE SEEDS TREATED WITH BIOSTIMULANT

Gonfio,FRP; Zucareli,V; Toledo,MZ;

Universidade Estadual de Maringá;

Studying sources to replace non-renewable sources of fuel has been currently a priority in many countries. Species such as safflower (*Carthamus tinctorius* L.) and crambe (*Crambe abyssinica* Hoechst) consist of a potential alternative for biodiesel production. However, there are still obstacles in producing high quality seeds to supply the demand that is already increasing. Safflower and crambe seeds are known to show primary dormancy, naturally overcome during storage. Another alternative is the use of biostimulants to enhance seed germination and seedling development. This study aimed to evaluate the effects biostimulant doses on physiological quality of safflower and crambe seeds. The experimental design was the completely randomized, with five replications. Biostimulant (cytokinin+indolbutiric acid+gibberellic acid) was applied on safflower and crambe seeds at doses 0, 50, 100, 200 and 400 mL 100 kg⁻¹ of seeds. After treatment, seed quality was assessed by germination, viability and vigor tests. Data was submitted to variance analysis. Species were compared by the Tukey test (p<0.05) and doses by regression analysis. Isolate effects of biostimulant doses on seed germination and viability were found for both species, with higher percentages observed for the 200-mL dose. It was noticeable the difference between the two crops as for initial quality; crambe seeds showed higher germination whereas development of safflower seedlings were significantly higher. Germination first count and percentage of abnormal seedlings were influenced by the interaction between species and biostimulant doses. Quality of crambe seeds was not affected by doses; conversely, quality of safflower seeds was increased by biostimulant doses up to 100 mL, followed by gradual reduction. Safflower root length and seedling dry matter did not vary with increasing doses; however, development of crambe seeds was reduced with higher doses inferring possible toxic effects of biostimulant on seedling growth. According to the results, it can be concluded that germination and viability of safflower and crambe seeds are enhanced by the application of 200 mL of biostimulant cytokinin+indolbutiric acid+gibberellic acid. Safflower seed vigor, evaluated by the first count test, is improved by the application of 100 mL of biostimulant as a consequent of decreased abnormalities in seedlings. Negative effects of biostimulant doses are noticed on crambe root development and seedling dry matter.



3273 - Seed Physiology, Production & Technology

Janice Regina Gmach Bortoli

NITROGEN FERTILIZATION AND SEED PHYSIOLOGICAL QUALITY OF WHEAT

Pereira,T; Coelho,CMM; Gmach,JR; Drum,G; Carvalho,CF; Souza,CA;

UNOESC;

The current study aimed to evaluate the influence of nitrogen on the physiological quality of wheat seeds. The experiment was conducted in 2010/11 season, in Campos Novos, SC, with BRS 220. The experimental design was randomized blocks with four replications, with applications at tillering and booting stages, respectively, with the following doses: T1 - 0 kg ha⁻¹ N (nitrogen), T2 - 33.75 kg N ha⁻¹ and 0 kg ha⁻¹, T3 - 67.5 kg ha⁻¹ N and 0 kg N ha⁻¹, T4 - 135 kg N ha⁻¹ and 0 kg N ha⁻¹, T5 - 67.5 kg ha⁻¹ N and 67.5 kg N ha⁻¹, T6 - 33.75 kg N ha⁻¹ and 33.75 kg N ha⁻¹, and urea as N source. After harvest, the moisture was standardized to 12%, an average sample of 700 g was obtained, which provided the research's sample for the realization of the following tests: total protein content (%), electrical conductivity (mS cm⁻¹.g⁻¹) and percentage of germination. The results were submitted to variance analysis and comparison of means by Tukey test (5%). The protein concentration ranged from 11.2% (T1) to 14.7% (T5), and the concentration's highest level was in T5, which indicates that the split application of nitrogen associated with higher N favored the increase of the total protein concentration in the seeds. The electrical conductivity was used as a test of strength, leading to the observation of a high leakage of solutes in the control (20 mS cm⁻¹.g⁻¹) with significant difference compared to T3. The germination ranged from 87% (T4 and T6) to 95% (T3), indicating that there was no difference in the number of normal seedlings in accordance with the treatments. Treatment 3 showed the highest percentage of germination and differed significantly from other treatments. From the results, it is possible to conclude that treatment 3 showed the highest germination and seed vigor, indicating that for BRS 220 the 67.5 kg N ha⁻¹ dose at the tillering was the one that provided the best quality seeds.



3384 - Seed Physiology, Production & Technology

Juliana de Souza Dode

Isozyme expression in sunflower seedlings under water stress

Dode,J; Chim,JF; Chaves,FC; Nora,L;

UFPEl;

Highly negative soil water potential leads to reduction in water uptake by the seeds, which may affect germination process. On the other hand osmotic conditioning can potentially speed up and regulate germination and emergence of seedlings of many plant species. Polyethylene glycol 6000 (PEG 6000) can be used in osmotic conditioning by reproducing a water potential reduction without being absorbed by the seeds. This study focused on investigating changes in the expression pattern of isozymes, acidic phosphatase, esterase, malate dehydrogenase, glutamate oxaloacetate transaminase and sorbitol dehydrogenase, in sunflower (*Helianthus annuus*) seedlings under different water stress conditions. Isozyme selection was based on previous knowledge of their involvement in stress responses and tissue specific expression. Sunflower seeds of cultivars MG2 and Agrobol were placed in Germitest[®] paper rolls soaked in PEG 6000 solutions representing the following water potentials: -0.1; -0.3; -0.5; -0.7 MPa. Seed germination was evaluated according to the seed analysis guidelines from the Brazilian Ministry of Agriculture. Five days after sowing, roots and green tissues were sampled for analyses. The lower the potential the strongest the effect on germination and emergence such that at -0.7 MPa seeds did not germinate. Isozyme expression was evaluated by gel electrophoresis and band intensity of all isozymes tested was highly correlated with stress intensity.



3142 - Seed Physiology, Production & Technology

Mariana Zampar Toledo

MINIMIZING PRE-HARVEST DESICCATION EFFECTS ON SOYBEAN SEED QUALITY WITH BIOESTIMULANTS AND MICRONUTRIENTS

Toledo,MZ; Cavariani,C; Bennett,MA; Françaneto,JB;

Universidade Estadual de Maringá - CAU/UEM;

In soybean, the physiological maturity stage is characterized for higher accumulation of dry matter in seeds with consequent improvement in germination and vigor. As moisture content in this period is still not compatible with mechanical harvest, the application of desiccants in R7 stage has become a routine practice. Seed producers have applied glyphosate in conventional soybean fields not being aware of phytotoxic effects that may decrease seed quality. This study aimed to evaluate soybean germination and seedling development affected by pre-harvest desiccation with glyphosate and later treatment of seeds with biostimulants and micronutrients. The experimental design was the completely randomized, with four replications. Seeds produced with and without desiccation with glyphosate (2 L ha⁻¹) at R7 stage were harvested and immediately treated with micronutrients (Co+Mo; Co+Mo+B+Zn) and a biostimulant (cytokinin + indolebutyric acid + gibberellins). Physiological quality was evaluated by tests of germination, seedling length and seedling dry matter. Also, an automated system for seedling evaluation (SVIS®) was applied to determine seedling growth, uniformity and then establish vigor index. Data was submitted to variance analysis and means were compared by the Tukey test (p<0.05), being analyzed as a 3x2 factorial. Pre-harvest desiccation with glyphosate reduced seed germination both in the first and second counts; nevertheless, negative effects were minimized by the application of micronutrient Co+Mo as the number of abnormal seedlings decreased. Additionally to plant desiccation reducing seedling length and dry matter, the application of Co+Mo and biostimulant to seeds even accentuated negative effects. Image analysis was not efficient to identify differences in seedling development parameters caused by pre-harvest desiccation with glyphosate; however, decreased vigor index was observed due to the application of Co+Mo and biostimulant reducing uniformity and growth, respectively. Desiccation of soybean plants with glyphosate decreases seed germination and seedling development; negative effects on germination can be minimized by the application of micronutrients Co+Mo, but this can accentuate phytotoxicity in seedling development.



2873 - Seed Physiology, Production & Technology

Mateus Olivo

SEEDLING RESPONSE OF RICE PADDY BRAZILIAN CULTIVARS TO IRON PRESENCE

Olivo,M; Kavalco,SAF; Baretta,D; Groli,EL; Santos,RL; Magalhães-Junior,AM; Oliveira,AC; Maia,LC;

Federal University of Pelotas;

Iron (Fe) is a necessary element for all live cells. However, in cultivated rice paddy at flooded soils it can cause a problem, called iron toxicity. It is a major problem in lowland environment worldwide. This occurs associated with large concentrations of reduced iron (Fe^{+2}), in the soil solution. The objective of this work is known the effect of iron on the seedling root length of Brazilian rice paddy cultivars. The experiment was conducted at the Teaching Laboratory Analysis of Seeds -FAEM/UFPEL, Pelotas city, Brazil. It was used eight Brazilian cultivars: BRS Querência; BRS Pampa; BR-IRGA 414; BRS 6 Chui; BRS Sinuelo CL; BR-IRGA 410; BRS Pelota; BRS 7 Taim. Four replication of 200 seeds were placed on "germitest" paper with ferrous solution in five level of Fe^{+2} presences. The levels were: 0.0 (control), 20.14, 100.72, 200.14, 302.17 mg.L^{-1} . The ferrous solution was prepared by dissolving ferrous sulfate heptahydrate ($\text{FeSO}_4 \cdot 7\text{H}_2\text{O}$), in distilled water. The pH values in all solution, was adjusted to 4.5. The "germitest" paper was wetted with ferrous solution using 2.5 times paper weight and placed into germinator at 25°C. After 14 days all the normal seedlings were measured using ruler and the results were obtained in centimeter. The data analysis was conducted using computational program Genes, the experimental design was randomized complete block. Analyzing the result of root length using regression curve tendency, was possible observer 2 main different behavior when in Fe^{+2} , presence. Six of eight cultivars: BR-IRGA 414; BRS 6 Chui; BRS Sinuelo CL; BR-IRGA 410; BRS Pelota; BRS 7 Taim showed decrease of root length for all level presence in respect of the control. The others two cultivars: BRS Querência; BRS Pampa showed their best result for root length, when there are Fe^{+2} , at ferrous solution, having theirs best result in level of Fe^{+2} , 76,5 and 64,14 mg.L^{-1} respectively. At 302.17 mg.L^{-1} of Fe^{+2} in the ferrous solution, all eight cultivars, has showed decrease in root length, greater than 55% in respect of control dosage. Taking as a reference of these results of this work we can conclude: (1) Low dosage of Fe^{+2} , can help root elongation on seedling of rice paddy; (2) Brazilian rice paddy, cultivars have a different behavior when in Fe^{+2} , presence and a different tolerant limit.



3701 - Seed Physiology, Production & Technology

Patricia de Jesus dos Santos

THE INFLUENCE OF SPACING IN LINES AND OF COVERAGE NITROGEN FERTILIZATION IN PHYSIOLOGICAL QUALITY OF CORN SEEDS

Santos,PJ; Andrade,ER; Sandim,MS; Fagioli,M;

Universidade de Brasília;

The level of technology used in a crop will depend on the genotype, plant population, fertilizer base, the spacing between rows of weed control, the top dressing with nitrogen and micronutrients, irrigation, pest control and diseases chosen. The narrow row spacing and the splitting of nitrogen have been target of several studies for several years, contradictory results are found, however, most reports confirmed the feasibility of such practices in significant gain better yields. Furthermore, results from the influence of spacing and fertilization on seed quality are few and inconsistent, requiring more research. This report has as a purpose evaluating the influence of spacing in lines and of coverage nitrogen fertilization, into different moments (split or not), in physiological quality of corn seeds. The experiment was conducted in an irrigated area of the Ituiutaba Educational Foundation Experimental Farm, Campus of the Minas Gerais University, in Ituiutaba country and the laboratory evaluations were realized in the Seeds Technology and Analysis Laboratory. The following treatments were developed: spectator (interpretation); coverage nitrogen fertilization with one portion; coverage nitrogen fertilization with two portions; coverage nitrogen fertilization with three portions; into in line spacing of 0,50 and 0,80 m. Among the quality evaluations of the seeds the paper and sand germination tests were fulfilled for the vigor and weight of green material, seedling length, cold test and electric conductivity and the emergency of the seedling in the ground. For the emergency and laboratory analysis of seedlings in ground the entirely randomized delimitation was used, being the averages compared by the Tukey test, in a 5% probability test. By the interpretation of the results there was concluded that the reduction of the in line spacing and the interpretation, split or not, have produced different answers in the physiological quality of the corn seeds. The feasibility tests (germination), of vigor and the emergency of ground seedling were inconstant in the results for the corn seeds evaluation.



3220 - Seed Physiology, Production & Technology

Renata Juliana Ahlert

PERFORMANCE OF IRRIGATED RICE CULTIVARS IN RESPONSE TO IRON TOXICITY IN HYDROPONIC CULTURE

Ahlert,RJ; Mesquita,R; Muller,C; Santos,FIC; Almeida,AM; Maia,LC; Oliveira,AC;

Federal University of Pelotas;

Iron is an essential element for development of rice crop and necessary for essential plant functions. However, under irrigated cultivation conditions, low redox potential leads to reduction of iron in the soil solution which is readily available and can become toxic to plants if absorbed in excess. In rice production areas of Rio Grande do Sul, iron has caused problems of toxicity and tolerant cultivars becomes an important strategy to solve this problem. However, it is necessary to understand the tolerance mechanisms for application in breeding programs. This way, the means of this study was evaluate the performance of irrigated rice cultivars in response to iron toxicity in hydroponic culture. Four rice cultivars were used in this study, previously characterized for iron toxicity: BR-IRGA 409, BR-IRGA 410, IRGA 417 as sensitive and Epagri 107 as iron toxicity tolerant, which were subjected to treatment with 7mM FeSO₄EDTA. For roots and shoots were analyzed: dry weight, length, total of the micronutrients Fe, Zn, Mn and Cu, determined by atomic absorption; Thiobarbituric acid test was used to measure lipid peroxidation. Also, Fe(III) EDTA reduction by roots was measured by using bathophenanthrolinedisulphonate reagent. For shoot, iron treatment was significant for micronutrients, with a reduction of Mn, Zn and Cu and increased of Fe under stress. An interesting point was the high Mn content in the control of Epagri 107 shoot, characterized as tolerant, which showed no significant iron accumulation in roots and no significant reduction in root dry weight. Roots subjected to iron stress, showed a decrease in dry weight, reduction in Mn concentration and increase in Fe content. An increased on the degree of lipid peroxidation in leaves of cultivars subjected to stress, showed the presence of oxidative damage. In roots, only IRGA 417 showed no significant oxidative damage. Higher Fe(III)-EDTA reductase activity of roots was observed for Epagri 107 and IRGA 417 cultivars. Iron content in roots allowed to differentiate tolerant cultivar from others and high content of Mn in shoots may be related to this tolerance. The dry weight of roots also allowed discrimination of tolerant cultivar. The degree of lipid peroxidation and Fe (III)-EDTA reductase activity showed variation with iron stress and did not differentiate tolerant cultivar Epagri 107, but showed that IRGA 417 cultivar can present mechanisms of tolerance to oxidative stress in roots.



2874 - Seed Physiology, Production & Technology

Sabine Gruber

AN ARTIFICIAL SOIL CRUST TO ASSESS SEEDLING EMERGENCE UNDER SOIL EROSION

Gruber,S; Buehler,A; Claupein,W;

University of Hohenheim;

Soils exposed to heavy rainfall can form a crust at the surface so that proper and fast seedling emergence through the crust is inhibited. Aim of the study was to create artificial soil crusts with a standardised and uniform appearance for a simple test of seeds to emerge under conditions of a sealed soil. Liquid clay (LC), gelatine and wax were tested in a preliminary test for their general suitability as an artificial soil crust. The materials were applied in different thicknesses to pots sown with wheat (*Triticum aestivum*) in a greenhouse, and their performance was quantitatively assessed in terms of handling, penetration resistance and seedling emergence. LC turned out to be the most suitable material and thus it was used in the following main experiment. Winter wheat (TKM 47.0, 92% germinability) and oilseed rape (*Brassica napus*, TKM 4.4, 96% germinability) were sown in pots (100 seeds per pot) with standard soil substrate in a greenhouse and covered with soil and then with LC in thicknesses of 0, 5, 10 and 15mm. The difference to 20mm (target sowing depth) was added by the soil substrate so that the seeds were always located 20mm below the soil surface. The pots were arranged in a fully randomised block design with three replicates. Seedling emergence was counted over 14 days. Only LC spread out uniformly over the soil substrate, and affected seedling emergence least among all tested. All treatments showed shrinking cracks similar to those under field conditions. The total emergence rate was highest in the control and accounted for 92% for both wheat and oilseed rape. A crust of 5 or 10mm thickness resulted in emergence rates of 44-49 % (oilseed rape) and 32-80 % (wheat), and a crust of 15mm gave rise to 12% (oilseed rape) and 17% (wheat) emergence. Oilseed rape seedlings were not strong enough to penetrate a 15mm crust and only emerged in shrinkage cracks here. After removal of the soil crust at the end of the experiment, fatally germinated, deteriorated seedlings were found, which had not been able to penetrate the crust. An artificial soil crust made of LC is a simple and fast method to assess the vigour of seeds with different kernel mass to simulate erosive conditions. The results should be correlated with field data and actual penetration resistance of specific soils to predict seedling emergence.



3263 - Seed Physiology, Production & Technology

Sydney Antonio Frehner Kavalco

EFFECT OF DROUGHT STRESS IN DIFFERENT WHEAT CULTIVARS IN THE UPPER PARANAÍBA REGION

Desordi,R; Ribeiro,MDN; Kavalco,SAF; Pazza,R; Kavalco,KF;

Laboratório de Genética Ecológica e Evolutiva, Universidade Federal de Viçosa - Campus de Rio Paranaíba, MG.;

The wheat production in Minas Gerais - MG provides only 10% of the consumed in the state. A major problem faced by the state wheat farmers refers to water deficit, and this is a consequence of a continuous or transient period of drought, which causes reduction in plant development. The present study sought to identify the effect of water deficit on plant growth and yield of wheat in Minas Gerais, under dryland and irrigated farming. The experiment was conducted in a greenhouse in Rio Paranaíba - MG, in a randomized block design with three replicates for normal crop cultivation under irrigated and water restriction. Forty wheat cultivars were tested, 8 recommended for Minas Gerais and 32 for the Southern Brazil. The seeds were sown in plastic pots being conducted five plants per pot. Irrigation in both experiments was the same until the 60th day after emergence, and then stopped in water restricted experiment until 72th day. The analyzed characters were: days from emergence to flowering (DEF) days from flowering to maturity (DFM), the total development cycle (CYCLE), number of fertile tillers (NAF), number of grains per ear (NGE), weight of grains of the ears (PGE) and thousand grain weight (MMG). The data were subjected to analysis of variance of "t" test and the analysis of averages by the model of Tukey at 5% of significance with the GENES software (Cruz, 2006). The results indicated statistically significant differences between the two environments. Four cultivars were reduced, and two showed a significant increase for the character DEF on the environment with stress, the rest did not differ between environments. This result indicates that this feature was not much influenced by stress. All cultivars subjected to water stress had a significant decrease in character DFM and consequently in CYCLE. The characters NAF, NGE, PGE and MMG were significantly influenced by stress, showing lower average in the environment with stress to some cultivars. It is evident that the cultivation of irrigated wheat in the region of Alto Paranaíba - Minas Gerais, significantly affects the development of some cultivars and consequently their productivity, since this crop is subject to water stress conditions. The drought stress reduces the development cycle and yield of wheat, directly affecting the grain yield components (NAF, PGE and NGE).



Workshops



Progress in breeding for submergence tolerance in rice

Abdelbagi M. Ismail¹, Endang Septiningsih¹, Bertrand Collard¹, Uma S. Singh¹, and David J. Mackill²

¹International Rice Research Institute (IRRI); DAPO 7777, Metro Manila, Philippines

²MARS Food Global, University of California, Davis, California, USA.

Flooding is a major abiotic constraint for rice production in vast areas of rainfed and flood-prone lowlands in the tropics. The hydrological conditions of these areas are unpredictable, leading to low and unstable productivity, with ensuing incidences of food shortages and high poverty. Flooding at any stage can severely damage the rice crop because modern varieties are extremely sensitive. Early floods can lead to poor crop establishment, and transient complete submergence during vegetative stage causes high mortality. Even partial floods can be devastating if they persist for longer duration, as in stagnant floods and deepwater areas; where only local landraces are currently being grown but have low yields. Recent advances in genomics have provided faster approaches to develop varieties adapted to unfavorable areas such as those affected by excess water. Transient submergence for 1 to 2 weeks regularly affects over 20 million ha of rice producing areas in Asia. The discovery of the *SUB1* QTL and cloning of the *SUB1A* gene as the main contributor for tolerance have facilitated the transfer of tolerance into high-yielding varieties using marker assisted backcrossing, and their subsequent deployment to farmers. *SUB1* confers tolerance of complete submergence for 4 to 20 days, with no undesirable consequences, and is effective at almost all growth stages, from a week after seeding until just before heading. Its effectiveness was validated in farmers' fields with yield advantages of 1 to over 3 t.ha⁻¹, depending on the submergence duration and floodwater conditions, but with similar yield in absence of submergence. Eight *Sub1* varieties were recently developed in the background of varieties that are popular in Asia. Five of them were officially commercialized in several countries, and the remaining lines are under advanced stage of evaluation. Moreover, additional varieties are being introgressed with the *SUB1* gene in several countries in partnership between IRRI and local programs. Efforts are also ongoing to enhance the level of tolerance beyond that conferred by *SUB1*. Significant progress has been made in developing varieties that can tolerate anaerobic conditions during germination, an important trait for direct seeding systems. This system is receiving increasing interests in recent years over the transplanted system. Traits associated with tolerance were studied and major QTLs were identified and are being fine-mapped for gene cloning and for use in breeding. Rice accessions and breeding lines with reasonable tolerance of stagnant floods were recently identified; some of them also carry the *SUB1* gene. Developing varieties that tolerate complete flooding during germination and vegetative stage as well as yield well under partial long-term stagnant floods will have considerable impacts on increasing and stabilizing rice production in rainfed and flood-prone rice areas.



Maize Breeding in Brazil – Advances and Future Perspectives

Ademir Luiz Capelaro;

R&D Infrastructure Leader, Syngenta, Rodovia BR 452, km 142, Caixa Postal 585, CEP 38400-974, Uberlândia, MG, Brasil. E-mail: ademir.capelaro@syngenta.com

Corn breeding in Brazil can be considered as a successful story. The introduction of hybrid started in the 50s, when the first double hybrids were released. Thereafter there was a very fast development and every year the farmers had access to new hybrids more productive and better adapted to Brazilian conditions. With the introduction of the first single crosses hybrids there was a change of level of productivity and response of the technology addition. This combination of hybrids with better yield potential, increase in the level of applied technology, and better management of crops raised the productivity steadily reaching levels above 10 tons/ha. Currently, farmers who use a higher technological level have reached yields around 12 tons/ha. It should be noted that this is not the reality of all corn production in the country, where the average national productivity, despite of all technology available, remains at levels below 4 tons/ha. The advent of biotechnology, with the introduction of the first events to control lepidopteron insects brought an important contribution to increasing productivity, since the crops now have protection against these insects from the beginning, reducing the initial losses. All work and development done so far can undoubtedly be considered as very successful, but there are still major challenges that must be considered for the next years. Challenge concerning gain sanity still without a definitive solution and is also necessary to move significantly concerning the complex of leaf diseases, which has grown in importance in recent years. Regarding GMOs, remains the importance of continuing the development of new events that increase tolerance to insects and also weeds, keeping the progress made so far. But new challenges, especially regarding the optimization of water use and better use of fertilizer, especially N, are mandatory to guarantee that the crop yield potential can be reached. Another key factor is concerning the field crop management. Notwithstanding the progress, it is still necessary to still improving cultivation techniques and treatment of the crops and to develop cultivars that allow a better use of available areas and increase the productivity. Furthermore, it is noteworthy that the point of view of the farmer, plant breeding is just part of the solution. All the underlying technologies have an important role in the success of the farmer and also in the breeding process. The use of fungicides for example, has allowed breeders to devote further efforts to obtain hybrids with more productivity potential, considering the use of fungicides as part of the solution in controlling diseases. Finally, another challenge will undoubtedly be finding a way that all this available technology be transferred to part of the farmers who still have no access because of different reasons. It will be necessary to create programs that can allow access to this technology and ensure that all benefits can be incorporated. No doubt the effects will be fast and very significant, making the average corn productivity in Brazil to grow substantially and moves away from current levels, which are much below the potential this crop has.



Transcriptome analysis of genetic and environmental factors controlling sugarcane root development.

Thais L.G. Carvalho¹; A. Carolina J.S. Bomfim¹; Livia Vargas¹, Lucas Almendra¹, Vanessa Yurif¹, Renato Vicentini², J. Ivo Baldani³; Paulo C. G. Ferreira¹, Adriana S.Hemerly¹. hemerly@bioqmed.ufrj.br

¹Laboratório de Biologia Molecular de Plantas, Instituto de Bioquímica Médica, Centro de Ciências da Saúde, UFRJ, Rio de Janeiro, RJ, Brazil;

²Centro de Biologia Molecular e Engenharia Genética, Universidade Estadual de Campinas, Campinas, SP, Brazil,

³Embrapa Agrobiologia, Seropédica, RJ, Brazil.

Plant growth is achieved basically by events of cell division, followed by cell expansion and differentiation, therefore a potential strategy to increase productivity and biomass could be the manipulation of regulatory networks controlling cell proliferation. Since plants adopt a modular and indeterminate construction of the body by self-perpetuating meristems, plant growth and development can be shaped by environmental signals, including biotic factors such as beneficial microorganisms. The associations that occur between nitrogen-fixing endophytic bacteria and important crops such as sugarcane, rice and maize have raised a large interest in their use in agriculture, in the view that several studies have demonstrated the positive effects of inoculation of these bacteria on the promotion of root development and increase in total plant biomass. Remarkably, different diazotrophic bacteria differentially modulate the final root architecture by promotion of lateral root formation. It is well known that the success of the association depends not only on the selection of best bacterial strains, but it is also under control of the plant genotype and it is especially affected by the environment where the association is established. Our group has been studying the molecular mechanisms involved in the establishment of this particular type of endophytic interaction. Plant gene expression profiling during association with diazotrophic endophytic bacteria have confirmed the involvement of plant genes in the association. Next generation sequencing technologies are currently being applied to compare expression profile of regulatory networks controlling root development in different sugarcane genotypes and in response to environment. All together, the data suggest that (i) some plant regulatory networks are actively involved in the association with the endophytic diazotrophic bacteria; (ii) the modulated plant gene expression during association is not a general stress response against microorganisms, but seems to be specific for beneficial associations and to be controlled by the plant genotype; (iii) environmental conditions control regulatory networks that are important during the establishment of the beneficial association.

This work was supported by INCT, CNPq, FAPERJ & CAPES.



Development of high-iron rice to improve global health

Alexander A. T. Johnson^{1,2,*}, Bianca Kyriacou^{2,3}, Damien L. Callahan¹, James Stangoulis³, Enzo Lombi⁴ and Mark Tester²

¹School of Botany, The University of Melbourne, Victoria 3010, Australia;

²Australian Centre for Plant Functional Genomics, University of Adelaide, PMB1, Glen Osmond, South Australia 5064, Australia;

³School of Biological Sciences, Flinders University of South Australia, GPO Box 2100, South Australia 5001, Australia;

⁴Centre for Environmental Risk Assessment and Remediation, University of South Australia, Building X, Mawson Lakes Campus, Mawson Lakes, South Australia 5095, Australia

Rice has the lowest iron (Fe) concentration of the cultivated cereals crops and billions of people in rice-based areas of the world suffer from iron deficiency. To generate biofortified rice lines with increased concentrations of Fe, the three rice nicotianamine synthase (NAS) genes – OsNAS1, OsNAS2, and OsNAS3 – were constitutively overexpressed using the 35S cauliflower mosaic promoter¹. Elemental analysis of transgenic plants by inductively coupled plasma optical emission spectroscopy (ICP-OES) indicated that both iron and zinc (Zn) concentrations were significantly increased in unpolished and polished grain of all three of the 35S::OsNAS populations, relative to controls, and highest in the 35S::OsNAS2 population. Concentrations of nicotianamine and the phytosiderophore deoxymugineic acid were increased in transgenic grain and positively correlated with Fe and Zn concentrations, providing evidence that both of these chelators are responsible for loading of Fe and Zn into grain of the transgenic rice. Studies of elemental distribution using synchrotron X-ray fluorescence spectroscopy demonstrated significant enrichment of Fe and Zn in aleurone, subaleurone and endosperm layers of the transgenic rice grain. Enriched Fe and Zn concentrations in the endosperm tissue were not associated with phytate and are therefore likely to be bioavailable in a human diet. In addition to continued molecular characterization of the 35S::OsNAS rice, we have initiated backcrossing experiments to introduce the high Fe trait into both Indica and Japonica varieties of rice.

¹Johnson AAT, Kyriacou B, Callahan DL, Carruthers L, Stangoulis J, Lombi E, Tester M (2011) Constitutive overexpression of the OsNAS gene family reveals single-gene strategies for effective iron- and zinc-biofortification of rice endosperm. PLoS ONE 6, e24476.



Transgenic Technologies for Eucalyptus

Ana Gabriela M. C. Bassa, MSc, Maud Hinchee, Ph.D., William Rottmann, Ph.D., Brian Kwan, Michael Cunningham, Ph.D., Marina Kalyaeva, PhD.

ArborGen, Ridgeville, South Carolina, USA.

ArborGen, Campinas, São Paulo, Brazil

To meet the demand of the commercial forestry industry needs trees that can do more — produce more wood, on less land. We combine our leading technology with our well-established forestry expertise to develop trees that grow faster, yield more wood, are more resistant to cold and disease and can be processed more efficiently. All these traits are being tested in different projects. To improve growth we are testing genes to improve allocation of carbon, stress tolerance and nitrogen use efficiency. To increase processing efficiency we have Eucalyptus plants with increased wood density. And also production of plants with increased cellulose or plants that are able to release of fermentable sugar easier by using genes that regulate cell wall biosynthesis. We have tested plants with an increased cellulose yield by reducing total lignin content. Reduced lignin enhances sugar release because lignin prevents cellulose from being broken down into sugars so it is converted more easily by fermentation technologies into biofuels. Chemistry of lignin can also be engineered by manipulating the amount of syringyl and guaicyl lignins. With a higher syringyl lignin pulping efficiency is increased and costs in a pulp mill are reduced with chemical savings. For the frost resistance we developed a freeze tolerant tropical Eucalyptus product, currently under USDA review, that combines the fast-growing characteristics of the tropical Eucalyptus grown extensively in Brazil with the ability to grow in geographic areas further north than conventional tropical Eucalyptus can grow. While not currently widely grown in the Southeastern United States, Eucalyptus has the potential to be a ready source of biomass for the biopower and biofuels markets as well as a source of high quality wood for the pulp and paper market. The advanced and technology-enhanced products are designed to improve growth rates, yields, stress tolerance, uniformity, wood quality and processing efficiency of trees. Combining superior nursery management practices and methods, conventional tree breeding, species selection, advanced tree improvement and biotechnology to produce trait-specific superior trees, ArborGen is working to ensure that our customers get more out of every tree they grow.



Wheat spike fertility: genetics and breeding applications of a key ecophysiological yield component

Pontaroli, A.C.^{1,2*}; Abbate, P.E.¹; Lázaro, L.³; Gutheim, F.⁴; Martino, D.L.¹; Mirabella, N.E.¹; Deperi, S.I.¹; Alonso, M.P.^{1,5}; Ramírez, I.A.¹

¹Unidad Integrada Balcarce (Estación Experimental Agropecuaria Balcarce, Instituto Nacional de Tecnología Agropecuaria – Facultad de Ciencias Agrarias, Universidad Nacional de Mar del Plata); CC 276 (7620) Balcarce, Buenos Aires, Argentina.

²Consejo Nacional de Investigaciones Científicas y Técnicas, Argentina.

³Facultad de Agronomía, Universidad Nacional del Centro de la Provincia de Buenos Aires; CC 178 (7300) Azul, Buenos Aires, Argentina.

⁴Chacra Experimental Miramar, Ministerio de Asuntos Agrarios de la Provincia de Buenos Aires; CC 35 (7607) Miramar, Buenos Aires, Argentina.

⁵Comisión de Investigaciones Científicas de la Provincia de Buenos Aires, Argentina. *apontaroli@balcarce.inta.gov.ar

One of the main components of grain yield in wheat, grain number m^{-2} , is determined by chaff weight m^{-2} and the number of grains per unit of spike chaff weight (i.e. a spike fertility parameter, or SF). SF explains a great proportion of yield variation among cultivars. Therefore, selection for high SF could contribute to an increase in grain yield, which is paramount in wheat breeding programs worldwide. Recent works strongly suggest that SF appears to be stable in a wide range of environments, even sub-potential ones. However, the feasibility of using wheat SF as a selection criterion depends greatly upon the availability of a high throughput method for collecting and processing samples. The reference method for SF determination (i.e. in anthesis and at the plot level) is tedious, time consuming and destructive, and hence not amenable to be applied in a breeding program, where a large number of breeding materials have to be screened simultaneously and the seed has to be conserved for subsequent generations. We have established an appropriate method for fast and simple SF determination at maturity in a small sample of individual spikes that yields substantially similar results to those obtained with the reference method. Furthermore, preliminary work indicates that training for visual selection of F2 plants for spike attributes associated with high SF can fairly substitute for SF determination. In order to generate an experimental framework for investigating the genetic and molecular mechanisms underlying wheat SF, controlled crosses were made between wheat cultivars with contrasting SF under different mating designs. Variance components were estimated for the 15 parents, 21 F1 families, two F2 families (~200 individuals each), and the derived F3 and F5 generations. Overall, these results suggest that SF is controlled by a few genes, with low genetic x environmental interaction and medium to high heritability. Molecular marker analysis is being currently carried out in two mapping populations; so far, several markers co-segregating with SF have been detected, which warrant further investigation.



A systemic approach to genetics and crop management, leading to a sustainable wheat revolution

Comeau, A.¹, Langevin¹, F., Scheeren², P., Caetano, V.R.³, Eudes, F.⁴, Randhawa, H.⁴, Dion, Y.⁵, Voldeng, H.⁶

¹CRDSGC, AAFC (Agriculture and Agri-Food Canada), Quebec, QC,

²Canada EMBRAPA Trigo, CP 451, 99001-970, Passo Fundo, RS, Brazil

³EMBRAPA CLIMA TEMPERADO, CP 403, Pelotas, RS, Brazil

⁴AAFC Research Centre, Lethbridge, AB, Canada

⁵CÉROM, Saint-Mathieu-de-Beloeil, QC, Canada

⁶ECORC, AAFC, Ottawa, ON, Canada

The systemic approach gave faster genetic progress in bread wheat for complex goals, both in Canada and in Brazil. More attention must be given to the relationships between genetics and the projected environment in which cultivars are due to be grown 15 years later. If selection is done in less sustainable conditions (high inputs), a genetic base adapted only to high inputs will be develop over time. If selection is done only for the current climate, which is due to change over 15 years, this becomes a high-risk scenario. New cultivars may well be maladapted to a changing environment, on the very day they are released. Scientific collaboration between Canadian and Brazilian scientists on those issues helped major methodological progress. We became able to create germplasm and cultivars adapted to a wide range of environments and cultural methods. Fusarium Head Blight (FHB), for which resistance factors are quite complex, was one test case. The systemic approach gave evidence of true victory against FHB in less than 4 years, in Canada: we got very good resistance with good agronomics. Other methods had allowed only slow progress against this disease. Complex traits, for which the systemic approach works well, include many yield factors, bread-making quality, straw strength, and other valuable traits. In the near future, a scenario for a pesticide-free wheat culture may evolve, based on more research towards this desirable result. Replacing fertilizer in part by symbiotic bacteria and fungi is a logical step envisioned. The systemic approach concept is partly published in a book chapter. Making better use of the complex relationships between traits (including genes) and environments is at the core of the approach. A genome allows interactions (GxE, gene x gene, etc.) that are often many orders of magnitude more numerous than the number of genes. Multivariate analysis revealed many unexpected relationships between traits and environments. Methods based on the understanding of interactions were developed. This shortens the time to cultivar creation by 40% and increases the annual rate of genetic progress for difficult goals. Moreover, the systemic approach is unique in allowing the use of much broader genetic diversity in crosses, faster recycling of good genetics into crossing blocks, and faster selection of genotypes that embody multiple disease and stress resistance. In fact the annual progress rate is still accelerating. Systemic methods enjoyed rapid, convincing success and must receive much more attention from breeders of wheat and other crops. Collaboration with crop management experts is needed for coevolution of genetics with sustainable cropping methods.



Genetic Mapping in Polyploids

Antonio Augusto Franco Garcia¹, Marcelo Mollinari¹, Thiago Gibbin Marconi², Melina C Mancini², Estela A Costa², Robert Henry³, Peter C. Bundoock⁴, Luciana R. Pinto⁵, Anete P. Souza².

¹Luiz de Queiroz College of Agriculture, Department of Genetics, University of São Paulo, Brazil;

²CBMEG - State University of Campinas, Brazil

³The University of Queensland, Australia

⁴Southern Cross University, Australia

⁵Instituto Agronômico de Campinas (IAC), Centro de Cana, Brazil

Polyploid plant species are very common in nature. Due to its genetic complexity, they do not fully benefit from modern marker technologies (with a few exceptions, such as autotetraploids). Results about genetic maps, QTL and association mapping are scarce, making it difficult for geneticists to study the genetic architecture of quantitative traits important for breeding and evolution. In this talk, it will be shown that the combination of SNP-based marker systems, combined with new statistical models, could provide an appropriate framework to deal with this complicated scenario. Examples of applications will be presented for sugarcane, showing that it is possible to making the SNP call, estimating ploidy level and number of copies of each SNP allele. Once these results are obtained, it is possible to build multipoint linkage maps, which are required for QTL studies and for genome assembling. The implications of these results will be addressed.



Regulatory elements linking genes co-regulated in response to abiotic stresses

Antonio Costa de Oliveira, Luciano Carlos da Maia, Taciane Finatto, Camila Pegoraro, Daniel da Rosa Farias, Lara Isys Dias

Plant Genomics and Breeding Center, Federal University of Pelotas, PO Box 354, Pelotas-RS, Brazil.

The overwhelming amount of data originating from plant genome sequencing projects has posed novel challenges for scientists: the understanding of the functional roles of many genes in the organisms. The study of genes and gene families involved in abiotic stress responses may help to elucidate the role of genes related to stress tolerance and potential candidates to introduce in elite varieties. The study of cis-acting elements and the association of promoter landscape and gene expression can aid the identification of co-regulated genes. Our group has been working on genome structure and characterization through the development of bioinformatics tools for the development of genome elements. The abundance of cis-elements and the characterization of complex and simple regulation of abiotic stress responsive genes in the rice genome are discussed.



LARGE-SCALE TRANSCRIPTOMIC ANALYSES IN SUGARCANE:

SEARCHING FOR GENES ASSOCIATED WITH DROUGHT TOLERANCE

ANTONIO FIGUEIRA¹, JOAO FELIPE NEBÓ^{1,4}, SILVANA CRESTE², DANIEL NUNES², PAULO E. MARCHIORI³, RICARDO S. MACHADO³, RAFAEL V. RIBEIRO³, MARIANA BELLOTI¹, ALINE HARISSIS¹, JONI LIMA¹, RAY MING⁴, JAMES WALSH⁴, GLAUCIA SOUZA⁵, MARCOS LANDELL², PATRÍCIA REZENDE⁶, ROGÉRIO A. B. SOARES⁶.

¹Centro de Energia Nuclear na Agricultura, Universidade de São Paulo, Piracicaba, SP, Brazil;

²Centro de Cana, Instituto Agrônomo de Campinas, Ribeirão Preto, SP, Brazil;

³Centro de Ecofisiologia e Biofísica, Instituto Agrônomo de Campinas, Campinas, SP, Brazil;

⁴Department of Plant Biology, University of Illinois at Urbana-Champaign, USA;

⁵Instituto de Química, Universidade de São Paulo, São Paulo, SP, Brazil;

⁶Jalles Machado Mill, Goianésia, GO, Brazil.

High throughput sequencing technologies have allowed the development of large-scale transcriptomic analyses, with important progress in non-model species. Sugarcane (*Saccharum* spp.) presents a large analytical challenge due to the complex nature of its genome (highly heterozygous, polyploid, with aneuploidy). We have compared large-scale transcript profiling approaches (microarray and RNA-seq) to search for genes with roles in drought tolerance. Leaf samples from two contrasting genotypes for response to drought were collected from plants grown under irrigation or drought conditions in a field trial at two moments (early and after severe drought), and used to perform microarray analysis. From a set of 14,522 genes, 91 were differentially expressed between irrigated or non-irrigated treatments during early drought, whereas 576 were differentially expressed during severe drought between water treatments, from which 438 were differentially expressed between genotypes. Similarly, samples from the same genotypes grown in contrasting water regime under greenhouse conditions were used for gene expression profiling by RNAseq. From a reference sugarcane dataset with 43,141 genes, 2,300 (5.3%) genes were identified as differentially expressed. The open system of gene expression analysis (RNA-seq) was more successful in identifying novel genes involved in drought response than microarrays (closed system). Most of the genes identified through microarrays were also observed in the RNAseq with high correlation for differentially expressed genes between both approaches (0.78 and 0.84 for tolerant and sensitive genotypes, respectively). Genes related to drought response were validated through qPCR. Known drought responsive as well as novel genes were detected, that may play a role in sugarcane drought tolerance. Main discriminating mechanisms associated with drought tolerance included maintenance of photosynthesis, redox metabolism and transcription regulation during drought.

Financial support: FAPESP



CROP PHYSIOLOGISTS : Tour guides, discoverers or team players?

A.J.Hall,

IFEVA (FAUBA/CONICET), Av. San Martín 4453, C1417DSE, CA Buenos Aires, Argentina.
hall@ifeva.edu.ar

The Crop Science Community is currently facing difficult, important and –above all- urgent challenges, including: the development and implementation of effective responses-between now and 2050- to the looming problem of global food security; the mitigation of losses of reactive nitrogen from farmed soils to the environment; and the improvement of our understanding of – and hence, the design of effective responses to – the effects on crops of the predicted increases in frequency and intensity of episodes of drought and high temperature stress. This commentary concentrates on the first item of this shortlist and attempts a prospective view of the roles of Crop physiology in facing this challenge, as a stand-alone discipline and, more importantly, as a member of a team of sister disciplines. This team is simplistically viewed as including agronomy, crop modelling, crop yield improvement, and crop yield biotechnology. Current linkages of crop physiology with agronomy and crop modelling are considered effective, those with crop yield improvement controversial, and those with crop yield biotechnology poor. Particular attention is paid to the crop physiology / crop yield improvement linkages in view of a more extended joint history and published comments by some authors. Especial significance is attached to the recent formation of a cross-disciplinary approach (involving all five disciplines) to wheat yield improvement. This is viewed as a possibly useful model for the future. It is argued that in the near future crop physiologists, as well as attending to considerable unfinished business, should also invest some time in fostering interdisciplinary approaches to the main challenges facing the crop science community. Possible actions include building bridges to disciplines with which linkages are currently controversial or weak; encouraging funding bodies to support interdisciplinarity; encouraging research organisations to establish specific policies aimed at increasing and supporting interdisciplinarity; and urging universities to produce graduates better able to comfortably navigate the whole chain of disciplines between agronomy and molecular genetics.



Improving nitrogen use efficiency in crops for sustainable agriculture

Bertrand Hirel

Adaptation des Plantes à leur Environnement. Unité de Recherche 511, Institut Jean-Pierre Bourgin, Institut National de la Recherche Agronomique, Centre de Versailles- Grignon, E-Mail: hirel@versailles.inra.fr

In this review, we present the recent developments and future prospects of improving nitrogen use efficiency (NUE) in crops using various complementary approaches. These include conventional breeding and molecular genetics, in addition to alternative farming techniques based on no-till continuous cover cropping cultures and/or organic nitrogen (N) nutrition. Whatever the mode of N fertilisation, an increased knowledge of the mechanisms controlling plant N economy is essential for improving NUE and for reducing excessive input of fertilisers, while maintaining an acceptable yield and sufficient profit margin for the farmers. Using plants grown under agronomic conditions, with different tillage conditions, in pure or associated cultures, at low and high N mineral fertilizer input, or using organic fertilisation, it is now possible to develop further whole plant agronomic and physiological studies. These can be combined with gene, protein and metabolite profiling to build up a comprehensive picture depicting the different steps of N uptake, assimilation and recycling to produce either biomass in vegetative organs or proteins in storage organs. We provide a critical overview as to how our understanding of the agro-ecophysiological, physiological and molecular controls of N assimilation in crops, under varying environmental conditions, has been improved. We have used combined approaches, based on agronomic studies, whole plant physiology, quantitative genetics, forward and reverse genetics and the emerging systems biology. Long-term sustainability may require a gradual transition from synthetic N inputs to legume-based crop rotation, including continuous cover cropping systems, where these may be possible in certain areas of the world, depending on climatic conditions. Current knowledge and prospects for future agronomic development and application for breeding crops adapted to lower mineral fertiliser input and to alternative farming techniques are explored, whilst taking into account the constraints of both the current world economic situation and the environment.



Animal production on Tropical Pastures in Brazil

Cacilda Borges do Valle and Valéria Pacheco Batista Euclides
Embrapa Beef Cattle – Campo Grande, MS, Brazil.
cacilda@cnpqg.embrapa.br; val@cnpqg.embrapa.br

Animal production in the tropics is done mostly on native and cultivated pastures. Brazil is predominantly tropical and is the fifth largest country in the world with about 20% of its area covered by pastures (174 million ha). It has a natural aptitude for livestock production also as climate and topography are concerned. Soils however, are acid and poor, with more than 90% dystrophic (soil base saturation less than 50%) in Central Brazil, the most significant region for livestock production. The majority of the cattle of 209 million head is on pastures, mostly of grasses and planted to a few *Brachiaria* and *Panicum* cultivars, characterizing extensive monocultures. Estimates are of only 3% finished in intensive systems. Pasture diversification as well as recovery of degraded old pastures is the major target of research and public policies nowadays in Brazil. Since 2004 Brazil is the largest exporter and second largest producer of beef in the world. It is also the largest producer and exporter of tropical forage seed, a market of about 1 million dollars a year, triggering interest from multinational companies to begin exploring this sector. Technology has increasingly been used in livestock or integrated with crop-forest-livestock systems. Together with research-oriented inputs, productivity has increased despite decrease in the area of pastures. Major issues of sustainability and animal welfare have been raised towards Brazilian beef despite the fact that the country has 68% of its area in original forests. Efforts to observe good agricultural practices and to reduce greenhouse gas emissions from ruminants are being undertaken to make Brazilian livestock industry ever more efficient and competitive. Tropical forage breeding is a recent activity worldwide and started with legume breeding in Australia and at CIAT in Colombia. Regrettably almost of all those programs have been discontinued and results have not really impacted production systems in the tropics. In Brazil, breeding and selection of tropical forages began in the mid-1980's focusing mostly on *Panicum maximum*, *Brachiaria* sp., *Andropogon*, *Stylosanthes*, *Arachis* and *Leucaena*. Recently released cultivars in Brazil, selected either from germplasm collections or from bred progenies are expected to fulfill expectations of increased productivity with sustainable production. A very important contribution comes from the private sector through the partnership with UNIPASTO (Seed Companies Association) since 2002. As exclusive seed producers and distributors of Embrapa's cultivars, both in Brazil and abroad it assists in the rapid adoption and dissemination of these cultivars.



Cassava Breeding Technology: Constraints, solutions and opportunities to enhance root yield and quality for industrial utilization

Chikelu Mba

Plant Production and Protection Division, Food and Agriculture Organization of the United Nations, Rome, Italy

Cassava, (*Manihot esculenta*, Crantz), a south American herbaceous plant, is cultivated for its starchy storage roots in the tropics. In sub-Saharan Africa into which it was introduced in the 16th century, it is a major food security crop that is becoming increasingly important as feedstock, substrate for biofuel and source of industrial starch just as it had become in a number of Asian countries. Despite the crop's robust tolerance to abiotic stresses, especially drought, and amenability to low input agriculture, considerable production constraints must be overcome and poor quality attributes ameliorated in order to attain meaningful levels of productivity and acceptable quality that can warrant its envisaged multi-purpose uses for food and in myriad industries. These constraints include viral and bacterial diseases and infestations by insect pests. Sub-optimal yields (especially in sub-Saharan Africa), low contents and poor qualities of starch, low dry matter contents, postharvest physiological deterioration, plant architectures, harvestability and contents of anti-nutritional factors are some of the compelling breeding objectives for the crop. Cassava varieties with market-specific traits, e.g. for bioethanol production and contents of waxy starch, are also increasingly being bred for. Several national programs, two centres of the Consultative Group on International Agricultural Research and a number of advanced laboratories are employing, usually in collaborative endeavours, a suite of interventions encompassing classical and molecular breeding strategies in improving cassava. Induced mutagenesis is being used to generate novel alleles in the crop's genome just as efficiency enhancing molecular tools are aiding the efforts at the uncovering of new sources of heritable traits including from the crop's uncultivated and wild relatives. Broadening the genetic base of the crop's breeding materials – that can be facilitated greatly by enhanced exchange of germplasm and pre-breeding -- and the further development and deployment of genomics tools can contribute greatly to the efficient development of new elite cassava varieties. These varieties are needed to safeguard the crop's food security status without compromising the ubiquitous efforts to harness its potentials for industrial applications in the context of the burgeoning climatic, demographic and economic pressures that characterize agricultural production in the 21st century.



Global Partnership Initiative for Plant Breeding Capacity Building (GIPB): The Crop Improvement Coalition

Chikelu Mba

Plant Production and Protection Division, Food and Agriculture Organization of the United Nations, Rome, Italy

Significant individual skill and institutional capacity gaps still exist, especially in developing countries, for applying both classical and powerful novel tools in translating the potentials inherent in plant genetic resources into superior crop varieties. With the coming into force of the International Treaty on Plant Genetic Resources for Food and Agriculture, this shortcoming became even more glaring with the consensus that a majority of the contracting parties were incapable of implementing effectively its Article 6 relating to the sustainable use of plant genetic resources for food and agriculture (PGRFA). The imperative of reversing this trend of sub-optimal capacities led to the convening of the multi-stakeholder platform, the Global Partnership Initiative for Plant Breeding Capacity Building (GIPB) that is hosted by the Food and Agriculture Organization of the United Nations. The GIPB adopts the multi-pronged approach of supporting the development of relevant policy instruments; enhancing human and institutional capacities; facilitating access to technologies; fostering the exchange of PGRFA; and disseminating information. The GIPB-commissioned studies on the statuses of national capacities in crop improvement have provided baseline information that are aiding the development of intervention strategies. Supporting the acquisition of skills in pre-breeding has been one of GIPB's main activities. For instance, GIPB supported the training of many scientists in pre-breeding and related biotechnologies through four training courses. Also, in order to reach the widest possible target audience, GIPB has rolled out an e-learning course on pre-breeding. GIPB also leverages the mechanisms of its partnering organizations for providing technical assistance. For instance, to contribute to the strengthening of capacity for germplasm enhancement, six pre-breeding projects were funded under a collaborative initiative involving the Global Crop Diversity Trust and the Generation Challenge Program of the Consultative Group on International Agricultural Research. GIPB's Knowledge Resource Centre portal provides relevant information on plant breeding and other PGRFA related issues that were either previously unavailable or not easily accessible through several mechanisms including a discussion forum, the PB-Forum. The user base of GIPB's knowledge portal which comprises the *Plant Breeding News* - a monthly newsletter that is distributed to about 2000 subscribers is continuously growing. The GIPB's interactive database on plant breeders and other relevant scientists, the PB-Directory, also facilitates the building of collaborations.



The genomics of peanut and its wild relatives.

David J. Bertoli¹, Bruna Vidigal^{1,2}, Soraya C.M. Leal-Bertoli², Lutz Froenicke³, Christopher Beitel³, Stephan Nielen^{2,4}, Millind Ratnaparkhe⁵, Ana C. Brasileiro², Patricia M. Guimarães², Trude Schwarzacher⁶, Richard Michelmore³, Andrew H. Paterson⁵, Pat Heslop-Harrison⁶, Ana C.G. Araujo².

¹University of Brasilia, Department of Genetics, Campus Universitário, 70910-900 Brasília DF, Brazil.

²Embrapa Genetic Resources and Biotechnology, Brasilia, DF, Brazil.

³UC Davis Genome Center, Davis, CA, USA

⁴Now at: Plant Breeding and Genetics Section, Joint FAO/IAEA Division of Nuclear Techniques in Food and Agriculture, International Atomic Energy Agency, Vienna, Austria.

⁵Plant Genome Mapping Laboratory, The University of Georgia, Athens 30605, USA.

⁶Department of Biology, University of Leicester, Leicester, UK.

Cultivated peanut (*A. hypogaea* L. is a very important tropical oilseed, valued both for subsistence and as a cash crop. It is an allotetraploid of recent origin with an AB type genome ($2n = 4x = 40$) and has very low DNA polymorphism, a characteristic that has hampered genetic studies. The two sub-genomes diverged from a common ancestor about three and a half million years ago, more recently than the sub-genomes of cotton or soya. The genome of peanut is estimated at about 2.8 Gb (only slightly smaller than the human genome) and has a high repetitive DNA content. During meiosis, peanut chromosomes pairing is almost entirely bivalent, an indication of genetic divergence of the A and B chromosomes. A significant divergence is also indicated by *in situ* hybridization analyses, which show that the repetitive contents of the A and B genomes are substantially different. Interestingly, evidence regarding the low copy fraction of the genome is converse: strong colinearity is observed between the A and B genome genetic maps, and indeed in many genome regions, gene order appears to have changed little over the last 55 million years. These diverging lines of evidence point to an intriguing question in the evolution of genome structure: how can the evolutionary flux of the structurally predominant repetitive DNA be reconciled with evolutionary conservation in low copy number DNA? Analysis of genomic sequences from the A and B genomes indicated that a large proportion of the sequence space is accounted for by relatively few transposons that have been active since the evolutionary divergence of the two subgenomes. The activity of these transposons has been a very significant driver of the erosion of A-B genome sequence similarity. Notably, this erosion is not evenly distributed; it is concentrated in intergenic regions.



Resolving developmental networks that control inflorescence architecture in maize.

Peter Bommert¹, Andrea L. Eveland¹, Byoung Il Je¹, Mai Komatsu⁵, Alexander Goldshmidt¹, Michael Pautler¹, Kengo Morohashi², Erich Grotewold², Erik Vollbrecht³, Doreen Ware^{1,4},

Hajime Sakai⁵ and David Jackson^{1*}

¹Cold Spring Harbor Laboratory, Cold Spring Harbor, NY, USA;

²Ohio State University, Columbus, OH, USA;

³Iowa State University, Ames, IA, USA;

⁴USDA-ARS, Cornell, NY, USA;

⁵Dupont Crop Genetics, Wilmington, DE, USA. *For correspondence: jacksond@cshl.edu.

The activities of stem cells (“meristems”) in crop plants is vital to plant productivity. Developmental decisions programmed by meristems have also been major targets of selection during crop domestication and improvement. Stem cell proliferation in the shoot apical meristem is regulated by the CLAVATA (CLV)-WUSCHEL signaling pathway. The CLAVATA signaling pathway is complicated, involving the action of at least three major receptor complexes in *Arabidopsis*. The CLAVATA pathway appears to be conserved in maize, since orthologs of *CLV1* and *CLV2*, *THICK TASSEL DWARF1* (*TD1*) and *FASCIATED EAR2* (*FEA2*) have similar fasciation phenotypes. We have found evidence that *FEA2* corresponds to a QTL for kernel number, suggesting that it contributed to the increase in ear size during maize improvement. We have also identified new members of the CLAVATA pathways in maize, including an additional receptor, *FASCIATED EAR3*, which appears to act in parallel to the other receptors, and a downstream signaling factor. We are also taking a systems approach to inflorescence architecture. Branching patterns of grass inflorescences are determined by developmental fate of stem cell populations called axillary meristems. We investigated transcriptional networks controlling axillary meristem determinacy using a mRNA-seq strategy to generate genome-wide transcript profiles capturing spatiotemporal expression changes during development in ear and tassel primordia, and those resulting from genetic perturbation. Expression signatures from developmentally staged ears of branching mutants were compared with those of maize tassels, which show distinct patterns and degrees of branching. The mRNA-seq datasets were integrated to resolve co-expression networks of TFs and their potential targets in relation to the *RAMOSA* branching pathway. We identified classes of TFs as putative candidates in the regulation of branching, and which intersect multiple hormone pathways as well as distinct signaling networks. To expand this co-expression network, we performed ChIP seq using maize transgenic *RAMOSA1* tagged lines, and are integrating genome-wide DNA occupancy profiles for *RA1* in relation to expression differences. Also, enrichment of regulatory elements, and the potential for combinatorial binding of developmentally-regulated TFs were performed. Collectively, these data provide a framework for elucidating key components of a developmental program with agronomic importance.

Funding from NSF, NIFA and Dupont- Pioneer is gratefully acknowledged.



6th International Crop Science Congress

August 6th to 10th, 2012

Fundaparque Event Center
Bento Gonçalves - RS - Brazil

Biotech Varieties for the Future: Examples from Monsanto's Pipeline

David A. Somers

Monsanto Company, Monsanto Mystic Research Center, Mystic, CT USA

This presentation will cover trends shaping agriculture today and in the future and how biotechnology will play a major role in increasing crop production. Biotechnology product development will be described and technologies that have accelerated biotechnology crop improvement will be highlighted. Examples of biotechnology product trends will be drawn from Monsanto's pipeline.



Maize Reproductive Response to Nitrogen

Dale Loussaert

DuPont Pioneer Hi-Bred, Johnston, Iowa 50131-1004, USA

Reproductive parameters responsive to nitrogen inputs are more useful parameters for elucidating nitrogen use efficiency improvements in maize. Unfortunately, it is difficult to grow maize in controlled environments in the quantity required to conduct reproductive research. A maize, Gaspe Flint line has been developed that has nearly the same cycle time as Arabidopsis and has been used to conduct research on maize reproductive responses to nitrogen input. Physiological responses observed in this model system have been reproduced in full season maize hybrids demonstrating that major physiological responses observed in this model system maize can be translated to full season, field results. Ear development and responses to nitrate input and timing have been analyzed. Insufficient levels of nitrate at different stages of plant growth may affect reproductive development independently from vegetative development. These experiments confirm the importance of nitrate assimilation in ear development in maize.



THE ROLE OF BIOTECHNOLOGY IN FOOD SECURITY FOR AFRICA - SOUTH AFRICAN EXPERIENCE

DIANA MARAIS

Department of Plant Production and Soil Science, University of Pretoria, Pretoria, Gauteng,
South Africa. Diana.maraais@up.ac.za

South Africa is the leader in Africa in terms of embracing bio-engineered crops. This started with the introduction of Bt Maize (*Zea mays*) and Bt Cotton (*Gossypium hirsutum*) in the early 2000's followed by RR Maize, RR Cotton and RR Soybean (*Glycine max*) as well as Bt + RR Maize and Bt + RR Cotton. The range in Cotton is further broaden by the inclusion of numerous other staple genes to improve the resistance of the crop to pests in the last five years. Currently research and formulation of legislation on the Drought tolerant gene in Maize are being conducted in South Africa. This is spearheaded by Monsanto as part of the WEMA (Water efficient maize for Africa) project funded by the Bill and Melinda Gates Foundation. South Africa has thus come far in adopting this technology and embracing new GMO crops which could lead to even better production for both commercial and small holder farmers. However, before we can assess the role of biotechnology in food security, it is important to know what we mean by food security and the main reasons for a country to be food insecure. For this talk food security will imply that food is readily available, that it fulfil in the nutritional needs of the human body and that the source is sustainable. Readily available includes distribution, money to buy and enough, quantity wise. Malnutrition in South Africa is mainly in terms of Zn, Fe, Vitamin A and protein, with obesity also being a huge problem. Apart from these problems, the food source is often not sustainable due to production constraints. Therefore it is often these production constraints which prevent food security. The main production constraints in South Africa are: seed quality, input costs and availability of these inputs (fertilizers, crop protection and soil cultivation), and erratic or low rainfall. For commercial farmers, seed quality and input costs are usually not such a big problem as faced by the small scale farmers, while water constraints can be experienced by both. On the one hand we thus have biotechnology to assist, but on the other hand there is constraints which cannot be addressed by the current biotechnology. In this paper we will thus be looking at where the journey started with bio-engineered crops in South Africa, the adoption rate by South African producers, the constraints experienced by the producers, and the way forward.



Agricultural Policies and Food Security Issues in Africa: Deterrents or Enhancements Agricultural Biotechnology Perspectives

Diran Makinde

NEPAD Agency African Biosafety Network of Expertise Ouagadougou, Burkina Faso

The quest for effective mechanisms to regulate modern biotechnology has elicited policy responses at various levels the world over, with the main multilateral framework being the Cartagena Protocol on Biosafety. African countries are at various stages towards developing and implementing domestic frameworks that comply with this Protocol. In addition, several efforts have been made towards regional cooperation in biosafety. The New Partnership for Africa's Development (NEPAD) Agency's African Network of Biosafety Expertise (ABNE) has in the last few years been at the forefront of efforts to help African countries develop and implement biosafety systems that will ensure that the technology plays a key role in multi-faceted efforts towards the continent's socio-economic self-sufficiency. Like elsewhere in the world, African countries have engaged in the debate on the pros and cons of modern biotechnologies and products thereof for a greater part of the last two decades. Efforts to develop and implement regulatory systems have also been on-going across the continent for the same length of time, with varying levels of success across countries and regions for the desired policy change. The debate and policy trajectories have incessantly been altered both in content and nature by a number of internal and external factors, not least the developments unravelled by conclusion and implementation of the provisions the Cartagena Protocol on Biosafety. Africa's geographical and socio-economic peculiarities also shape the content and nature of the debates, and their outcomes. Key among these peculiarities are: the economic and social importance of agriculture in Africa; the degree of food insecurity and poverty on the continent; the pressures exerted on natural resources by the continent's population as they endeavour to satisfy food and nutritional needs; the vulnerable nature of Africa's agriculture due to climate change, diseases and predators; the need to explore new ways of developing agriculture to overcome food insecurity and alleviate poverty; and all this while needing to protect biodiversity, the environment and human and animal health. This raises both the importance of biotechnology in the development of Africa's agriculture economic development, as well as the need for effective regulatory mechanisms to ensure maximisation of benefits and minimisation of risks. The presentation will focus on a related set of questions which interrogates the duration and direction of most of the policy processes. The contention and indeed the evidence is that the processes are too long and tend to move in multiple, uncoordinated directions, resulting not only in delays or failure to accomplish targets and desired policy change, but in dissipation of resources and diverging outputs. It is important for all stakeholders to continuously confront the fact that to implement biosafety frameworks, they are doing so out of competition among themselves, and with other policy arenas that also require the financial and human resource attention of governments.



6th International Crop Science Congress

August 6th to 10th, 2012

Fundaparque Event Center
Bento Gonçalves - RS - Brazil

Soybean Production and Improvement in Brazil

Éberson Sanches Calvo

TMG – Tropical Genética & Melhoramento Ltda.

Cambé, PR, Brazil. e-mail : ebersoncalvo@tmg.agr.br

In spite of its origin in a temperate region, soybean has succeeded as one of the main agricultural crops in tropical and subtropical environments of Brazil. The presentation will comment on the trajectory of the crop in the country and the reasons that contributed for this success. Special emphasis will be given on the past, present and future efforts on soybean genetics and breeding in Brazil.



MONSANTO'S BEACHELL-BORLAUG INTERNATIONAL SCHOLARS PROGRAM

E. C. A. Runge, Program Director and Judging Panel Chair

Soil & Crop Sciences Department, Texas A&M University, College Station, TX 77843-2474

Monsanto's Beachell-Borlaug International Scholars Program is a unique program that honors two of the World's best known plant breeders who are widely credited for bringing the green revolution to rice and wheat production. The dramatic increase in rice and wheat production per unit area of land prevented starvation for billions of people and spared land for other activities. Monsanto funded MBBIS program at \$2 million per year for 5 years for a total of \$10 million but expects the MBBIScholars to work in the public sector upon graduation. Monsanto recently announced that they would extend funding the MBBIScholars program for an additional 3 years. The program provides complete support for PhD students in rice and wheat breeding. The MBBIS program was announced on Dr.

Norman Borlaug's 95th birthday on March 25, 2009. The 1st, 2nd, 3rd and 4th rounds of applications were evaluated by an internationally acclaimed panel of judges and 12, 14, 12, and 14 scholars were selected for support. Of the 52 students receiving funds, 31 are in wheat breeding and 21 are in rice breeding. Students are from Argentina (2), Bangladesh, Brazil (2), China (4), Colombia (3), Ecuador, England, Ethiopia (4), Kenya, Korea, India (14), Iran (2), Italy, Mexico (3), Nepal (2), Philippines, Syria (2), Tajikistan, Thailand, Tunisia, and USA (4). Funds are encumbered for the duration of the PhD program and transferred yearly. The program is unique in that it requires scholars to complete part of their PhD program in Australia, Canada, United States or Western Europe and part in another country of the World. If students are enrolled in a university in Australia, Canada, USA or Western Europe they must complete part of their study in a developing or transition country. Conversely, if students are enrolled in a university in a developing or transition country they must complete part of their study in Australia, Canada, USA or Western Europe. The equivalent of one year is desired for the alternative experience on the students PhD program. Program activities with CGIAR Center scientists are encouraged. Students with two or more years remaining on their PhD program are eligible for support. Funding is limited to a maximum of 4 years with 3 years being the norm. More student applications from Eastern Europe, Central Asia and Africa are desired. Applications for the 5th round of funding will be accepted from November 1, 2012 through February 1, 2013. Students work with their advising professor or scientist from the degree granting institution from anywhere in the World and the advising professor submits the application for the student. To learn more about the program, how to apply, application form, and requirements please go to www.monsanto.com/mbbischolars.



Presentation Title: A web-based platform for RNA-Seq data analysis and storage: a case study on soybean gene expression experiments

Eliseu Binneck and Lucas Soares do Nascimento Institution of origin including city, state and country: Embrapa Soybean, Londrina, PR, Brazil

The availability of the soybean genome sequence and the rapid evolution of DNA sequencing technologies in recent years bring us exciting new promises for scientific discovery and its conversion into required technological breakthroughs in the production and use of soybean. In addition to be a major protein source in animal feeds, soybean is ranked number one among the chief oil crops in the world and is becoming a major crop for biodiesel production. As a leguminous crop, soybean fixes nitrogen in association with *Bradyrhizobium*, which significantly reduces the needs for ammonium-based fertilizer even in other crops. In this presentation, it will be described using a web-based platform, Soybean Gene Express, for analyzing and storing RNA-Seq data from whole-genome transcription profiling experiments. It will be presented first hand how Soybean Gene Express supports researchers going from raw data to visual reports comparing the different genes within same sample or comparing gene expression across different biological samples/conditions. Also, it will be explored the power of link-based integration with other sources of biological information and databases such as ontologies, KEGG pathways, Pfam, and others, to uncover the biological meaning of these data. The ultimate goal is to facilitate the discovery of new biological insights into fundamental molecular processes as responses to biotic and abiotic stresses in soybean.



Our research on ecophysiological bases for maize management

Fernando H. Andrade

Inta Balcarce, Facultad de Ciencias Agrarias UNMP. Balcarce, Buenos Aires Province, Argentina.

The knowledge of factors and mechanisms that determine crop growth and yield is critical for a high, efficient and sustainable production because it i) guides the design and selection of the most appropriate management practices, ii) provides information for efficient and adequate use of agricultural inputs, and iii) provides to breeders the conceptual and screening tools that could improve efficiency in the selection of genotypes with high yield potential and adaptation to the target environment. This presentation focuses on the mechanisms determining yield in maize using a comprehensive and simple conceptual framework. The concepts of light capture and growth, temperature and photoperiod effects on development, environmental effects on growth and radiation use efficiency, critical periods for grain yield determination, vegetative and reproductive plasticity, source-sink relationship during grain filling, and harvest-index stability constitute the bases for understanding crop yield as determined by management practices, environmental conditions and the interactions among these factors. Plant density, inter-row distance, uniform planting, sowing date, cultivar selection, water and nutrient management, among other practices, are analyzed relative to their effect on the physiological condition of the crop or the plant within the crop. Management practices should ensure that the crop maximizes crop growth rate, biomass accumulation and biomass partitioning to reproductive structures especially during the most critical period for grain yield determination. Examples are given to emphasize that basic ecophysiological information is valuable to i) evaluate and predict the effect of agricultural management practices on crop yield and ii) design knowledge intensive crop management strategies oriented to a high and sustainable production.



Crop physiology contributions to crop productivity

Fernando H. Andrade

Inta Balcarce, Facultad de Ciencias Agrarias UNMP. Balcarce, Buenos Aires Province, Argentina.

Agronomists face the great challenge of increasing agricultural production and simultaneously reducing environmental impact. To avoid the expansion of cultivated land towards fragile areas highly vulnerable to degradation, agricultural production must be expanded mostly through increasing the number of crops per year and crop yield per unit area. Crop physiology will contribute to these objectives since the knowledge of factors and mechanisms that determine crop growth and yield is critical for a high, efficient and sustainable production. Basic ecophysiological information is valuable to evaluate and predict the effect of agricultural management practices on crop yield and to design knowledge intensive and sustainable crop management strategies oriented to increase productivity per unit area and per unit time, with an efficient capture and use of resources and inputs. Crop physiology could also contribute to plant breeding in the identification of relevant traits for yield potential and crop adaptation to the target environment, because it helps to understand trait attenuation and magnification of interactions resulting from scaling up across levels of organization. An important contribution of crop physiology is envisioned in characterizing target environments, identifying key primary and secondary traits for high and stable yields, and interpreting the interaction of those traits with the environment. Finally, the potential interaction between crop physiology and crop breeding is analyzed in view of the currently available biotechnologies. These novel techniques could help to bridge the gap and stimulate creative interactions between both disciplines.



Nutrient management and fertilization in soybean: A perspective from the crop

Fernando Salvagiotti

Agronomy Department, INTA Oliveros, Ruta 11 km 353 (C 2206), Santa Fe, Argentina.

e-mail: fsalvagiotti@correo.inta.gov.ar

Nutrient management in crops is crucial for guaranteeing global food security and fertilizers are an important tool for achieving this goal. Fertilizer management strategies must accomplish two goals: assure crop production and quality and avoid negative consequences on the environment. Best fertilizer practices involve the use of soil and/or plant tests capable of identifying sites that are more likely to respond to fertilizer addition. Soil tests are chemical reagents that indirectly reflect soil nutrient availability. However, several times these reagents cannot identify responsive sites. Some soil tests has been successfully implemented in the Pampas region of Argentina for recognizing sites responsive to phosphorus fertilization, but there has been no success in finding soil tests for predicting soybean response to sulfur fertilization. Plant analysis has been proposed as a more reliable predictor of nutrient responsive sites. This presentation will show the use of: (i) seed nitrogen (N) and sulfur (S) content in soybean at maturity as a retrospective diagnosis for deciding fertilization in the succeeding crop using stoichiometry concepts and, (ii) plant analysis in all plant parts at maturity in soybean for modeling nutrient requirements and nutrient uptake efficiency following the QUEFTS approach. Nutrient stoichiometry considers the relative proportions of elements (e.g. nutrients) in living organisms. Deviations from optimal allometry relationships among nutrients may be used for managing multiple nutrients in crops or for detecting nutrient imbalances. We found that nitrogen-sulfur stoichiometric relationships in soybean seeds were all isometric. Differences in the stoichiometric parameters of the N-S relationship reflected shifts in S content under constant N status in seeds. These changes allowed the development of an S deficient index for identifying S responsive sites and deciding S fertilization in the succeeding crop. Many times deficiencies of different nutrients appear simultaneously in real conditions. Nutrient ratios may be useful tools for managing multiple nutrient deficiencies, and thus, be a part of an integrated nutrient management strategy (i.e. balanced fertilization). QUEFTS (Quantitative Evaluation of the Fertility of Tropical Soils) accounts for interactions among macronutrients affecting internal efficiency and allows differentiation according to different yield levels. Equations derived from this approach can be used for modeling nutrient uptake. We developed preliminary envelope functions among macronutrients uptake and seed yield in soybean describing border lines that define maximum and minimum accumulation of nutrients. Likewise we characterized indigenous soil nutrient supply using macro and micronutrient omission plots. This information may help in designing field-specific nutrient management strategies.



The role of Seed Associations on Crop Production: How to Globalize Brazil in the World Seed Market?

The Role of ISTA in Conveying Seed Science to the Production Sector

Francisco Carlos Krzyzanowski ; Officer of ISTA ;

Research Scientist of Embrapa Soybean, Londrina, PR, Brazil; E-mail: fck@cnpsa.embrapa.br

ISTA - International Seed Testing Association, founded in 1924 aiming to develop and publish standard procedures in the field of seed testing, is a non-profit association of public and private seed testing laboratories and persons under the Governance of the Government of member countries. ISTA works to achieve reproducibility in seed quality determination on a worldwide basis. Currently there are 58 countries with at least one ISTA accredited laboratory. The number of member laboratories is 211 from which 123 are accredited ones. The goals of ISTA are international standardization of: reporting results (Orange Certificate); methodologies for testing seeds (Rules), laboratory performance (Accreditation Programme) and international exchange of scientific results (Journal of Seed Science and Technology, Seed Symposiums and Seed Seminars). Since 1933 ISTA has published the International Rules for Testing Seeds. The ISTA Rules can be modified and amended annually by members and non-members, public and private laboratories or persons working in the area of seed science and technology during ISTA Annual Meeting held every year in a different country. To update the Rules, ISTA has 17 technical committees which are responsible for the study and validation of the proposed new seed evaluation method. The technical committees are also responsible for training, education and publication within its area of expertise. To achieve reproducibility of seed quality determination, the standardization of laboratory performance is highly important through: the continuous monitoring of performance through proficiency tests, development of a quality assurance system according to one international standards within the laboratory, regular auditing of the laboratories through an independent body and the further training and education of seed analysts in international training and education workshops. The ISTA accreditation programme is open for seed testing laboratories from the public and private sectors. The ISTA accreditation and audit programme is globally accepted and used worldwide. The accredited laboratories are entitled to issue ISTA Certificates, which are accepted by all countries and are mandatory for seed imports in a growing number of countries. ISTA is actively facilitating the international seed trade.



Diversity of Capsicum in Brazil and its genetic and agronomic potential

Francisco J. B. Reifschneider

Embrapa (Brazilian Agricultural Research Corporation) and CNPQ Fellow (National Research Council), Brasília, DF, Brazil. fjbr@cnph.embrapa.br

Several species of *Capsicum* are found in Brazil and domesticated as well as semi-domesticated species such as *C. annuum*, *C. baccatum*, *C. chinense*, *C. frutescens*, *C. baccatum* var. *praetermissum* are important horticultural crops in the country, consumed either as sweet or as hot peppers, in many ways. The Embrapa-based *Capsicum* research program has had activities that go from expeditions to collect germplasm in remote areas of the country to molecular markers, volatile determination and processing characteristics, bridging knowledge and technology gaps of relevance to both public and private sectors; its focus has been the development of disease-resistant lines, cultivars and hybrids of both hot as well as sweet peppers. The program is financed by federal funds (Embrapa and CNPq) as well as by contract research with the private sector. The *Capsicum* collection at Embrapa has over four thousand accessions, which have supported a major 30-year-old breeding program that today has over 30 thousand lines and populations. Germplasm collection has followed traditional processes as well as innovative schemes that mobilized individuals from technical schools. The collection has been characterized in part by both morphological as well as molecular means. Major contributions by the program and associated researchers include the establishment of the germplasm collection and of a satellite collection at IFG Campus Ceres with over 300 genotypes from central Brazil; the establishment of a *Capsicum* research group at CNPq; the discovery of new species (*C. pereirae*, *C. friburgense* and *C. hunzikerianum*); the organization of an internet-based network of over 500 *Capsicum*-related professionals from both private and public; the release of several disease resistant lines such as CNPH 148 and CNPH 703; the release of disease resistant cultivars such as BRS Sarakura (*C. annuum*), BRS Mari (*C. baccatum*), BRS Moema (*C. chinense*); and the support to young talents interested in *Capsicum* conservation, characterization and sustainable use.



Multi- trait QTL modelling for sets of related traits

Fred van Eeuwijk^{1,3}, Huange Wang¹; Maaïke Wubs¹; Ep Heuvelink²; Nurudeen Alimi¹; Marco Bink¹

¹Biometris, Wageningen UR, The Netherlands;

²Horticultural Production Chains, Wageningen University, The Netherlands;

³Centre for BioSystems Genomics, Wageningen, The Netherlands.

An attractive approach to the improvement of complex traits is by dissection of the complex traits into simpler component traits. The philosophy behind this approach is that the complex trait is based on many QTLs that show QTL by environment and epistatic interactions, while the underlying components will have a small number of QTLs without interactions. To identify co-location of QTLs for complex traits with those for component traits, QTL mapping approaches need to consider multiple traits simultaneously. Another frequently occurring context in which multiple traits would require simultaneous modelling is that of the modelling of metabolites belonging to a particular pathway. A traditional preferred statistical tool for modelling QTLs for multiple traits, and also multiple environments, is the mixed model. In the traditional multi- trait mixed model approach, a multivariate normal model is assumed for which the mean is determined by fixed trait intercepts together with QTL effects, while the random part, containing the residual, polygenic genetic effects determines a multivariate variance covariance matrix. In the classical mixed model approach, all traits are treated in a parallel fashion, i.e., no hierarchical, or 'causal', relations are assumed to exist between the traits. However, when modelling physiological or metabolic processes, typically part of the relations between traits is clearly hierarchical. In the presentation, the mixed model approach to multi- trait QTL modelling will be described and possible extensions in the direction of hierarchical and causal modelling will be discussed.



The soybean root hair: a single cell model for systems biology

Gary Stacey, University of Missouri, Columbia, MO, USA

The root hair is a single cell extension of the root epidermis whose primary function is to expand the root surface area to facilitate water and nutrient uptake. However, the root hair is also the primary site of infection by rhizobia, leading to the formation of a nitrogen fixing symbiosis. Our laboratory continues our characterization of the soybean root hair cell as a model to investigate the rhizobial infection process and, more importantly, as a platform for systems biology. Published and unpublished work has now characterized the early stages of the rhizobial infection process at the level of the transcriptome, proteome, metabolome, phosphoproteome, as well as profiling small RNA expression and the chemistry of the root hair cell wall. Our data show that the root hair cell is extensively remodeling as a consequence of rhizobial infection. The data generated from our project is deposited in our soyKB.org database, which provides tools to integrate the various data and to carry out a variety of analyses. This database is evolving into a platform not only for storage and analysis but to generate new hypotheses that can be experimentally tested. Complex regulation is a feature of the rhizobial infection process and new algorithms for the analysis of co-expression data are providing avenues to investigate this complexity. Recent highlights in the laboratory relate to the study of protein phosphorylation that occurs very rapidly in the root hair cell upon rhizobial infection. We identified 240 proteins whose phosphorylation varies significantly after inoculation. Our work on small RNA is also providing some interesting new insights. We identified over 90 miRNAs whose expression levels responded to rhizobial inoculation. We have identified the mRNA targets for these miRNAs. In the few cases examined, we see that ectopic expression of specific miRNA can either significantly increase or decrease nodule numbers, supporting a key role for these regulators in nodulation. These and other results will be described, as well as how we intend to extend this model system to explore abiotic stress.



Conservation and use of underutilized genetic resources in Latin America and policy aspects

Gea Galluzzi¹, Isabel Lopez Noriega², Marleni Ramirez¹

¹Bioversity International, Regional Office for the Americas, c/o CIAT, km 17 Recta Cali Palmira, Colombia.

²Bioversity International, Via dei tre Denari 472/a, 00057 Maccarese, Rome, Italy.

In Latin America, a continent home to a number of centers of crop domestication, native agrobiodiversity includes many under-utilized or neglected species and varieties. This genetic treasure holds great potential for diversifying agro-ecosystems, stabilizing production and addressing climate change challenges, while improving people's food security and sovereignty. However, for these expectations to be met, research strategies and policy measures are needed which effectively strengthen conservation, improvement and increased use of these resources. Concerns have been voiced about the tendency of international policy frameworks to directly or indirectly contribute to the marginalization of already neglected genetic resources, for example by focusing on a narrow set of "major" crops or determining difficulties in access to and exchange of other species and traditional varieties. Results of a study on the influence of international policy frameworks on continued conservation and use of underutilized and neglected genetic resources highlighted experts' perceptions on the status of minor crops and varieties in Latin America as well as cases and contexts in which international policies and their implementation at national level have indeed introduced additional complexities or on the contrary, provided support to overcoming existing challenges. Further analyses looked at a number of national or local level experiences aimed at the rescue, conservation, and use of underutilized and neglected species especially at the on-farm level, where most diversity of these crops is maintained by small scale farmers. It is suggested that if the role that minor crops may play in food security, nutritional and ecosystem diversification is to be enhanced, multidisciplinary and flexible interventions are needed, supported by similarly flexible and innovative policy and institutional arrangements to make results sustainable over time. The main challenge resides in the ability and vision to bridge formal (scientific, market-based and policy) approaches with the realm of informal and dynamic institutions through which minor crops and varieties are maintained by farming communities. Those interventions which applied holistic research and development approaches and took into account traditional practices and informal institutions alongside more formal public and private sector interventions were most successful. Participatory approaches, involving communities in activities ranging from monitoring genetic erosion to crop breeding, seed production and dissemination, were especially effective when accompanied by more formal policy support and recognition. In light of these examples, overall challenges, gaps and opportunities in terms of type and scale of interventions to promote conservation and use of underutilized genetic resources are discussed.



Progress in breeding for drought and flooding tolerance in soybean

J. Grover Shannon, Safiullah Pathan and Henry T. Nguyen,

Division of Plant Sciences, University of Missouri, Columbia, MO 65211 USA
shannong@missouri.edu

Abiotic stress in soybean is primarily due to too little or too much water. Drought and flooding are abiotic stresses that are first and second, respectively in reducing soybean yields worldwide. Soybean strains and germplasm lines have been identified that have higher tolerance to stress that occurs on drought-prone soils and wet, slowly drained soils. Plants use different mechanisms to cope with drought stress, namely drought avoidance and drought resistance. Mechanisms for drought resistance include water use efficiency slow canopy wilting, root plasticity, sustained nitrogen fixation under drought stress, and tolerance to dehydration stress. Flooding in soybean often occurs when soil is poorly drained or when rainfall or irrigation is excessive. Flooding tolerance has been associated with resistance to phytophthora root rot and morphological changes associated with the formation of aerenchyma tissue or continuous gas-filled channels for transport of oxygen from the above-ground shoot to the root. Sources of tolerance to drought and flooding have been identified among exotic plant introductions. Breeding lines and/or varieties with good productivity have been developed for use in breeding programs to improve soybeans for both drought and flooding. In addition, genes have been identified which are positively associated with improved productivity under these two abiotic stresses. Understanding genetic mechanisms related to physiological and morphological factors responsible for plant tolerance will be a key for much greater improvement to overcome soybean injury from too little or too much water. Insertion of genes via biotechnology offers great promise for improving stress tolerance but, regulatory approval and intellectual property issues to get biotech traits to the market place is very costly and can take many years. Natural genetic variation is a key resource to improve abiotic stress tolerance in soybeans. Although there are nearly 200,000 soybean accessions maintained by 160 institutions and 70 countries, studies that report variation among available soybean germplasm for tolerance to drought, and flooding are limited. Genes for higher tolerance to these stresses is likely to be found within accessions in world soybean collections. However, evaluation for tolerance to drought, and flooding is difficult and dependent on screening environments and methods where each stress can be consistently imposed year after year and selection for tolerance is reliable. Varieties with higher tolerance will greatly improve production of soybeans under such extreme conditions.

Keywords Abiotic stress, Stress tolerance, Drought, Flooding, *Glycine max*



Novel diversity in wild peanut relatives and the importance of their conservation in South America

Guillermo Seijo, Germán Robledo, Alejandra Ortiz, Marina Grabiele, Sebastian Samoluk, Diego Carísimo, Antonio Krapovickas and Graciela Lavia

Northeast Botanical Institute (IBONE, UNNE-CONICET) and Faculty of Exact and Natural Sciences, Northeast National University, Corrientes, Argentina.

Most of the collections of *Arachis* germplasm have been performed during the 70's, 80's and 90's when the accessibility to many of the natural localities where the species grow was very difficult, especially in Bolivia. Field collections performed during the last ten years, particularly in Bolivia and Argentina, allowed a better screening of the distribution of the genus in these countries and the collection of many samples of different species. The biosystematics analysis of these new materials together those present in ex-situ collections revealed novel variability in the wild germplasm. Taxonomically, 8-10 new species are being formally described. Morpho-anatomical studies revealed some new features, particularly in fruits. From a chromosome point of view, the species showed a wide variability in karyotype structure, which were used to arrange the species of section *Arachis* in a new genome classification. The isolation of DNA repetitive elements and the analysis of their distribution and representativeness in the karyotypes of the species, demonstrated that they are one of the most important component in determining the variations detected in the chromosome structure. Nuclear and chloroplast sequences of non-transcribed or spacer regions demonstrated a high variability among and within species. The nuclear 5S rDNA sequences showed that the alleles are restricted to species, while the variability detected in chloroplast marker is not restricted to species, but instead, it is geographically structured. The bulk of data strongly suggest that the variability present in nature is extremely underrepresented in the international and local germplasm banks of *Arachis*. In this context and because the habitats where *Arachis* species lived are being rapidly transformed, there is an urgent need of collection and evaluation of new materials to gain a comprehensive knowledge of the variability present in *Arachis* wild germplasm and to optimize its use in breeding programs.



"CIMMYT's breeding strategies for raising yield potential of wheat"

Hans-Joachim Braun

CIMMYT-Mexico. e-mail: H.J.Braun@cgiar.org

Wheat provides in both developing and developed countries on average around 20% of the food calories and 20% of the protein for human consumption. To meet the increased demand for wheat during the next decades from a growing population, average global wheat productivity needs to increase from currently around 1% to 1.6% per year. We believe these yield increases can be achieved and will come in developing countries from breeding for increased genetic yield potential and disease resistance and equally important, improved agronomic practices. CIMMYT's wheat breeding philosophy and methodology strives to develop germplasm with high and stable yields across a range of environments, geographically or temporally. We believe that wide adaptation to a broad range of environments, in place and time, becomes increasingly important to develop cultivars that can cope with the climate extremes that occur across a range of locations, or at one location over years. There is also empirical evidence that wheat yield potential is expressed across a wide range of environments including those affected by water deficit, high temperatures, salinity and at low N levels. The need to enhance the genetic yield potential of wheat is widely accepted, as genetic gains from wheat breeding and improved agronomic practices have decreased in recent years, creating a sense of urgency. To maintain historic genetic yield gains of 0.8% - 1% per year – other productivity gains come from better agronomy practices– a wide range of interventions are required. Scientific evidence suggests that the yield potential of wheat could be increased by 50% or more through the genetic improvement of photosynthetic capacity, while parallel improvements in plant architecture would guarantee positive impacts in farmers' fields. To meet this long-term research challenge, a wheat yield consortium has been formed with more than 30 international partners to increase photosynthetic capacity, optimize spike fertility and maintain lodging resistance under increased grain weight. In the meantime yield increases will be realized through conventional and molecular approaches and will continue to come from sharing elite lines for crossing; sharing data of international nurseries; better parental characterization through precision phenotyping platforms and combining molecular, physiological, quality and field trial data; breeding methods that allow to handle larger number of plants in segregating populations; increased number of lines evaluated in yield trials; routine application of physiological tools in selection; exploitation of distant gene pools, e.g. winter x spring crosses, use of synthetic derived wheat lines and a much more systematic utilization of genetic resources and use of translocations. Genomic Selection as a new breeding tool is currently evaluated. CIMMYT is also working on transgenic and hybrid wheat.



Exploiting the root system to improve crop adaptation to climate change

Henry T. Nguyen and Valliyodan Babu

National Center for Soybean Biotechnology and Division of Plant Sciences, University of Missouri, Columbia, MO 65211, USA

Climate change is expected to cause a higher frequency of drought and temperature extremes, which will severely affect crop yields and food security in the future. Understanding the root system architecture will contribute to the strategies for genetic improvement of crop adaptation and productivity under water and temperature stress environments. Deeper and proliferate root system help extract enough water and nutrients under these environmental conditions. Extensive screening for natural genetic variation in root system architecture in major crop plants including soybean has identified germplasm which exhibit genetic diversity in root system developmental plasticity in response to climate changes. These discoveries enable physiological and genetic analysis of the regulatory mechanisms involved in the stress adaptation processes in crops. Research programs focusing on an integrated genetics and genomics approach in major crops including rice, maize and soybean help understand molecular processes from transcriptome to phenome. Comprehensive expression profiling using current 'omic' technologies and comparative genomic analyses were performed to dissect regulatory networks and genes associated with the root development and root system architecture under these stress conditions. Drought and temperature stress responsive gene discovery and the translational genomics of these candidates using model plants provided encouraging results; however the field testing of transgenic crop plants for better performance and yield is still minimal. This presentation will highlight the global research strategies and recent discoveries towards better root system architecture in some important food crops such as rice, maize, and soybean for enhanced stress resistance and yield.



Marker-assisted selection in the era of whole genome sequencing

Henry T. Nguyen

National Center for Soybean Biotechnology and Division of Plant Sciences, University of Missouri, Columbia, MO 65211, USA

In recent years, the remarkable development of next-generation sequencing technologies allowed plant molecular breeding to experience major progress in marker-assisted selection (MAS). Next generation sequencing technologies are revolutionizing traditional biparental population mapping, association mapping and molecular breeding. The advent of sequencing –based genotyping approaches enables the construction of ultra-high density linkage maps, precise mapping of genes/QTLs, and genome-wide association studies. These technologies significantly contribute towards better understanding of the genetic architecture of complex traits and it has been shown its application in breeding program for crop improvement through whole genome association studies and genomic selection. This strategy has been successfully demonstrated in the model plant *Arabidopsis* and different crop plants, such as rice, maize, barley, and soybean, as results of the integration of genetic mapping, marker development, marker-trait association validation, and MAS application. Cost and time effectiveness are major logistical concerns in marker-assisted breeding programs. However, with the significant reduction in genotyping costs due to large-scale high-throughput genotyping platforms in conjunction with precision phenotyping methodologies have made it possible to execute MAS, marker-assisted recurrent selection (MARS), and genomic selection (GS) for complex agronomic traits that were previously inaccessible.



Genetic transformation of fruit crops.

Carlos Aguirre, Catalina Álvarez, Hayron Canchignia, Álvaro Castro, María Miccono, Christian Montes, Marisol Muñoz, Blanca Olmedo, Marcelo Ortega, Alejandra Ramírez, Julia Rubio, Evelyn Sánchez, Fabián Santander, Eduardo Tapia, and Humberto Prieto.

Instituto de Investigaciones Agropecuarias, La Platina Research Station, Santiago, Chile.

Biofrutales Consortium for fruit technology, Santiago, Chile.

Genetic transformation provides the means for adding single horticultural traits in existing cultivars without modify their commercial characteristics. This capability is particularly valuable for perennial plants and fruit tree species, in which conventional breeding is hampered by their long generation time and juvenile periods, complex reproductive biology, high levels of heterozygosity, limited genetic sources and linkage drag of undesirable traits from wild relatives. In addition, gene transfer technologies for fruit trees and perennial species take the inherent advantage of vegetative propagation used for their reproduction, allowing the application of a high scale production of the desired transgenic line starting from one successful transformed line. Despite this opportunity, final setting of transformation protocols in this type of species, including fruit trees, endures major limiting factors preventing the development of new varieties: a) explants recalcitrance to regenerate adventitious transformed shoots and b) a limited regeneration capability, usually extended to just few genotypes. It will be presented the road between the establishment of transformation methodologies on particular species of both *Vitis* spp. and *Prunus* spp. and the achievement of transformation procedures for new, eventually more recalcitrant, cultivars or genus members. Genetic transformation of *Vitis* sp. has mainly relied on the use and availability of somatic embryogenesis (SE) procedures. Regeneration of whole Gloryvine (*V. vinifera* x *V. rupestris*) plants was first achieved from SE previously obtained in this hybrid by culturing of anthers. Since then, successful procedures have made possible SE in *V. vinifera*, *V. labruscana* and *V. rotundifolia*. Recently, SE in 'Thompson Seedless' was scaled-up using an *air-lift* bioreactor. This knowledge fused to the characterization of some of the kinetic parameters involved in grapevine SE, led to the design of new developments in SE for rootstocks ('Harmony', 'Freedom' or 'Salt Creek') and more recalcitrant cultivars ('Red Globe'). In case of *Prunus*, European (*P. domestica* L.) and Japanese (*P. salicina* L.) plums have been the more successful rosaceous fruit models to regenerate and transform within this genus. Former regeneration protocols using *P. domestica* seed-derived explants led to the generation of the *Plum Pox Virus* (PPV) resistant C5 event ('HoneySweet') which has been deregulated in 2009. Dissection of four derived media based on the system used in C5, did not show differences in the regenerative responses of *P. salicina*, leading to the regeneration of two *P. salicina* varieties ('Larry Ann' and 'Angeleno'). Stable *P. salicina* GM lines have been already generated by this strategy in order to introduce the green fluorescent protein gene and more recently, a hairpin dsRNA inducing construct to evaluate silencing of the PPV coat protein gene.



Management System for weeds and stalk control in Glyphosate Tolerant Cotton Fields

Igor Rezenze Coelho

Monsanto do Brasil Ltda.

Weed resistance is a growing problem. And regardless of the farming system and what weed control product used, a single herbicide mode-of-action is simply no longer adequate to protect your yields and long-term profitability. In high productive environments we should avoid the negative effects caused by weeds, so management practices are extremely important. Here are some tips that can make all the difference: Use practice integrated weed management during the off season mainly (use of association of herbicides with different modes of action and covers); Start the culture in clean (make an effective control early in the drying and if necessary use a pre-emerging in areas of high weed pressure); Apply the correct dose of the products used in its control system, observing the best conditions for the application; Monitor the results of the application, avoiding the establishment of populations remaining in the culture; Use the best agronomic practices to maximize crop competitiveness with weeds, avoiding also the dispersal of seeds by farm implements. The control of cotton stalk has always been seen as of great difficulty for the time when the crop is harvested (drought and low plant vegetation) and by the characteristics of a plant species that has a large root system and is a perennial crop conducted as an annual crop. For Roundup Ready Cotton, the control is mainly done chemically through the use of 2,4-D, complemented by mechanical methods. The 2,4-D can have foliar and root absorption giving a residual effect for 20 days. The minimal dose to be considered is around 2L/ha in each application. Good soil moisture conditions has great favorable effect in this type of control. Sequential applications of 2,4-D during post harvest over resprouted plants and over the planting line right after mowing has a positive effect on chemical control. 2,4-D application right after mowing and 45 days posterior to mowing over the planting lane of the culture. According to Bianchini(2005), two sequential applications separated by 45 days each of 2,4-D + glyphosate + mechanical intervention demonstrated great result. Cotton Stalk with weak sprouting in the basal area – herbicide application over the entire plant before mowing. Cotton stalk with intense sprouting in the basal area – herbicide application before and after mowing. Recent works have demonstrated that two applications of 2,4-D associated with Amonium Gluphosinate has great effect in controlling and reducing sprouting of cotton stalk.



TRAITS AND TOOLS TO IMPROVE WHEAT NITROGEN USE EFFICIENCY

Le Gouis Jacques, Bogard Matthieu, Bordes Jacques, Balfourier François, Allard Vincent

INRA, UMR 1095, Génétique, Diversité et Ecophysiologie des Céréales, F-63039, Clermont-Ferrand, France

UBP, UMR Génétique, Diversité et Ecophysiologie des Céréales, Clermont-Ferrand, France

A large part of nitrogen (N) fertilizer used worldwide is applied on bread wheat. Economical and ecological factors plead for an optimization of the ways in which this input is used by the crop. A better understanding of the genetic determinism would help in breeding more efficient cultivars. Three main integrative traits were considered: (i) N use efficiency and its components (utilization and absorption efficiencies), (ii) grain protein deviation which is the deviation from the negative relationship between grain yield and grain protein concentration and (iii) the response to N limitation. Using different panels and populations, we first showed that a large genetic variation existed for these traits and their components. This genetic variability was characterized using both direct measurement of agronomically important traits and non destructive indirect measurement such as near-infrared spectrometry giving an access to the kinetic of relevant traits (leaf N...). Aboveground organs were mainly considered and complementary studies were conducted on root traits. We showed that root biomass and root N could be ignored in a first step when estimating N use efficiency because of their extremely low participation to the whole plant N budget. We then carried quantitative trait loci (QTL) detection using bi-parental mapping populations, connected mapping populations and panel of association genetics. Several QTL linked to N use efficiency and grain protein deviation were identified. A large part of these QTL colocalized with major QTL for flowering time, exemplifying the close relationship between plant development and N use. This was particularly the case when looking at QTL involved in grain protein content and post-anthesis leaf senescence. We also identified chromosomal regions linked to the response to N fertilizer level using a panel of association genetics. Finally, one chromosomal region on chromosome 3B was further dissected. A meta-analysis confirmed the implication of this region in several wheat mapping populations and possibly other cereal species. Physical mapping and sequencing enabled to identify conserved genes within the confidence interval of the QTL. The most probable candidate is a glutamate synthase (GOGAT), an enzyme involved in N assimilation. All these studies, combined with the development of high throughput phenotyping methods, should bring new opportunities to improve wheat N use efficiency for grain yield and grain protein production.



Ecology Based Breeding and Seed Systems for African Crops

Speaker: Dr. Jane Ininda

Access to improved seed is viewed as the principal constraint to raising small holder productivity in Africa. The development of improved crops for Africa has taken a new dimension in the last decade. This is because of increased international support to local breeding programs and seed systems for Africa aimed at increasing the number of improved crop varieties. The approach known as ecology-based breeding systems focuses on localized model for crop variety development, release and access to seed for farmers in Africa. In the past crop varieties available to farmers were those with broad adaptation. This limited the farmer acceptability of released varieties and the result has been that farmers got trapped to growing landraces or old varieties developed 30-40 years ago. Variety development for Africa requires adaptation to specific ecologies and should take care of inherent cultural, crop species and/or cultivar diversity. This also implies that Africa must deviate from the centralized breeding and seed systems adopted earlier for food crops because this system has not benefited farmers. Africa is lagging behind US and Asia when it comes to access to improved varieties for her farmers. Farmers in Africa are precise in their preference for taste, ease of processing, storage, and are adaption to their environments. This paper will also highlight results of the AGRA 'Program for Africa's Seed Systems', a localized breeding approach in process for Africa today. Since 2007 the Program for Africa's Seed Systems has supported 120 breeding operations in twelve important crops for Africa; maize, rice, wheat, sorghum, millet, beans, cowpea, soybean, groundnuts, cassava, sweetpotato, and banana. This has led to the development and release of 367 improved crop varieties of which 218 have been commercialized through local private seed companies in Africa. Variety release in the last five years is localized on ecology and needs of farmers. The total number of varieties released differ from country to country; Burkina Faso, 14 varieties released; Ethiopia, 9; Ghana, 14; Kenya, 67; Malawi, 23; Mali, 65; Mozambique, 45; Nigeria, 6; Rwanda, 38; SierraLeone, 16; Sudan, 9; Tanzania, 31; Uganda, 30 and Zambia, 4. The development and release of maize hybrids is more advanced in Kenya where 27 hybrids have been released in the last five years; while in Tanzania it is cassava, 16 varieties; for Mozambique it is cassava (12 varieties) and sweet potato(15 varieties); Rwanda, 28 varieties of beans have been released in the last five years, and in Uganda, 10 varieties of groundnuts while in Mali 18 varieties of rice. The availability of these improved crops has stimulated development of 70 local seed companies and production of 40,000 MT annually.



“Nutritionally Enhanced Crops”

Iron biofortification in rice: what have we learned so far?

Janette Palma Fett

Universidade Federal do Rio Grande do Sul, Centro de Biotecnologia and
Departamento de Botânica, Porto Alegre, RS, Brazil.

Rice and most staple cereals contain low iron levels, most of which is lost during grain processing. Populations with diets consisting mainly of cereals are especially prone to iron deficiency, which affects about two billion people. Supplementation or food fortification programs have not always been successful. Crop iron fertilization is also not very effective due to iron soil insolubility. An alternative solution is iron biofortification by generating cultivars that efficiently mobilize, uptake and translocate iron to the edible parts. The strategies used for iron biofortification of rice include conventional breeding and directed genetic modification, which offer the most rapid way to develop iron-rich rice plants. While classical breeding is able to modify the contents of inhibitors of Fe absorption, transgenic approaches have focused on enhanced iron uptake from soil, xylem and phloem loading and grain sink strength. The percentages of the recommended dietary Fe intake reached by independently developed transgenic plants were calculated and will be presented. Although the discovery of new QTLs and genes related to iron biofortification is extremely important, interdisciplinary research is needed for future success in this area. Novel results will be shown, suggesting that mineral remobilization from vegetative tissues to rice grains is dependent of plant Fe nutrition and that continued uptake and translocation of minerals from the roots during seed fill are probably more important than mineral remobilization from other plant organs.



Meeting Education Needs in Southeast Asia and Africa

C. Jerry Nelson, Professor Emeritus of Plant Sciences, University of Missouri, Columbia, MO 65211, USA.

Increased use of the internet and social networking inspires developing countries to have life styles and food supplies like developed countries. The Arab Spring of 2011 taught the international community how rapidly change can occur. Objectives are to share experiences and perspectives on developmental steps and how education can assist. Crop science is foundational, but it alone can not drive the change. It provides new tools and technologies that offer potential, while other disciplines play expanding roles in advocacy and public support to adopt change. Subsistence agriculture has an almost exclusive goal of food production. As incomes increase there is a gradual shift in public priorities to add non-food outcomes including, almost sequentially, reduced soil erosion, improved water quality, improved food safety, improved food quality, and maximal biodiversity of plants and wildlife. Simultaneously, as crop production improves in a sustainable way, increased social values of agriculture are expected including worker safety, human rights, animal rights and aesthetic qualities of the landscape. Already, about 50% of the market value of rice in Japan and South Korea supports primary production while the remaining 50% subsidizes ecosystem and social services. The continued demand for organic production in developed countries adds more challenges, whereas growing acceptance of GM crops in developing countries adds more potential. Public expectations will always prevail in market economies. Thus, education is essential for agriculturalists to improve crop production in developing countries, but it is also essential for policy makers, innovators and the general public to effect change. Population growth in Southeast Asia, Africa and even India, will accentuate needs for food; a challenge that is further heightened by projected changes in global climate. Education efforts on production technologies must be integrated with those for marketing, processing and distributing the food, often initiated at the community level. Engagement of private industry is essential. Several documented cases indicate it takes a generation for marked change, about 20 to 30 years, but it needs to be shortened quickly. Examples from Asia and Africa will be compared.



Progress in breeding for drought stress tolerant maize in Eastern and Southern Africa

Jill E Cairns¹, Gary N Atlin², Tsedeke Abate³, Wilfred Mwangi³, Peter Setimela¹, Babu Raman⁴, Christian Thierfelder¹, PH Zaidi⁴, Sudha Nair⁴, Biswanath Das³, Cosmos Magorokosho¹, Amsal Tarekegne¹, Jose Crossa⁵, George Mahuku⁵, Benhilda Masuka¹, John MacRobert¹, and BM Prasanna³

¹International Maize and Wheat Improvement Centre (CIMMYT), Harare, Zimbabwe

²CIMMYT, Department of Plant Breeding and Genetics, Cornell University, Ithaca, USA

³CIMMYT, Nairobi, Kenya

⁴CIMMYT, Patancheru, India

⁵CIMMYT, El Batan, Mexico

Drought is a major cause of low maize yields in eastern and southern Africa (ESA). In the late 1990's CIMMYT initiated a product-orientated maize breeding program in southern Africa to increase maize yields in drought prone environments. Early hybrids from this program had a 40 % yield advantage compared to commercially available hybrids. Recent on-farm trials of new hybrids have a 35 % yield advantage against farmers' own varieties in low yielding environments. However the anticipated negative impacts of climate change on maize production in this region, combined with predicted population growth, highlight the urgent need to further improve maize yields in ESA. Recent advances in phenotyping, conventional and molecular breeding will provide powerful tools to accelerate breeding gains and dissect stress adaptation. Double haploid (DH) technology increases the efficiency of line development by reducing the time taken to reach homozygosity in conventional breeding from approximately six seasons to one season. Tropical-adapted maize inducer lines have recently been developed with an induction rate of 10%. The ability to apply DH technology within the tropical maize breeding will significantly improve the genetic gains in the breeding programmes. Climate projections show growing season temperatures will increase within drought prone regions. Earlier research in model species suggested the combined effect for drought and heat stress is unique. Our results show tolerance to combined drought and heat stress in maize is genetically distinct from tolerance to the individual stresses, and tolerance to either drought or heat stress alone does not confer tolerance to the combined effect of drought and heat stress. Many current drought donors are susceptible to drought stress at elevated temperatures and new donors with tolerance to combined drought and heat stress must be incorporated into maize breeding pipelines. Recent analyses of managed drought trials highlighted the need to reduce the size of the residual variance relative to the genetic component of variance to increase genetic gains. Work is underway to decrease the effects of field variability, thereby increase the genetic signal to noise ratio to detect real differences between lines. Association mapping (AM) and genomic selection, using 55 K SNP data, are also being applied in maize breeding for ESA. AM has identified nine genomic regions associated with grain yield under drought stress. Individually, the regions explained 4.6 to 7.6 per cent of phenotypic variance and approximately 12 to 22 per cent genetic variance for GY under stress. Several rare alleles with large positive effects on grain yield were also identified. Yield improvements through both conventional and molecular breeding will be critical to the resilience of maize cropping systems in the face of climate change. However further improvements in yields can be made if genetic approaches are combined with improved management options. Conservation agriculture practises have been shown to improve the soil water balance thus reducing the severity of a drought episode. This multi-disciplinary approach to improving maize yields in ESA will play an essential role in adapting maize-based cropping systems to the potential effects of climate change.



Corn production in Brazil: Past and Future Perspectives

João Carlos Garcia

Embrapa Milho e Sorgo – Sete Lagoas, Minas Gerais - Brazil

Corn is a strategic product for Brazilian agriculture. It is grown throughout the country, by the majority of the Brazilian farmers and is fundamental for production of animal protein at low cost. It is also an important component of the Brazilian agribusiness exports, as grain, or as feed for export products such as poultry, pork and beef. The corn crop in Brazil is produced in two seasons. The Summer season that begins in late August in the South region and continues until October/November in the Southeast and part of Center West regions (in the Northeast this period occurs at the beginning of the year) and the corn second crop season, which is planted in February/March, in the Center West region and in Parana and São Paulo states. The corn area in the Summer season has decreased by competition with soybeans, what was partially offset by the second crop season area. The corn producing regions in Brazil can be divided into four clusters. Summer subtropical - regions that allow the establishment of Summer (corn and soybeans) and Winter (wheat, oats, etc.) crops and have temperature limitations for corn in the Winter. Summer tropical - regions with tropical climate and dry Winter, which do not allow the establishment of Winter crops. Second crop season - planting of Autumn/Winter in areas where the rainy season is longer, but with lower risk of frost in Winter. Northeast - the semi-arid region, that presents low and variable rainfall and short period favorable for corn crops. In the subtropical harvest it is possible greater variations in Summer/Winter crop rotations and the use of maize hybrids with regional characteristics. In the season of Summer tropical production, the production systems are very similar to the ones of the Summer subtropical, but the options for ground coverage is reduced in the Winter. The use of *Brachiaria* for this propose is increasing. In the second crop season, the corn is important for no-tillage system, allowing the soybeans/corn rotation in the same year. Second crop season plantations were performed with low input at the beginning but currently the plantings at this period are conducted using production systems adapted to the more restrictive conditions of climate, raising the crop yields year by year. The corn production in the Northeast is the challenge for new corn technology development in Brazil, due to the need to supplement the regional supply and the variable climate conditions that increase the economic risk of using modern inputs. The outlook for corn production in Brazil is favorable due to the proved ability to develop viable production systems in regions with climatic limitations. In addition, the new international market conditions enable the growth of agricultural productivity, opening a channel for export the surplus production. Productivity gains will come largely from increased managerial capacity of farmers to use the most advanced technology possible, at competitive costs.



Energy Cane-related Grasses as Bioenergy Feedstocks for Texas

John Jifon and Jorge DaSilva

Texas A&M AgriLife Research Center, Weslaco, TX, 78596, U.S.A., jljifon@ag.tamu.edu.

Sugarcane (*Saccharum spp.*) and its tropical relatives are among the leading candidates as dedicated feedstock crops for production of biofuels from lignocellulosic biomass, thanks to their high-yield potential. Besides high-yield, the suitability of these species as biofuel feedstocks also depends on their cell wall characteristics, since the relative proportions of cellulose, hemicellulose, and lignin are major factors determining the appropriate conversion technology. These two aspects of feedstock characteristics are part of a research effort to identify advanced feedstocks that are adapted to tropical and subtropical production regions of the U.S. We have recently screened over twenty high-fiber, low-sugar accessions from the sugarcane breeding program for yield potential and cell wall characteristics. Key traits of interest include fast growth, tiller density, high productivity per unit land area, high dry matter content at harvest, cell wall characteristics, energy content, and high resource-use efficiency. Non-optimized dry biomass yields of plant cane and first ratoon crops ranged from 31.7 to 49.9 Mg/ha, and varied considerably among the genotypes evaluated. Productivity of the highest-yielding genotypes was better correlated with tiller density than any other yield component. These genotypes also had higher fiber and low moisture contents at harvest compared to the low-yield genotypes. Continued physiological and agronomic characterization of input requirements will help identify genotypes well-suited to marginal lands and hence avoid potential competition with food production.



Potential use of sugarcane and relatives as a feedstock for BioEnergy production

José Bressiani, PhD, Graal Bio Investimentos SA. São Paulo, Brazil

Mauro Xavier, PhD, Instituto Agronomico de Campinas. Ribeirão Preto, Brazil Mauro

Violante, MS, Monsanto. Campinas, Brazil

Gonçalo Pereira, PhD, University of Campinas. Campinas, Brazil

The last century was the scene of an extraordinary social and economic development of mankind. This development had the fossil energy as one of its pillars. The discovery of petrol led the society to shape a development model highly dependent on this source of energy, which has finite resources and also promotes a big increase on the greenhouse gases, with unforeseeable consequences for the human beings as well as the entire life. It is imperative that we change the pillars of energy from fossil to renewables that will be more sustainable and less aggressive to the environment. One of the sources of this new energy platform, probably the best, is biomass. By the other hand to produce biomass we will use land and when we talk about land we must be very analytical because it is imperative that we do not competes with food production and respect the forest and water preservation. Fibrous plants bring several advantages and fit well within the requirements deemed important to be elected as producers of biomass. Among these characteristics we have the high processing capacity of solar energy into biomass, fast growth, long-term canopy, possibility of large-scale production. Despite of that this plants are adapted to suboptimal environments that allows its production not compete with food production because it requires less energy input, bringing marginal lands into production with its all social-benefit consequences. Among the fibrous plants, SUGARCANE or, better, ENERGYCANE has one of the biggest potential for biomass productions. Energy Cane was first named in Louisiana and Puerto Rico (Giamalva et al., 1984, Samuels et al., 1984). At that time, Alexander (1985) demonstrated that, with a penalty of 25 to 35% in sucrose, it would be possible to increase the total biomass of up to 100%. In Barbados, Rao et al. (2007) found results of 45 tons of dry matter per hectare (TDMH), 72% over a range of commercial varieties. In Brazil, at Canavialis, Matsuoka et al. (2012) found results of 40 tons of fiber per hectare (equivalent to 60TDMH), 100% over the commercial varieties. More recently, Xavier (personal communication, 2012) identified clones of energy cane in IAC breeding program producing 2.5 to 3.0 times more biomass over commercial varieties. Besides the current breeding programs in Brazil that are looking for energy cane varieties, two other private breeding programs were started specifically to develop energy cane varieties. One of these, the GraalBio is also creating a big platform in the country that covers not only Energy Cane varieties development, but also biochemical plants based on enzymatic conversion, a laboratory and pilot plant to promote increase and/or development in the pre-treatments, hydrolysis and fermentation process. The main goal is to create a new refinery platform where the nafta will be not fossil, but green. And we believe that among the biomass crops, Energy Cane will be the most attractive due to the big potential to produce biomass in comparison with other fibrous plants, like sugarcane (2x), eucalyptus (3x) and elephant grass (4x) and also with other grasses like sorghum (1.5x).



MAIZE PRODUCTION AS FACTOR OF THE NO-TILL SYSTEM SUCCESS

José Eloir Denardin¹; Rainoldo Alberto Kochhann²

¹Researcher, Embrapa Trigo, Rodovia BR 285, km 294, Caixa Postal 451, CEP 99001-970 Passo Fundo, RS, Brasil. E-mail: jose.denardin@embrapa.br

²Researcher, Embrapa Trigo, retired, Passo Fundo, RS, Brasil. E-mail: rainoldoak@gmail.com

No-till is a conservation practice described as seeding without intense soil mobilization. This practice fulfils only two precepts of conservation agriculture - soil minimum tillage and crop residues maintenance on the soil surface. Under conditions of the tropical and subtropical regions of Brazil, these precepts are insufficient to promote soil conservation. The main reason for this is the high crop residues decomposition rate, which prevents permanent soil coverage. Thus, the no-till adoption in these regions needs to be approached as a management system - no-till system. Therefore, the success of no-till system adoption is based on the following practices: soil mobilization only in the seeding row; crop residues maintenance on the soil surface; crop species diversity; harvesting-seeding process, namely minimization of the interval time between harvest and seeding; organic material input to the soil in quantity, quality and frequency compatible with the soil biological demand; and permanent soil coverage. In this context, the harvesting-seeding process is a way to: facilitate the plant species diversification in different production systems; increase the opportunity for greater number of crops per year; maintain permanent soil cover; and improve the organic material input to the soil. In Brazil the main grain production system is focused in monoculture of soybean (*Glycine max*) under no-till. This production system does not promote soil conservation nor ensures the benefits expected of no-till system, due to the low quantity and frequency of crop residue input to the soil and its fast decomposition. For tropical and subtropical conditions, the grasses in the production systems play an important conservation role. Thus, to mitigate this problem, the Brazilian agricultural production systems have been diversified with integration of plant and animal species including grain, pasture and forest in intercropping or crop rotation. In consequence the number of crops per year has been incremented from one up to three. The feasibility of this innovation has been promoted by inclusion of some grasses in the soybean production system as second harvest in the year or as cover crop. However, maize (*Zea mays*) and intercropping maize-*Brachiaria* spp. has been highlighted for promoting two grain harvests per year, and also supplying pasture during four months. This production model is a result of no-till system success and generates high technical and economic benefits.



The potential of native germplasm for forage production

José F. M. Valls (jose.valls@embrapa.br and jose.valls@pq.cnpq.br)

Embrapa Genetic Resources and Biotechnology and CNPQ Fellow (National Research Council), Brasília, DF, Brazil

Brazilian forage breeding programs are below the needs for a country of continental dimensions. They target too few species, and grass cultivars are mostly exotic. The main forage cultivars resulted of phenotypic selection based on agronomic merit, and, just a short time ago, this kind of selection would depart from very small collections. Present trends include acceptance of the value of broad collections, a clear concern on the mode of reproduction, potential introgression of genes from allied species, and a drive for greater use of native species, mostly of the legume genera *Arachis* and *Stylosanthes*, but also of *Paspalum*. Results of such programs are reaching the market, yet at long intervals. Expanded use of native species finds obstacles on lack of information, and frequently on reproductive barriers, to be overcome by cytogenetic studies and pre-breeding activities, that still need to capture the breeder's attention. Many native grasses and legumes have a potential for use as cultivars. For centuries, native plants have been the biological basis for sustainable livestock raising in many Brazilian states. There is a good insight on which species are the main components of productivity in Brazilian natural pastures. Accessions of many native species are now available in genebanks, in spite of their rarity in breeder's working collections. Identification of elite species has been recently stressed, under the "Plants for the Future" governmental project, especially concerning the Southern and West Central Brazilian regions. Initiatives involving outstanding native legumes and grasses will be commented. While in exotic germplasm, the search for expanded knowledge on reproductive mechanisms aims at the incorporation of such knowledge in breeding strategies, the search for biosystematic knowledge of native species has dual purpose: The sustainable management of native pastures, considering the adequate conservation of major components of their yield and environmental services, and balanced survival of plant populations with distinct ecological niches, and the use of such knowledge in pre-breeding activities and breeding programs. Identification of limiting factors for the establishment of a broad span of native cultivars of forage grasses and legumes, adapted to the diverse ecological conditions of the Brazilian territory, will help to find a better niche for native species in the spectrum of commercial forage plants for sustainable pasture establishment.



Integrated conservation and sustainable use of regional crop wild relatives

José F. M. Valls (jose.valls@embrapa.br and jose.valls@pq.cnpq.br)

Embrapa Genetic Resources and Biotechnology and CNPQ Fellow (National Research Council), Brasília, DF, Brazil

South America includes some mega-diverse countries, but genetic resources locally used for food and agriculture are mostly of exotic origin. Exclusively exotic crops, with no local germplasm, sometimes are key elements behind successful agribusiness. The local importance of coffee, soybeans, sugar-cane, as well as of species of *Citrus* and *Eucalyptus* illustrates the strong dependence on exotic germplasm, with the resulting vulnerability. However, the region also includes plant genetic resources of global importance, gathering diverse wild relatives of crops. Breeding programs of exotic crops such as rice, barley, pearl millet or finger millet could benefit from the addition of local congeneric wild species. In parallel, the breeding of American crops such as maize or lima beans may benefit from the addition of germplasm of local landraces, derived from remote introduction of such crops in South America, from their areas of origin in Mexico and Central America. But the greatest impact of the regional plant genetic resources refers to traditional South American crops, such as pineapple, peppers, and groundnut, of which the area is rich in wild relatives. Three crops of Brazilian origin, cassava, cashew, and rubber-tree, enrich this group, of which most wild relatives occur in Brazil, many of them being endemic. Besides typical wild relatives of crop plants, some species native to Brazil and adjacent countries have shown a potential to become commercial crops. This applies to many native forage plants, fruit trees, and palms. In the last three decades, some elite wild plants, *Arachis pintoii* and *Stylosanthes seabrana*, both exclusive to Brazil, confirmed this potential, reaching the World market. Information will be presented on what is being done, and still needs to be accomplished, towards the conservation of such crop wild relatives, both *ex situ* and *in situ*, especially at a time of strong modifications in the land use systems and practices in South America, while facing threats of climate change. Detailed information on three regional crop gene pools will follow, stressing the growing amount of taxonomic and genetic information piled up on the groundnut wild relatives, on the struggle to conserve the wild *Manihot* species, when their preferred biome, the Cerrado, is under drastic agricultural impact, and on how much diversity is being constantly unveiled on South American species of *Capsicum*, and how this knowledge relates to agronomic advances.



The role of Seed Associations on Crop Production: How to Globalize Brazil in the World Seed Market?

França-Neto, José de Barros; President of ABRATES; Research Scientist of Embrapa Soybean, Londrina, PR, Brazil; E-mail: jbfranca@cnpso.embrapa.br

ABRATES (Brazilian Association of Seed Technology) is a scientific non-profit organization, founded in 1970. Its members consist of research scientists, professors, students and other professionals related to the seed sector, and seed producing companies. The major objectives of ABRATES are: support and stimulate scientific work and teaching on seed technology; disseminate results of scientific and technical papers of interest to the seed sector; cooperate with individuals or entities, public or private, on issues related to seed technology; suggest methods and uniform practices, aimed at improving seed technology in the country. These objectives are achieved by implementing various actions. Three Brazilian Seed Seminars and 17 editions of the Brazilian Seed Congress have been offered. In these events, 7,797 papers were delivered. Eleven editions of the Brazilian Symposium on Seed Pathology, five of the Brazilian Symposium of Forest Seeds, and three of the Brazilian Workshop on Seed Quality Control have been offered by ABRATES. The association edits the Brazilian Seed Journal (Revista Brasileira de Sementes), first published in 1979. A total of 1,722 research papers have been published so far. Since 1990, ABRATES has edited the ABRATES Newsletter (Informativo ABRATES), containing more practical technical articles, news and the abstracts of the Brazilian Seed Congress and other scientific events promoted by the association. In 2012, a new electronic publication was implemented: ABRATES in Focus (ABRATES em Foco), which is a monthly newsletter delivering technical news, interviews, and other information by e-mail. All these three publications can be accessed by the association site (www.abrates.org.br). The association is also in the social network, using Facebook and Twitter. ABRATES edits books and handbooks related to the seed area, dealing with subjects such as seed vigor procedures, sampling, analysis, seed processing, seed pathology and forest seeds. Since 2011, it has been involved in offering training courses to the seed sector, dealing with the specialization of Seed Physiology, Seed Sampling, Seed Analysis, and Seed and Seedling Image Analysis. Basically, all this effort is devoted to the seed production sector, aiming the production of high quality seeds and seedlings of several species.



The Role of Legumes in Forage Production Systems in Tropical Latin America

Judson F. Valentim; Carlos Mauricio S. de Andrade; Giselle Mariano L. de Assis

Research Agronomist at the Agroforestry Research Center of Acre – Embrapa Acre. Rio Branco-AC, Brazil. E-mails: judson@cpafac.embrapa.br; mauricio@cpafac.embrapa.br; giselle@cpafac.embrapa.br

Projections are that the world population will grow from the current 7 billion to some 9.2 billion by 2050, while available land for expansion of agriculture will become economically and environmentally unattractive. Urbanization, growing population and income in developing countries, associated with changes in food preferences are fueling a Tropical Revolution with a massive increase in demand for energy, fiber and food, particularly livestock products. The livestock sector accounts for 40% of the world agricultural gross domestic product. It is also socially and politically very important since it employs 1.3 billion people and creates livelihoods for over one billion of the world's poor. This sector is the single world largest anthropogenic land user, accounting for 30% of Earth's surface and 70% all agricultural land. Pasture expansion has been and still is a key driver of deforestation, particularly in tropical Latin America. Meat and dairy production in this Region is almost solely dependent upon forage grasses. Estimates are that around 40% of these pastures are in some degree of agricultural degradation, mostly due to overgrazing, low soil fertilization and biotic problems. This presentation reviews the benefits of forage legumes to sustainable cattle production systems, particularly through their ability to supply nitrogen which is the primary nutrient limiting plant and animal production in tropical Latin America. Forage legumes contribute to increase forage quality and pasture productivity, improve animal diet and productivity, increase above and below-ground biodiversity, reduce weed infestation, increase pasture resiliency and longevity, reduce production costs and environmental impacts of cattle production in the Region. This presentation also focuses on some success histories of transition towards sustainable cattle production systems in tropical Latin America. Forage legumes such as *Stylosanthes capitata* & *S. macrocephala* cv. Campo Grande, *Arachis pintoi* and *Pueraria phaseoloides* have been successfully used in more than 1.5 million hectares of grass-legumes pastures in Brazil and Colombia. Finally, it highlights the contributions of forage legumes to meet the challenges of reconciling the objectives of increasing world food production, promoting economic growth, improving food security, income and human welfare, mitigating environmental impacts of cattle production and ensuring environmental conservation in Latin America.



WEED MANAGEMENT AND STALKS CONTROL IN HERBICIDE TOLERANT COTTON

FIELDS

Julio Cesar Bogiani¹, Alexandre de Cunha Barcellos Ferreira², Ana Luiza Dias Coelho Borin²

¹Embrapa Cotton, Brazilian Agriculture Research Cooperation, P.O. Box 198, 47850-000, Luís Eduardo Magalhães, BA, Brazil. E-mail: julio.bogiani@embrapa.br

²Embrapa Cotton, Brazilian Agriculture Research Cooperation, P.O. Box 179, 75375-000, Santo Antônio de Goiás, GO, Brazil. E-mail: alexandre-cunha.ferreira@embrapa.br, ana.borin@embrapa.br

Cotton production system using varieties genetically modified for herbicide tolerance increases every year around the world. In Brazil, there are transgenic cotton expressing tolerance to over-the-top applications glufosinate ammonium (Cotton LL) and glyphosate (RR and RR Flex Cotton). In RR Flex cotton over-the-top applications of glyphosate can be made during throughout the season, unlike what happens with the first generation of RR cotton, which is very sensitive to the herbicide was applied during the reproductive stage. Introduction of tolerance genes for these herbicides provides an additional option for weed management in cotton crops because this technology allows controlling a large amount of weeds without detrimental effect on fibers yield. However, this technology needs attention and care. The major easy to weed control using this technology can promote successive plantings of cotton and other crops with tolerant to same herbicide, caused the selection of weed species resistant to this herbicide in the crop areas. In several states of Brazil and in the world, frequently occurring infestations of weeds tolerant to herbicides. The presence of these species in glyphosate resistant cotton crops, for example, may cause difficulty to control it only with over-the-top application of glyphosate. Therefore, the use of best weed management practices should be adopted to avoid this problem. Practices such as weeds identification in the area before and after the crops, perfect desiccation to plant crop free of weeds, use of herbicides with residual action, rotation of herbicides with different action mechanisms, survivors weeds elimination after herbicides applications, crop rotation using plants tolerance to different herbicide, use of doses recommended by manufacturer, control of late weed infestation to prevent seed production, among others, because certainly will decrease the percentage of problems with weeds management in cotton crops. Cotton stalks control is provided by law and aimed to reduce pest population and disease inoculum. In conventional tillage system this practice is usually done using machines, but in no-tillage system is done chemically after to mow the crop harvested. So are made successive applications of herbicides to control of herbaceous cotton ratoons. In the case of herbicide tolerant cotton, applications are usually made using herbicide different of the tolerance genetically inserted, most often in admixture with the 2,4-D.



Modelling genotype and environment effects to aid crop improvement

Karine Chenu¹, Graeme L Hammer², Scott C Chapman^{2,3}

¹The University of Queensland, Queensland Alliance for Agriculture and Food Innovation (QAAFI), Toowoomba, QLD 4350, Australia

²The University of Queensland, QAAFI, St Lucia, QLD 4072, Australia

³CSIRO Plant Industry, St Lucia, QLD 4072, Australia

Substantial genotype x environment interactions impede breeding progress for yield. Identifying genetic controls associated with yield response is confounded by poor genetic correlations across testing environments. Part of this problem is related to our inability to account for the interplay of genetic controls, physiological traits, and environmental conditions throughout the crop cycle. Here we outline several approaches based on modelling to bridge this predictability gap. First, crop models incorporating physiological understanding of traits were used to scale-up known effects of 'simple' traits from organ to crop level. Breaking down yield into simpler traits allows identification of more stable genetic controls. Modelling can help estimate the impact of those genetic controls and the associated genotype x environment interactions on yield. Second, models were used to quantify abiotic-stress timing and intensity that crops experience during their life cycle. Such environment characterisation helps to interpret genotype x environment interactions in multi-environment trials. Third, biophysical and plant breeding models were combined to explore efficiencies in breeding programs. Simulations were conducted to examine rates of genetic gain associated with different strategies (e.g. which cross to perform, multi-environment testing). Case studies will be presented to illustrate these different approaches and their value for crop improvement.



Implementing Genomic Selection in Barley

Kevin P. Smith¹, Vikas Vikram¹, Aaron Lorenz², and Jean-Luc Jannink³

¹University of Minnesota, St. Paul, MN USA

²University of Nebraska, Lincoln, NE USA

³U.S. Dept. of Agriculture, Ithaca, NY USA

Genomic selection (GS) was implemented in a Midwest U.S. barley breeding program to improve resistance to Fusarium head blight (FHB), a fungal pathogen that infects kernels and produces a mycotoxin called deoxynivalenol (DON). Improvement of FHB resistance by traditional phenotypic selection has been slow. Genetic studies from bi-parental mapping populations have identified several larger effect QTL, however, resistance at these loci is linked to traits that are unfavorable (eg. high grain protein) or that confound measurement of disease (eg. late flowering time). This has left limited targets for traditional marker assisted selection (MAS). Recent association mapping studies with elite breeding germplasm indicate that QTL are of relatively small effect and distributed across the genome. The combination of quantitative inheritance and expensive and inconsistent phenotyping make the use of GS an attractive option. We generated genomic estimated breeding values (GEBV) using disease and genotype data sets from three Midwest U.S. breeding programs focused on developing six-rowed malting barley varieties with enhanced FHB resistance. In cross-validation studies, we found that marker platforms of 384 SNPs and training population sizes of 200 – 300 were sufficient to generate prediction accuracies that would substantially improve gain from selection over phenotypic selection. Training populations from a single breeding program used to predict performance of breeding lines from the same program were more accurate than when training and prediction populations were from different breeding programs. Based on these results we initiated GS on a set of 1,440 F₂ progenies resulting from crosses among and between the Minnesota (MN) and North Dakota (ND) breeding programs. A ridge regression BLUP model using 1,536 SNP markers and a training population of 768 breeding lines was used to generate GEBVs. Three sets of 100 random lines from these F₂'s corresponding to the three cross types (MN x MN, MN x ND, ND x ND), were advanced to the F₄ and evaluated in four replicated disease nurseries in 2011. We used the three training populations to predict the three cross types and calculated the accuracy as the correlation between GEBV and the observed phenotype. As expected the MN training population predicted DON for the MN x MN crosses more accurately ($r = 0.60$) than for the ND x ND crosses ($r = 0.08$). A similar trend was observed when using the ND training population. The MN & ND training population predicted the MN x ND crosses with greater accuracy ($r = 0.37$) than using either of the single breeding program training populations ($r = 0.28, 0.15$). These empirical results from one cycle of GS are promising and suggest that with properly constructed training populations we should be able to double the rate of gain from selection and substantially reduce the need for field screening of FHB in early generations.



Integrating genetic diversity, metabolites profiles, transcript profiles, and protein profile allowed identification of gene sets useful to improve storage root quality in cassava storage root.

Luiz Joaquim Castelo Branco Carvalho, James V Anderson, Claudia Regina Batista de Souza, Eduardo Alano Vieira.

A research program at EMBRAPA Genetic Resources and Biotechnology exploits natural genetic variation to overcome genetic bottlenecks during domestication and to improve yield and quality of cassava storage root. Here, we integrate results genetic diversity, metabolite profiles (carotenoid synthesis), microarray-based transcript and proteomic profile to unveil complex biological and metabolic networks using diversity from landraces and F1 progeny. Based on correlation analysis, we mined candidate regulatory genes to identify putative biological pathway network that differentiate storage root phenotypes and genes coding for enzymes in carotenoid synthesis to identify putative mutations in the pathway. Proteomic profile was used to mine candidate proteins associated to carotenoid accumulation. Results from this analysis provided evidences to indicate that carotenoid metabolite revealed by HPLC profiles correlate differentially with specific expressed genes coding for enzymes such PSY, PDS and LyCb as well as with specific putative regulatory genes network with gene nodes as FLC, ABI1, JAR1, MPK4, BRI1 and ATG50240. Proteomic profile revealed that small Heat Shock Proteins (sHSP) were the most abundant protein in the carotenoid-protein complex and that HSP21 protein play major roles in the accumulation of β -carotene in cassava storage root. It was also observed that the gene coding for HSP18.1 and HSP21 are highly expressed in intense yellow root than in white.



Opportunities and Constraints for Animal Production on Warm-Climate Grasslands

Lynn E. Sollenberger

Agronomy Department, University of Florida, Gainesville, Florida, USA

Populations of most ruminant livestock species are greater in warm than temperate climates, and grasslands serve as their primary source of energy and protein. Individual animal production has generally been less in warm- than temperate-climate regions due to a number of constraints. These include highly seasonal forage production, challenges associated with conserved forage, relatively low nutritive value of most C4 grasses, minimal legume contribution, and nutrient limitations to plant growth and persistence. There are additional challenges that have arisen in recent years. These include land-use changes driven by market forces that relegate forage-livestock systems to even poorer production environments. Additionally, in most parts of the world there has been greatly diminished research capacity in grassland science. In other areas where funding has been sustained, the emphasis has been on rapid throughput of graduate students and researcher performance evaluation based primarily on number of publications. This has led to a focus on short-term studies of questionable relevance to the real-world problems of producers. Lastly, in some areas the non-agricultural public has increased its expectations of agriculture, going beyond food, to managing natural resources in a sustainable way. Opportunities exist to address many of these challenges. For example, pasture plant improvement is an extremely important area of need in warm-climate systems. There is increasing realization in the USA that jettisoning plant genetic improvement efforts by public entities (e.g., universities and state and federal research agencies) was misguided. Plant selection and breeding of forages has potential to address the constraints of seasonality of production, nutritive value, legume contribution, and pasture persistence. Beyond plant improvement, there have been recent successes in designing practical management systems for legumes, and opportunity exists to explore novel approaches to establishment and grazing management including spatial separation of grasses and legumes and greater emphasis on matching compatible growth habits to increase likelihood of mixture success. Ecosystem services provided by grasslands are a fertile area of research interest. Lastly, highly specialized agriculture that has physically separated animal and crop production has led to challenging problems including disposal of animal waste, unbroken pest cycles, depletion of soil organic matter and nutrient-supplying ability. Integrated crop-livestock systems have potential to address some of these constraints, and there is a significant opportunity for forages to play a major role in these systems. Thus there are major challenges facing animal production systems on warm-climate grasslands, but clearly there are exciting opportunities for creative and dedicated scientists to make an impact in the future.



Conservation and use of genetic resources of watermelon in Brazil

Manoel Abilio de Queiróz

State University of Bahia – UNEB, Juazeiro-BA, Brazil. manoelabiliomaq@gmail.com

The watermelon crop is very important in Brazil, since it covers more than 80,000 hectares and is cropped in different regions. The South and Northeast regions are the most important ones. However, watermelon is an African crop that was introduced in Brazil in two different periods. The more recent one was in the end of the fifties when American and Japanese immigrants introduced few improved cultivars in the State of São Paulo and from there it was spread out using only very few cultivars, all of them replaced by Crimson Sweet types all over the country, since it was less prone to calcium deficiency, very common in the long fruited cultivars as Charleston Gray. But, the improved cultivars introduced were very susceptible to several biotic stresses despite good fruit characteristics. On the other hand, the old introduction from Africa by slaves and European immigrants in the coastal area from the State of Rio de Janeiro to Maranhão, brought many watermelon samples of seeds from different areas of the African continent and different tribes had different contributions. The seeds were, first used in the small gardens near the slave houses as depicted by Albert Eckhout and from there were spread for the interior, particularly in Northeast region when small farmers used watermelon seeds for their plantings sometimes few plants intercropped with food crops to bigger planted area for commercial purposes as it occurs in Massaroca, county of Juazeiro-BA. The farmers' selection aided by the seed dormancy has kept a sizable genetic variability, firstly caused by a big founder effect since it is supposed that a very big amount of watermelon seed samples were introduced and secondly by intercrossing of different populations introduced. As a result, the traditional agriculture in the country, present a great genetic variability that has little recognition in the scientific environment. Even though, seed samples from the traditional agriculture were rescued and four Active Germplasm Banks (BAGs) were set in the country. The oldest is the Federal University of Viçosa, MG, followed by the BAGs of Embrapa Vegetable Center in Brasília-DF, Embrapa Semiarid (Petrolina-PE) and Embrapa Temperate Climate (Pelotas, RS). The use of the variability rescued has been very modest, since prebreeding has been scarcely practiced. Therefore, there is a great space for use the existing genetic variability to develop improved lines and hybrids for use in the country watermelon farming.



Crop resistance to abiotic stresses – mechanisms, traits and mitigation strategies

Chaves MM

Instituto de Tecnologia Química e Biológica. Oeiras. Universidade Nova de Lisboa. Portugal.
mchaves@itqb.unl.pt

Crop production is facing in many areas of the globe the challenge of coping with new climatic conditions, comprising an extended dry summer period, heat waves and saline soils (IPCC 2007). Although fertilization by rising CO₂ may partly offset the effects of these changes on plant growth and development, a detrimental effect on food and feed production is predicted to occur in many of the major food-producing regions of the world (Lobell et al. 2008). It is therefore important to combine expertise from different disciplines to identify and overcome crop genetic and agronomic limitations to yield under unfavourable environments. The comprehension of the mechanisms underlying plant resistance to abiotic stresses (often acting in conjunction) allows the development of new ideotypes with a different set of physiological traits, the use of new crops and of new management techniques that are vital to increase food production in less favorable environments. The screening of a wide range of germplasm for our major crops in order to identify genetic variation in major traits involved in stress resistance is still a major tool for crop improvement. Among abiotic stresses, drought has a major impact on crop production as a result of diminished leaf carbon fixation, inhibition of growth and poor fruit set. A review will be made of the main plant physiological mechanisms that are key drivers in plant adaptation to water scarcity such as the optimization of water use, both through maximizing uptake (e. g., long roots, hydraulic redistribution, osmotic adjustment) and controlling losses (stomatal regulation). When the dry season lasts too long and/or other stresses co-occur (such as excess irradiance and high temperature) drought avoidance mechanisms may no longer be able to sustain plant water status; under such conditions the capacity for metabolic acclimation to stress play an important role in plant performance and survival. Fine tuned regulations of these responses at the gene and metabolic levels are being unravelled (Pinheiro and Chaves 2011). Issues related to crop phenology, root/shoot partitioning, stem reserves and leaf morphology and structure will also be addressed as important players in plant strategy against stress. The use of this knowledge in precision agriculture for increased crop water use efficiency and quality under sustained yield will be presented as case studies.

IPCC 2007. Climate change 2007: The physical basis summary for policy makers, Cambridge. Cambridge University.

Press. Lobell DB, Burke MB, Tebaldi C, Mastrandrea MD, Falcon WP, Naylor RL 2008. Prioritizing climate change adaptation needs for food security in 2030. *Science* 319, 607–610. doi:10.1126/science.1152339 Pinheiro C, Chaves MM 2011 Photosynthesis and drought: can we make metabolic connections from available data? *Journal of Experimental Botany*. 62, 869–882. DOI: 10.1093/JXB/ERQ340.



ASR genes and aluminum responses in Rice

Rafael Augusto ARENHART^{1,2}, Julio César DE LIMA¹, Marcelo PEDRON¹, Felipe de Oliveria NETO¹, Lauro Bucker NETO¹, Mariana SCHUNEMAN¹, Andreia CAVERZAN¹, Rogério MARGIS^{1,2} & Márcia MARGIS-PINHEIRO^{1,2}

¹Programa de Pós-Graduação em Genética e Biologia Molecular, Universidade Federal do Rio Grande do Sul, Porto Alegre

²Programa de Pós-Graduação em Biologia Celular e Molecular, Universidade Federal do Rio Grande do Sul, Porto Alegre

Among cereal crops, rice is considered the most aluminum (Al) tolerant species. However, variability among rice genotypes leads to remarkable differences in the degree of Al tolerance for distinct cultivars. A number of studies have demonstrated that rice plants achieve Al tolerance through internal and external mechanisms. We have analyzed expression changes of the rice *ASR* (Aba, Stress and Ripening) gene family as a function of Al treatment. The gene *ASR5* was differentially regulated in the Al-tolerant rice *ssp. Japonica* cv Nipponbare. However, *ASR5* expression did not respond to Al exposure in *Indica* cv Taim rice roots, which are highly Al-sensitive. Transgenic plants carrying RNAi constructs that targeted the *ASR* genes displayed increased Al susceptibility in T1 plants. Rice embryogenic calli expressing an *ASR5*-GFP fusion revealed that *ASR5* was localized in both the nucleus and cytosol. In transformed protoplasts, *ASR5*-GFP appears in chloroplast cells. In order to identify genes with differential modulation under Al stress in rice, and search for genes affected by *ASR5* silencing, RNA-seq was made in non-transformed plants and *ASR5*_RNAi plants in control conditions and after Al treatment. These analyses revealed that 961 genes responded to Al in non-transformed rice roots under Al stress. A total of 309 genes responded to Al in *ASR5*_RNAi plants. Only 52 genes overlapped between non-transformed and *ASR5*_RNAi plants when comparing genes modulated by Al, showing that *ASR*-silenced plants lost the ability to modulate a set of genes in response to Al treatment. Furthermore, our analysis revealed that *ASR5* can regulate the expression of *STAR1*, among other genes. Our results indicate that *ASR5* act as a transcription factor in rice and that it regulates Al-responsive genes conferring tolerance in rice against Al toxicity.



"Isolation and characterization flower specific promoters in cotton and their potential as a tool for biotechnology"

Marcio Alves-Ferreira, Maria Fatima Grossi-de-Sá, Sinara Artico, Julia Lambret e Sarah Nardeli

Laboratório de Genética Molecular Vegetal (LGMV), Inst. de Biologia, Universidade Federal do Rio de Janeiro (UFRJ), Rio de Janeiro, Brazil.

The isolation and characterization of plant promoters are crucial for the development of genetically modified (GM) crops. Most of transgenic plant commercially available today is based on the use of the CaMV 35S promoter. The 35S promoter has two major concerns: its activity is variable in certain tissues, such as flowers, and it presents potential hazard effects on non-target organisms when associate to genes encoding to toxic proteins. Cotton (*Gossypium spp.*) is the world's most important source of natural fiber and also an important source of edible oil. In spite of that, cotton production in Brazil is heavily damage by the attack of boll weevil (*Anthonomus grandis*). The endophytic habit of the *A. grandis* larvae inside floral buds triggers the destruction of the fiber quality, hampers the chemical control, causing considerable yield losses. The best method to control *A. grandis* is the development of genetically resistant cotton lines that suppress the insect larval development. We identified, by data-mining, 19 putative flower specific genes in cotton. qPCR analysis allowed us to select four genes (*GhPGFS-1* to *-4*) with a strong expression in stamens and carpels. To better characterize the expression of these four genes, we performed *in situ* hybridization experiments. The hybridization signal for the four genes was observed mostly in cotton anther tissues and carpels. The promoter region of these four genes was isolated by Genome Walker and further sequenced. Promoter fragments, ranging from 300 to 2000 pbs, were cloned in binary vector baring the report genes GUS (*uidA*). The constructs were used for Agrobacterium-mediated transformation of *Arabidopsis thaliana* and also for transient expression assays in flower tissues of *G. hirsutum*. The GUS histochemical assays of T3 plants containing a single copy of the T-DNA of the four distinct cotton promoters showed that most of the constructs direct GUS expression to anther and carpels. Transient expression assays in *G. hirsutum* confirmed the expression flower tissues. These results showed that our strategy was successful for the identification of cotton promoters with flower specific activity. The promoters isolated, when evaluated by qPCR in transgenic *Arabidopsis*, showed a higher activity in flower tissue than the 35S promoter. Therefore, the use of these promoters should be effective to direct expression of toxic proteins in cotton to protect against *A. grandis* with minimal effects in non-target organisms.



Citrus genome and breeding in Brazil

Marcos A. Machado. Centro de Citricultura Sylvio Moreira,

Instituto Agronômico, Caixa Postal 04, Cordeirópolis – SP, CEP 13490-970. E-mail: marco@centrodecitricultura.br

The citrus industry is one of the leading activities of the agribusiness in Brazil, with the states of Sao Paulo, Sergipe and Bahia as the main citrus producers. Brazil is by far the main producer and exporter of frozen concentrated (FCOJ) and not from concentrated (NFC) orange juice in the world. The low Brazilian yield (approximately 2 boxes 40.8 kg/tree/year) is highly associated to the incidence of pests and diseases (resulting in a substantial influence over the production costs), the production in non-irrigated areas, and the narrow genetic basis that has been used. It is estimated that more than 60 % of the costs for citrus production in Brazil are associated with control of pests and diseases. The group named citrus shows great diversity in genus, species, varieties and clones, however a relatively small number is used on commercial groves nowadays mainly because of botanical and historical reasons. Traditional programs of genetic improvement using hybridization and recurrent selection always found genetic difficulties (high heterozygosity, incompatibility, long cycle for selection, etc) and botanical barriers (mainly adventitious nucellar apomixy and juvenility) that are characteristic of the citrus group. The need to expand the genetic basis of used citrus nowadays, likewise the enhancement of the material in use, demand keeping and promoting breeding programs supported on biotechnological tools. However, the main challenge by using such approaches is undoubtedly the integration of information on genome to genetics at the breeding level. Nevertheless, approaches such molecular markers (SSR, ESTs and DArt) for genetic mapping, analysis of transcriptome using microarray platforms and RNAseq, genetic transformation, re-sequencing of genomes, and complete genome of citrus have been used as tools to improve genetic breeding. The current database of citrus genome includes complete and reference haploid genome of a model species (*Citrus clementine*), and other diploid species as sweet orange, mandarin, Rangpur lime, and *Poncirus trifoliata*. But the challenge to transform a huge amount of information into knowledge and from that point to a final product persists and needs to be overcome.



Genomic Selection in Plants: Empirical Results and Implications for Plant Breeding

Mark E. Sorrells

Department of Plant Breeding & Genetics, Cornell University, Ithaca, NY 14853 USA

Advancements in genotyping technologies are rapidly reducing marker costs and increasing genome coverage allowing the widespread use of molecular markers and methods in plant breeding. Marker assisted selection and recurrent selection are based on the selection of statistically significant, marker-trait associations. However, MAS strategies are not well suited for agronomically important complex traits controlled by many genes. Genomic selection incorporates genome-wide marker information in a breeding value prediction model, thereby avoiding biased marker effect estimates and capturing more of the variation due to small effect QTL. In GS, a training population representative of the breeding germplasm is genotyped with genome-wide markers and phenotyped in a target set of environments. That data is used to train a prediction model that is used to estimate the breeding values of lines in a population using only the marker scores. Prediction models can incorporate performance over multiple environments, G x E effects, and identify a highly predictive subset of environments. Because of reduced generation time, annual genetic gain for GS is predicted to be two to three fold greater than for a conventional phenotypic selection program, even with only modest prediction accuracy greater than 0.50. We have developed a new strategy for using genome-wide marker effects to group environments and identify outliers. Results indicate that GS can outperform conventional breeding on a per year basis even at low accuracies. This new approach to crop improvement will facilitate a better understanding of the dynamic genome processes that generate and maintain new genetic variation.



“Nutritionally Enhanced Crops”

Getting more from our foods: Assessing and targeting nutrient bioavailability in our food crops

Michael A. Grusak

USDA-ARS Children's Nutrition Research Center, Department of Pediatrics, Baylor College of Medicine, Houston, TX, USA

We are interested in the improvement of iron nutritional status of humans living in developing world countries where iron deficiency anemia is quite severe. We also wish to promote the use of plant-based food sources to improve human iron status, and thus are focusing on staple food crops like common bean (*Phaseolus vulgaris*) and rice (*Oryza sativa*). Several groups are attempting to increase the iron concentration of edible crop plants, but efforts are also underway to improve the availability of iron that is in foods (i.e., its bioavailability), such that more iron can be absorbed from the diet. This latter effort can involve changes in the form of iron within the food, or changes in the levels of inhibitors or promoters of iron absorption within the food matrix. All of these options will be reviewed and discussed in this presentation. In addition, we will discuss recent efforts in which we used an *in vitro* cell culture method (Caco-2 cells) to measure iron bioavailability and to identify quantitative trait loci (QTL) related to improved dietary iron absorption. We studied 248 bean entries that were grown in Washington State and 212 rice genotypes that were grown in Texas. Ground bean samples or whole rice grains were mixed with water and cooked in a steam sterilizer, then lyophilized and ground in a mortar and pestle. For the bioavailability studies, the ground samples were mixed with a known quantity of iron, then digested with a mixture of digestive enzymes, prior to feeding this 'food' to the Caco-2 cells. Ferritin formation in the cells (after 24 h) was used as a proxy for iron bioavailability potential. We are currently using an association mapping strategy with both the bean and rice lines to identify QTLs for enhanced iron bioavailability; results of these analyses will be presented. This work is funded by USDA-NIFA and USDA-ARS. The author reports no conflicts of interest for this research.



A glimpse into energetic homeostasis and growth in *Arabidopsis thaliana*

Americo José Carvalho Viana; Cleverson Carlos Matioli; Gustavo Turqueto Duarte; Amanda Bortolini Siveira; Luiz Eduardo Vieira del Bem and Michel Vincentz

Centro de Biologia Molecular e engenharia Genética and Departamento de Biologia Vegetal, UNICAMP, Campinas Brazil

Plants, as sessile organisms evolved efficient regulatory networks which allow them to cope with ever changing environmental conditions. Sugars produced by photosynthesis represent an important source of energy and also are key metabolic signals that control gene expression. In combination with developmental signals and environmental cues such as mineral nutrition, water availability or biotic stresses, sugars modulate plant growth and development. How these different signals interact is largely unknown. We have shown that the transcription regulatory factor (TF) of the basic leucine zipper family (bZIP), AtbZIP63 of *Arabidopsis thaliana*, integrates Absciscic Acid (ABA) (i.e., abiotic stress) and glucose (i.e., energy) signals to tune the response to energetic starvation mediated by the sucrose non-fermenting 1 related kinase (SnRK1). Unexpectedly, AtbZIP63 appears to promote growth under short days and this effect could partly be explained by the regulation of cell wall expansion activity by atbZIP63. The circadian regulation of atbZIP63 expression shows an inverse correlation with starch accumulation (day) and degradation (night) and indicates that the activity of this TF is most likely restricted to the night period. We propose that the circadian control of growth and stress responses in phase with available energetic resources and stresses, may constitute an important aspect of AtbZIP63 function.



Improving sugarcane productivity: The challenge for traditional crop improvement.

Nils BERDING

SCII Consultancy Pty Ltd, and Adjunct Professor, School of Marine and Tropical Biology, James Cook University, Cairns, Queensland, AUSTRALIA.

nberding@sciiconsultancy.com

The rate of genetic improvement of sugarcane is often stated to be low. Comparison of improvement in sugar yield in the Queensland industry, which has had an active, scientific breeding program since 1954, with four crop industries renowned for benefiting from application of scientific breeding methodology – U.S. corn, U.S. soybean, Californian strawberry, and U.K. wheat – is interesting. The percent change over the period scanned is only above that for the strawberry industry, and well below the three grain crops, suggesting either a relatively ineffectual improvement program or commencement at a relatively high initial level. Expression of the current predicted yield relative to the maximum commercial yield shows Queensland's sugar yield is almost equal to that of U.K. wheat. Both are well ahead of the U.S. grain crops. Alternatively, expression of the maximum commercial yield as a ratio of the current predicted yield reinforces the conclusion that improvement in sugar yield in the Queensland industry is equal to the advance made in U.K. wheat, and can be regarded as excellent. The challenges for traditional sugarcane crop improvement are viewed in the context of six "Grand Challenges for Crop Science" recently released by the Crop Science Society of America. These identified transformative questions to guide future crop improvement efforts in the face of current or perceived objectives. These are very relevant for sugarcane crop improvement but their priority may not be their presented order. Sufficient research has been conducted in sugarcane to be quite prescriptive as to a general strategy for genetic improvement, e.g., selection criteria, parental and cross selection, population size and structure, and selection methodology and intensity. However, a minority of programs heed the lessons gained from comprehensive research on these aspects. Generally, newly released cultivars could be better 'packaged' to enhance their uptake and accelerated realization of their benefits. Contemporary sugarcane cultivars have an acknowledged narrow genetic base. A major impediment in broadening this has been a feeble international effort in conserving, describing, using, and enhancing basic germplasm. This contrasts with the collaboration invested in the International Sugarcane Biotechnology Consortium. Investment in germplasm is surely more basic, and should be the focus of an international initiative across industries. Sugarcane programs also are disadvantaged through compromised use of commercial equipment for planting and harvesting trials. In contrast with specialized equipment used in breeding programs in the majority of major crops sugarcane lags by several decades. While sugarcane is well placed in terms of rate and size of improvement relative to other crops, future gains will be increasingly hard won. Wider use of acknowledged research findings, an international focus on basic germplasm, and development of specialized research-plot equipment are suggested objectives for further, sustained advancement.



“Sunflower yield differences as related to environmental variables. Comparison with maize and soybean. Crop management strategies in the SE of the Pampas”

Calviño Pablo A. Private consultant and AACREA. Tandil, Buenos Aires, Argentina

Summer crops yields under rainfed conditions depends on water available at sowing and on season precipitation. Soil depth and texture influence water storage, and soil topography modifies temperature within paddocks. Sunflower, soybean and maize respond differently to these variables. Most of the variability within paddock can be reduced by re arranging paddock within the farm in homogeneous units. This strategy reduced yield variability within paddock from 50 to 16%. And allow using site-specific management tools within each paddock. The division of paddocks in homogeneous units improve yield, yield stability and farm profitably.



Grape breeding and genetic studies in Brazil

Camargo, U. A.¹; Maia, J. D. G.²; Revers, L.F.³; Leão, P.C. de S.; Quecini, V³; Ferreira, M. E⁵.; Ritschel, P³.

¹Vino Vitis Consulting, Bento Gonçalves, RS, Brazil;

²Embrapa Grape and Wine-EVT, Jales, SP, Brazil;

³Embrapa Grape and Wine, Bento Gonçalves, RS, Brazil;

⁴Embrapa Tropical Semiarid, Petrolina, PE, Brazil; ⁵Embrapa Genetic Resources and Biotechnology, Brasília, DF, Brazil. e-mail: patricia@cnpuv.embrapa.br

The development of new grape cultivars in Brazil has been carried out by the Grape Breeding Program and the Grapevine Germplasm Bank (GGB), established by Embrapa in 1977. The main results of this effort include the phenotypic characterization of 1,000 accessions maintained in the collection, the development of a group of 400 advanced selections and the release of 14 new grape cultivars in the last two decades (www.cnpuv.embrapa.br). The majority of the breeding activities are based on trait analysis in the field, including phenological, agronomical and disease resistance evaluations. The quality and nutraceutical potential of grape accessions are also being assessed, including traits such as sugar content, pH, total acidity, antioxidant capacity, polyphenol content and anthocyanin concentration. Embryo rescue is used on routine to obtain novel seedless cultivars. Biotechnological tools such as molecular markers have been used to genotype GGB accessions using multiplex panels of SSR markers. Hundreds of GGB accessions have been genotyped, allowing estimates of the grape genetic diversity stored in the bank, assessment of the genetic structure of the collection and tests of genetic identity between accessions. Genomic regions associated with the control of traits of interest, such as mildew resistance and seedlessness, are currently being mapped in a segregating population. Population diversity of important grape pathogens, such as *Plasmopara viticola*, has also been evaluated by DNA analysis of isolates collected in different regions of the country. It is expected that the incorporation of biotechnological tools in routine tasks of germplasm conservation and breeding in the coming years will contribute to improve the efficiency of activities associated to the development of new grape cultivars in Brazil.

Acknowledgments: This work is supported by the Brazilian Plant Genetic Resources Program and Grape Breeding Program (Embrapa-SEG-MP1 and MP2), AgroVerde (BID and Embrapa agreement) and CNPq.



Closing yield gaps with high input efficiency in intensive cropping systems

Patricio Grassini

Research Assistant Professor, Department of Agronomy and Horticulture, University of Nebraska-Lincoln, Nebraska, USA

Modern agriculture faces the challenge of closing the gap between potential and actual farmers' yields while achieving high input-use efficiency in order to reduce the negative environmental impact. Research focusing on how to conciliate production and environmental targets in current intensive cropping systems is relevant to anticipate arising questions from future production systems that will operate near yield potential level. This paper discusses opportunities and trade-offs between closing yield gaps and achieving high input-use efficiency in intensive irrigated maize systems in the western US Corn Belt. Analysis of yield, applied inputs, and energy balance, coupled with use of crop simulation models, was performed using a large, high-quality on-farm database collected from irrigated and rainfed maize fields in Nebraska by the Natural Resources Districts of Nebraska (USA). The database includes data on yield, N fertilizer, and applied irrigation water collected annually from 10,000+ fields in Nebraska since 2004. Results indicate that high and stable yields under irrigation help farmers optimize their crop management and input management, leading to relatively small gaps and high efficiencies in the use of fertilizer, water and energy inputs. Comparison of simulated yields versus actual farmers' yields show that irrigated fields are operating about 90% of their yield potential based on the field-specific weather and management. The small yield gap is consistent with observed lack of increase in actual irrigated maize yields in all districts in Nebraska during the last 10 years. Irrigated maize also exhibits high efficiencies in the use of water supply and N fertilizer (NUE) and favorable energy balance, especially when compared with less intensive, rainfed corn. According to simulations and actual on-farm data, adoption of specific set of management practices (earlier planting dates, longer hybrid maturities, and higher plant population densities) can increase the yield potential ceiling up to 13%, however, adoption of such practices by farmers is limited by higher production costs, risk of frost during grain filling, and delayed harvest. Closing the yield gap between actual yields and yield potential can also lead to increasing inefficiencies in the use of inputs, especially N fertilizer. However, analysis of on-farm data can help identify opportunities for achieving high efficiency at very high yield levels under the same or lower level of applied inputs. For example, high yields and high NUE, together, were found when pre-plant N applications were avoided and total N dose was splitted into several, relatively small doses during the growing season. Likewise, water productivity can be increased substantially through better irrigation scheduling with negligible effect on crop yields. We conclude that it is possible to achieve high yields and high efficiencies in intensive, irrigated cropping systems through fine tuning of crop and input management. On-farm databases provide an excellent opportunity to benchmark and track geospatial and time trends in yield, applied inputs, and efficiency and identify opportunities for improvement.



Physiological Constraints to Sugarcane Yield Potential

Paul H. Moore

AgriLife Research, Texas A&M System Weslaco, Texas, USA and Hawaii Agriculture Research Center Kunia, Hawaii, USA

Maximum crop yields are obtained when there are no yield-limiting factors. Historically, crop scientists have developed technologies to nullify the various factors that could prevent an adapted cultivar from attaining its maximum yield. The maximum yield of sugarcane is attained when a cultivar is grown in the environment to which it is adapted, with non-limited water and nutrients, and free of pests, diseases, weeds, lodging, and other stresses. We assume that the highest experimental yields obtained from a cultivar under non-limiting conditions reflect that cultivar's yield ceiling or potential yield limit. A crop yield ceiling is the result of genetically set physiological parameters that prevent the attainment of a calculable theoretical yield maximum based on the level of incident solar irradiance and a theoretical photosynthetic efficiency. The high sunlight areas of the world growing sugarcane have reported the crop to have radiation use efficiencies (RUE) of 1.7 to 2.0 g MJ⁻¹ which is higher than the RUE of other crops. However, the calculated theoretical RUE of sugarcane is 3.5 g MJ⁻¹ or 75% higher than that thus far attained. The challenge for sugarcane scientists is somehow to change the sugarcane plant so that it more nearly achieves its theoretical limit. Based on reported experimental yield records of sugarcane grown in high sunlight areas, the yield ceiling for sugarcane biomass is nearly 100 t ha⁻¹ yr⁻¹. Although this productivity is very high, it is only 57% of the theoretical maximum of 175 t ha⁻¹ yr⁻¹. Quantifying the factors responsible for this difference between theoretical and actual yield limits should focus research on developing technologies to ameliorate these physiological limitations. Several crop development factors such as tiller mortality, lodging, and flowering have been shown to reduce yields under specific conditions, but even when these factors do not occur, the theoretical yield is not achieved. It appears that the primary factors responsible for the yield ceiling include a crop decline in specific leaf nitrogen, initiation of a sucrose feed-back inhibition of photosynthesis, and increased rates of maintenance respiration that occur during sugarcane development and maturation. In my view, these factors are likely greater in high sucrose storing genotypes than in low-sucrose, high-fiber genotypes, but this has yet to be demonstrated. Ramifications of these relationships will be discussed.



Genomic and Epigenetic Characterization of Sugarcane Hybrids and Wild Relatives

Clícia Grativol¹, Michael Regulski², Milos Tanurdzic², Rodrigo R. Latado³, Marcos A. Machado³, Renato Vicentini⁴, Laurent Farinelli⁵, Adriana Silva Hemerly¹, Robert A. Martienssen², and Paulo Cavalcanti Gomes Ferreira^{1*}

¹Laboratório de Biologia Molecular de Plantas, Instituto de Bioquímica Médica, Universidade Federal do Rio de Janeiro, RJ, Brazil;

²Cold Spring Harbor Laboratory, Cold Spring Harbor, NY 11724, USA; Centro de Biologia Molecular e Engenharia Genética (CBMEG), Universidade Estadual de Campinas, Campinas, SP, Brazil;

⁵Fasteris SA, Plan-les-Ouates, Switzerland.

*Corresponding author: Paulo Ferreira, paulof@bioqmed.ufrj.br; +55 21 2270-8647.

Modern sugarcane cultivars are hybrids of *Saccharum officinarum* and *Saccharum spontaneum* species. Hybrids have complex polyploidy genomes that difficult the studies of structure and organization of the genome. Here, we have used high-throughput Illumina sequencing to analyze repeat and genic regions of sugarcane. Genomic DNA was extracted from purified nuclei isolated from leaves of sugarcane SP70-1143 cultivar, and either sheared to 200bp or digested with McrBc. The sugarcane haploid genome size has been estimated at 800Mb; therefore the filtered reads used in this sequence survey represent an estimated 1.58x coverage of sugarcane haploid genome. We compared the Illumina survey sequences with the repeat classifications available from Plant Repeat Database (<http://plantrepeats.plantbiology.msu.edu/>) to classify each read on the basis of sequence similarity to known repeat sequences. The results provide a snapshot of overall composition of repeat content of sugarcane genome that is not yet sequenced. The McrBC fraction was divided in three samples; the first was sheared to 200 bp, then the 2kb and 5kb fractions were recircularized and sheared to 200 bp. The three fractions were then sequenced and the reads were mapped to the sorghum genome to estimate the coverage of the coding regions. To understand the structure of the repeat rich fraction of the sugarcane genome, total DNA from the wild parents and three commercial cultivars – B4362, RB867515 and RB72454 - was sheared to 200bp and sequenced by Illumina. Comparison of the main repeat fractions has shown significant differences in the abundance of the families of repeats among the genotypes, but also has shown that qualitative differences in repeat presence in the wild parents and commercial cultivars. This study is an initial step towards the discovering of structure and organization of sugarcane genome.

Supported by CNPq, FINEP/Genoprot, CAPES and INCT



Soybean Yield Gaps in Southern Brazil – Their Importance, Magnitude, and Causes

Paulo Cesar Sentelhas
Department of Biosystems Engineering
ESALQ – University of São Paulo
Piracicaba, SP, Brazil

The increasing demand for food, fibers and energy, caused by the expressive growing in the world population, is making agriculture a strategic activity for the food and energy security in many countries around the world. This scenario is more expressive in the countries where there still are lands available for agricultural expansion, with soil and climate potentials. Among these countries, Brazil stands out as one of the few countries around the world with lands available and technological level for increasing agricultural production. However, the expansion of agricultural lands will not be enough to attend the future demand for agricultural products, having also the need for improving the crop yields. For this to happen, a deep analysis of the crop yield patterns should be done in order to identify the magnitude and the causes of the yield gaps, looking for solutions at short, medium and long terms. In the case of soybean crop, it is evident that the actual yields are below to the levels that could be attained, as observed in southern Brazil, where the yield gap between attainable yields (Y_{at}), estimated by crop simulation models, and actual yields (Y_{ac}), reported by governmental statistics, is in average $1,200 \text{ kg.ha}^{-1}$. It shows that other factors than climatic ones are affecting the rainfed soybean crop performance. The agricultural efficiency (ratio between Y_{ac} and Y_{at}) of rainfed soybean crops in southern Brazil, more specifically in the state of Rio Grande do Sul, is around 60%, value greater than for other crops in the region, like wheat (43%) and maize (54%), however without presenting an expressive increase in the last 30 years, with some locations showing reduction in this efficiency. This situation reveals the importance of proactive actions in the crop management in order to diminish the gap between Y_{ac} and Y_{at} , including selection of the best cultivars for the region, with focus on drought tolerance, definition of the best sowing dates, based on the climatic risk zoning and actual climatic conditions, optimization of the plant population, soil correction and fertilization, and weeds, pests and diseases controls. Also, the use of irrigation could be a strategy to be considered together with best crop management, allowing to reduce the gap between Y_{ac} and potential yield (Y_{pt}), which is around 75%, and increasing the yields up to 4700 kg.ha^{-1} , considering the present average rainfed soybean yields in this Brazilian region.

Key-words: agriculture, food and energy security, potential yield, attainable yield, actual yield.



Co-evolution of breeding strategies and cropping systems for raising wheat yield potential on stressful environments

Pedro Luiz Scheeren¹, Vanderlei da Rosa Caetano²

¹Embrapa Trigo, Rodovia BR 285, km 294, PO Box 451, CEP 99001-970, Passo Fundo, RS, Brazil.

²Embrapa Clima Temperado, Rodovia BR 392, km 78, PO Box 403, CEP 99010-971, Pelotas, RS, Brazil. Email: scheeren@cnpt.embrapa.br

The average annual wheat area in Brazil has been around 2 million hectares during the last 10 years. Ninety percent of the wheat area and yield is concentrated in the states of Rio Grande do Sul and Paraná (Climate Regions Cfa and Cfb). About 95% of the cropping area in these states is under no-tillage. The average wheat yield is about 2.200 kg ha⁻¹ in rainfed areas and over 5.000 kg ha⁻¹ in irrigated areas. Less than 2% of the Brazilian wheat growing area is sown under irrigation, in the Cerrado Region. Most of the wheat area is cultivated with modern cultivars and less than 1% is sown with wheat landraces. Since 1925, the Brazilian wheat breeding programs released more than 450 cultivars for the different environments. The current abiotic constraints are: low rainfall (drought) and heat stress in the Cerrado region, and lodging, frost damage and pre-harvest sprouting in Southern Brazil. The most important diseases are: leaf rust (*Puccinia triticina*); scab (*Fusarium graminearum*); mildew (*Blumeria graminis*); glume blotch (*Stagonospora nodorum*); tan spot (*Drechslera tritici repentis*); spot blotch (*Bipolaris sorokiniana*); wheat blast (*Magnaporthe oryzae*); and virus diseases (BYDV and SBMV). Considering these constraints, the need for genetic progress is very challenging. The next generation of crop innovations in wheat and other crops can only be achieved by using the best scientific information, which means conventional breeding, advanced breeding and biotechnology. In 1978, in Southern Brazil, besides the conventional breeding strategies, a new methodology, called systemic breeding, was initiated. In this approach, selection is done on a large number of crosses (thousands of crosses per year), in the first generations. The approach was improved by applying multiple stress selection on F1s and complex F1s (cross of F1/F1), instead of beginning the selection in F2 populations. Such approach could also be suitable for breeding programs in underdeveloped countries, because it does not need high investments. Artificial stresses and pathogen inoculation were used in order to obtain fast solutions on several selected characteristics. Plant ideotype and bread wheat quality traits were also important goals. The first results of the new approach were breeding lines with a set of combined desirable traits. Cultivar BRS Parrudo was released in 2012. It presents a good plant ideotype, has a set of resistances to diseases, high yield potential and high gluten strength.



Breeding crops for boron deficiency: A case study of wheat breeding in Bangladesh

Gustafson¹, J.P., Emon², R.M., Jahiruddin³, M. and Islam², M.M.

¹Division of Plant Sciences, University of Missouri, Columbia, Missouri, USA

²Plant Breeding Division, Bangladesh Institute of Nuclear Agriculture, Mymensingh, Bangladesh

³Department of Soil Science, Bangladesh Agricultural University, Mymensingh, Bangladesh

Boron toxic and/or deficient soils are a problem to wheat production in many regions of the world. To establish the potential for improving wheat production in Bangladesh where boron deficient soils are common we gained access to farmer's fields and management practices all over Bangladesh for testing to establish whether or not the addition of boron to the soil would improve wheat production. The results indicated that the addition of one kilo of boron at planting time increased wheat yields up to 20%. All experiments were conducted in farmer's fields using their varieties and management practices. The experiments suggested that wheat yields, in Bangladesh could easily be improved with the addition of boron to the soil.



An integrated research framework to develop sugarcane for water-limited environments

Prakash Lakshmanan^{1*}, Jaya Basnayake², Philip Jackson, P³, Inman-Bamber, NG³

¹BSES Limited, 50 Meiers Road, Indooroopilly, QLD 4068, Australia

²BSES Limited, PO Box 117, Ayr, QLD 4807, Australia

³CSIRO PI, Australian Tropical Sciences and Innovation Precinct, Aitkenvale, QLD 4814, Australia

*Corresponding author: plakshmanan@bses.com.au

Water limitation is a major production constraint for sugarcane worldwide. In Australia alone water stress is estimated to cost the sugar industry an average of \$260 million (AUD) per annum in lost production. Despite its economic importance, there has been little effort in understanding and improving water stress tolerance in sugarcane. Thus a major research program to develop sugarcane for water-limited environments was initiated. Defining drought adaptation broadly, including both short and long periods of water stress, we took the first step in assessing the potential benefits of a number of traits for improving crop productivity in a simulation study. Among the traits studied increased rooting depth improved cane yield up to 21% in water stressed condition. Conservative water use by reducing stomatal conductance was only marginally useful in improving yield under stress environments. Simulation studies showed that increased transpiration efficiency (TE) at the leaf level through higher intrinsic water use efficiency would nearly always help improve sugarcane biomass yields in water-limited conditions. Concurrently field experiments were also conducted over four years under fully irrigated and managed water stress conditions at two locations in Northern Queensland in Australia to unravel the pattern of stress-adaptive trait responses. Eighty-nine genetically diverse clones were evaluated for this purpose. Water stress treatments reduced cane yield (tonnes of cane per hectare- TCH) and total dry matter (TDM) production by 17 to 52% and 20 to 56% depending on the severity of stress, respectively, compared with irrigated treatments in the same experiments. However, there was little genotype × environment interaction variation for TCH, TDM or commercial cane sugar (CCS) under mild to moderate stress, and hence high genetic correlations between the irrigated and water stress treatments in 1 out of 12 environments studied. Importantly commercial clones outperformed unselected clones under mild to moderate stress suggesting that high intrinsic vigour help them maintain relatively high productivity in a range of moderate stress conditions. In this presentation an integrated physiological, biochemical and molecular framework explaining the mechanistic basis of low GXE for growth and yield parameters, and the high productivity of commercial clones under stressed conditions will be discussed.



Success story of MAS for drought tolerance traits in chickpea

Rajeev K. Varshney

Centre of Excellence in Genomics (CEG), International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru- 502 324, India

Theme- Comparative and Applied Genomics (CAG), CGIAR Generation Challenge

Programme, c/o CIMMYT, Int APDO Postal 6-641, 06600 Mexico DF, Mexico

E-mail address: r.k.varshney@cgiar.org

Chickpea is the third most important grain legume grown in the arid and semi-arid regions of the world. Until recently, very limited genomic resources were available in the crop to initiate molecular breeding. With an objective of promoting genomics-assisted breeding in chickpea, a significant amount of genomic resources is being developed as community efforts (<http://www.icrisat.org/gt-bt/ICGGC/homepage.htm>). These resources include: (i) 1,655 novel simple sequence repeats (SSRs) from the SSR-enriched library and BAC-end sequences, (ii) DArT array with >16,000 features, (iii) 768 conserved orthologous sequences (COS based SNPs), (iv) ~ 2,000 KASPar assays and 96-BeadXpress system assays for cost-effective SNP genotyping, (v) >20,000 Sanger ESTs and 435,018 FLX-454 reads that provided 103,215 tentative unique sequences (TUSs). Furthermore, over 100 million Illumina/Solexa tags have been generated from drought and *Helicoverpa armigera* (insect) challenged tissues of four tolerant/ sensitive chickpea genotypes. By using a variety of markers and genotyping data from collaborators, an integrated reference genetic map comprising 1291 marker loci has been developed for an interspecific mapping population (*C. arietinum* ICC 4958 × *C. reticulatum* PI 489777). By using the same mapping population, a second-generation genetic map comprising 1328 marker loci including 939 gene-based loci with an average inter-marker distance of 0.59 cM has been developed. Both linkage as well as association mapping approaches have been used to identify the markers associated with tolerance to drought, a serious production constraint for chickpea production. In this context, in order to identify drought tolerance QTLs, phenotypic data for root traits for two environment and genotypic data for 294 SSR markers were obtained on an intraspecific mapping population (ICC 4958 × ICC 1882). Marker-trait analysis on these has revealed several QTLs for drought related traits and one major QTL contributing ~30% phenotypic variation for root traits is being introgressed into three elite chickpea lines (JG 11, ICC 92318 and KAK 2) using marker-assisted backcrossing (MABC), to develop superior cultivars with enhanced drought tolerance. Several of the MABC lines have been found to have higher root biomass in multi-location field trial in targeted environments of Africa and Asia. It is anticipated to have MAS products with enhanced drought tolerance in chickpea very soon.



Genome and genomics of pigeonpea

Rajeev K. Varshney

Centre of Excellence in Genomics (CEG), International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru- 502 324, India; &

Theme- Comparative and Applied Genomics (CAG), CGIAR Generation Challenge Programme, c/o CIMMYT, Int APDO Postal 6-641, 06600 Mexico DF, Mexico

E-mail address: r.k.varshney@cgiar.org

Pigeonpea (*Cajanus cajan*), a leading pulse crop of semi-arid region of the world suffers with low crop productivity (<1 ton/ha) due to its exposure with several biotic and abiotic stresses as the crop is generally grown in marginal environments by poor farmers. Although breeders have been engaged in developing superior varieties, modern breeding tools such as molecular breeding could not be deployed until recently mainly due to the low level of genetic diversity present in the primary gene pool and non-availability genomic resources such as molecular markers and mapping populations. As a result of intensive efforts of pigeonpea genomics community at international level, a significant amount of genomic resources like molecular markers, mapping populations, and genetic maps have been developed in pigeonpea. For instance several thousand simple sequence repeat (SSR, 3,094), single nucleotide polymorphism (SNP, 2,000), single feature polymorphism (SFPs, 5,692) and diversity array technology (DArT, 6,000) markers, bacterial artificial chromosome-end sequences (88,860), the first set of GoldenGate assays (768 SNPs) and KASPar assays (1,616 SNPs) for cost-effective SNP genotyping, the comprehensive Sanger EST resource (ca. 10,000), large scale transcript reads by using 454/FLX sequencing technologies in pigeonpea (ca. 500,000), 20 million Solexa/ Illumina reads, eight genetic linkage maps including the first genetic linkage map of pigeonpea, and QTL maps for sterility mosaic disease and fertility restoration have been developed. More recently, as International Initiative on Pigeonpea Genomics (IIPG) has generated genome sequence for 'Asha' variety using Illumina sequencing technology. A total of 73% pigeonpea genome could be assembled with an average N50 of 516.06 kb. Genome analysis predicted 48,680 genes for pigeonpea and also showed the potential role of some gene families during evolution/domestication, e.g. drought tolerance related genes. Efforts are underway to utilize genome sequence for using genotyping-by-sequencing (GBS) approaches for genotyping the reference set, a representative set of global germplasm diversity, and mapping populations. Detailed analysis of both the genotyping and phenotyping data will provide useful information on marker(s)/ gene(s)/ haplotype(s)- trait association that can be used in future molecular breeding programmes. In parallel to accelerate hybrid breeding in pigeonpea, mitochondrial genomes have been sequenced for male-sterile, maintainer, hybrid and wild progenitor lines and a range of 24 to 37 genes were identified across the pigeonpea lines. Comparison of mitochondrial genomes of male-sterile and maintainer lines have provided 13 chimeric open reading frames (ORFs) which may be responsible for male-sterility in pigeonpea. Furthermore, a SSR marker kit has been developed for assessing the purity of hybrid seeds. In summary, these pigeonpea genomics efforts will facilitate the identification of the genetic basis of important traits, and accelerate the development of improved pigeonpea varieties and hybrids.



Molecular dissection of auto-octoploid *Saccharum* genomes by transcriptome sequencing

Jisen Zhang, Qiong Zhang, Lei-Ting Li, Ray Ming

Department of Plant Biology, University of Illinois at Urbana-Champaign, Urbana, IL 61801, USA

Sugarcane (*Saccharum* spp.) has become increasingly important as a first generation biofuel crop. The complexity of the autopolyploid *Saccharum* genomes hindered the progress of genome research and application. Genome assembly is still not possible using the next generation sequencing technologies. To understand the genome structure and organization of *Saccharum* genomes, RNAseq was used to sequence the transcriptomes of 59 individuals in a segregating F1 population derived from *S. officinarum* LA Purple ($2n = 80$, $x = 10$) and *S. robustum* Mol 5829 ($2n = 80$, $x = 10$), yielding a total of 1.9 billion reads. A total of 11,157 and 8,998 single nucleotide polymorphisms (SNPs) markers were generated for LA Purple and Mol 5829, respectively, resulting two high density linkage maps consisting of 96 linkage groups (LGs) for LA Purple and 110 LGs for Mol 5829. The overall map lengths of LA Purple and Mol 5829 were 6718.3 cM and 6946.1 c, with an average genetic distance of 0.60 cM and 0.77 cM between adjacent markers, respectively. Intrachromosomal rearrangements were detected in all LGs of LA Purple and Mol 5829, whereas interchromosomal rearrangements were detected in four pairs of *Saccharum* and sorghum chromosomes. Genes are more evenly distributed along *Saccharum* chromosomes, not concentrated in the distal regions of chromosome arms as found in sorghum. Vast majority of *Saccharum* genes are collinear between *Saccharum* and sorghum genomes. This work provides two large collections of transcriptomes, two saturated genome maps, and detailed genome organization in two *Saccharum* species.



SUPPRESSORS OF GENE SILENCING IN THE PLANT VIRAL FAMILY LUTEOVIRIDAE

Régis L. Corrêa^{1,2}, Adriana F. Fusaro², Maité F. S. Vaslin¹, Peter M. Waterhouse²

¹UFRJ, Rio de Janeiro, Brazil;

²University of Sydney, Sydney, Australia;

Gene silencing is a conserved mechanism for controlling gene expression and in plants is associated with viral defense. During this process, sequence specificity is provided by small RNAs that bind to effector proteins called Argonautes. Members of the viral family Luteoviridae are divided into three genera: Luteovirus, Polerovirus and Enamovirus. The Polerovirus P0 protein was already shown to suppress plant RNA silencing defense through an F-box domain. We are exploring the existence and the mechanism of action of suppressor proteins in the two other genera of the family Luteoviridae. The Enamovirus P0 proved to be a strong suppressor of silencing. Expression of this suppressor in *Arabidopsis* induced developmental abnormalities that were associated with a reduction in the levels of endogenous small RNAs and an increase in the level of their targets. The action of the protein depends on the interaction with the SKP2 protein through an F-Box-like domain. The viral protein binds to and targets Argonaute proteins for degradation. In contrast to the Polerovirus P0, the degradation is abolished in the presence of a proteasome inhibitor. Members of the genera Luteovirus and Polerovirus are phloem-restricted. It is proposed that the action of the Enamovirus P0 on Argonautes and possibly on Dicers and dsRNA-binding proteins may be responsible for phloem relief in this viral genus.



Emerging opportunities for genomics-based breeding of climate resilient crop varieties for future food security

Robert J Henry

Queensland Alliance for Agriculture and Food innovation, University of Queensland, Brisbane Qld 4072 Australia

Meeting global food security needs requires the acceleration of delivery of climate resilient crops. Rapid advances in genomics are being driven by continued advances in DNA sequencing technologies. Approaches to applying this technology to ensure more rapid crop improvement will be reviewed. Whole genome sequencing, amplicon sequencing, transcriptome sequencing and population level sequencing can now be applied to breeding germplasm and crop wild relatives to identify and utilize new genes and sources of useful germplasm. International collaboration in this technology will be critical to ensuring success in delivery of outcomes.



Is there a rule for miRNA nucleotide addition?

Ana Paula Christoff^{1,2}; Luiz Felipe Valter de Oliveira^{1,3}; Rogério Margis^{1,2,3,*}

¹Center of Biotechnology and Department of Biophysics, UFRGS, Rio Grande do Sul, RS.

²Graduate Program in Cellular and Molecular Biology, UFRGS, Rio Grande do Sul, RS.

³Graduate Program in Genetics and Molecular Biology, UFRGS, Rio Grande do Sul, RS.

MicroRNAs are important regulators of gene expression. Several reports have demonstrated the importance of nucleotydyl-transferases in addition of extra nucleotides on miRNAs. Nucleotide additions were initially found in animals, where miRNAs 3' adenylation and uridylation are the most common additions. In plants only few works have evaluated miRNA additions. Using soybean data we demonstrate that different types of addition can occur in 3'end with no obvious preferences and established functions. As soon as these analyses will be extended to other plants, the mechanisms of miRNA nucleotide addition will become clearer and may reveal new pathways to miRNA regulation.



The Path to Discovery

Ronald L. Phillips, Regents Professor Emeritus
University of Minnesota, St. Paul, Minnesota, USA

“Do not follow where the path may lead, go instead where there is no path and leave a trail” (Ralph Waldo Emerson). This approach is key to applying creativity in solving important problems. Creativity is a must along with a prepared mind based on a broad understanding of the field. With the human population growing at a rate of about one billion people every 14 years, the young people in the field have a great challenge. The Crop Science Society of America has articulated the following grand challenges: crop adaptation to climate change, resistance to biotic stresses, management for resource-limited systems, crop management systems, biofuels, and bioresources. Fortunately, we crop scientists are standing on the shoulders of giants, such as Norman E. Borlaug, winner of the Nobel Peace Prize, who said “Never think for a minute that we are going to build permanent peace in this world on empty stomachs and human misery. It won’t happen, and the sooner our leaders at all levels of society reflect on that, the better.” Some personal philosophy to be discussed includes: 1) Believe in your data; 2) Look ahead – assume technology will improve; 3) Think about important research; 4) Maintain absolute integrity; 5) Gain an international perspective; 6) Recognize the importance of writing; and 7) Enjoy the best job in the world ---and watch for those serendipitous opportunities. In the Proceedings of the National Academy of Sciences (PNAS 107:21233), it was reported that “Even though prestigious journals are those that place the highest premium on perceived novelty and significance.....remember.....Many, if place the highest premium on perceived novelty and significance.....remember.....Many, if not most, important scientific findings come from serendipitous discovery”. I retraced my 42 years as a University professor of plant genetics, and found an element of serendipity in the discoveries in my lab spanning 55 graduate students and 23 postdoctoral scientists. Examples include the discovery of 8000 rRNA genes, the elucidation of a transposable element system that led to the cloning of brittle-1, the regeneration of complete maize plants from tissue culture used in producing genetically engineered types, the development of oat plants with maize chromosomes, the identification of a non-coding region controlling maize flowering time, and the finding of high oil corn. A successful scientist must be innovative, creative, collaborative, flexible, persuasive, productive, inspirational, entrepreneurial, curious, unconventional, passionate, analytical, and ethical (Job Board, April 2012, Science 336:33). Einstein said that “I am enough of an artist to draw freely upon my imagination. Imagination is more important than knowledge. Knowledge is limited. Imagination encircles the world.” Remember, the greatest minds look beyond what is to what could be (Scholars Walk, University of Minnesota)



DNA based breeding for improvement of pest resistance and quality traits of food-grade

soybeans

M.A. Rouf Mian*, Tae-Hwan Jun, and Andrew P. Michel M.A. Rouf Mian USDA-ARS and Department of Horticulture and Crop Science, The Ohio State University, 1680

Madison Avenue, Wooster, OH 44691, USA Tae-Hwan Jun · Andrew P. Michel Department of Entomology, The Ohio State Univ/OARDC, 1680 Madison Avenue, Wooster, OH 44691, USA

The importance of food-grade soybean (*Glycine max* L. Merr.) for human health worldwide is increasing with time. The conventional plant breeding approaches are being modified through incorporation of latest molecular technologies, including the DNA markers. The recent rapid advances in molecular and genomics researches in soybean have made this major crop a prime target for DNA marker assisted breeding. The complete genome sequence and hundreds of thousands of DNA markers, high-throughput genotyping platforms and an abundance of genetic materials are now available for DNA assisted breeding for improvement of this valuable crop. In the USDA-ARS soybean breeding program in Wooster, Ohio, USA, we are using DNA assisted breeding for a number of economically important soybean traits. The pest resistant traits includes: resistance to soybean aphid, frogeye leaf spot, Phytophthora root and stem rot, powdery mildew, and other diseases of soybeans. The quality traits such as high protein, high oleic acid, low linolenic acid are also being bred with DNA based selections. Single nucleotide polymorphism (SNP) is the primary DNA marker, however, simple sequence repeat (SSR) and other DNA markers are also in use. The high-throughput melting curve analyses on LightCycler 480® and BeadExpress® are the primary platforms for SNP marker assays. We also use high-resolution agarose gel assay for SSR marker screenings. We are stacking the genes for resistance to soybean aphid, powdery mildew and frogeye leaf spot in food-grade soybeans with high-protein and improved oil quality traits.



Overview of Brazilian advances in Agrichains

Samuel Ribeiro Giordano, Ph.D.

PENSA-University of São Paulo Agribusiness Knowledge Center

How can Brazil supply food and fuel to the world on a continuous and sustainable basis in the next 50 years? 1Natural Resources Brazil has an availability of natural resources for agriculture, availability of water, sun, land and plowable soil. 2State of the art in Tropical Technology for Agriculture and animal sciences Brazil has has efficient National research Agency-EMBRAPA. This agency have more than 35 years of activities and gives support in all latitudes of Brazil to every economic crop and animal breed. 3 Institutions supporting an almost totally deregulated market in agribusiness. Environmental regulation through law and enforcement. An almost complete elimination of subsidies to agriculture since the 1990's promoting it's competitiveness since then. Good business environment for production, domestic market and exports. Brazilian mainstays are: Sugar cane for Sugar, Fuel end Energy Soy bean and Corn for food, feed and oil. Animal Protein: Beef, broiler meat, pork, eggs, fisheries. Beef 2011 Production 9,8 million tons Domestic consumption 8,1 million tons Per capita consumption 43 kg/person/year Size of heard 204 million heads Exports 5,4 US\$ billion 1,1 million tons. Broiler Meat 2011 Production 13,1 million tons Domestic consumption 8,9 million tons Per capita consumption 46,5 kg/person/year Exports 7,5 US\$ billion 4 million. Pork meat 2011 Production 3,4 million tons Domestic consumption 2,7 million tons Per capita consumption 14,3 kg/person/year Exports US\$ 1,43 billion 548 thousand tons. Sugar Cane 2011 Area: 8,4 million ha Production: 571,5 million t Yield: 68,28 t/ha. Sugar : 36,8 million t Ethanol: 22,8 billion liters Size of the Business: US\$ 28 billion. 1The fruit production in Brazil is the third largest in the world, around 43 million tons /year. 2English potato production in 2010 was 3,46 million tons according to IBGE. 3 The Cassava/Manioc/ayuca production is around 24 million tons /year. 4 According to EMBRAPA the vegetable production in Brazil is more than 11 million tons/year. 5 The Milk production is around 32 billion liters/year according to EMBRAPA and the per capita consumption is around 170 l. Effects of institutions in Brazilian Agribusiness 1.An environmental code is being discussed by the society and its representants in a democratic way 2. An agricultural aptitude zoning is being done in Brazil in order to regulate which agor animal activity can be done in the regions of the country 3. The income increase of the population is directly related with the good numbers of the Global Hunger Index and theformation of a strong domestic market. 4. The production and the exports of food and fiber are growing expressively in the last ten years showing the strenght of the Brazilian Agribusiness and itsw answer capacity to supply the world demands for food, fuel and fiber. Conclusions: In spite of some flaws like infrastructure(roads, harbours, railroad net) problems, Brazil can be the one of the world suppliers of food, fiber and fuel in the next 50 years due to: 1Availability of natural resources 2Availability of Tropical Technology 3Availability of Human Resources 4Organized Institutional System and democratic political environment 5Increasing Performance of Agriculture and Animal production in the last 20 years.



Genomes for Crop Legumes

Scott A. Jackson

University of Georgia, Athens, GA USA

Since the last International Crop Science meeting, many legume genomes have either been published or become public including soybean, *Medicago truncatula*, *Lotus japonicus*, common bean, pigeonpea and more. The availability of 'gene maps' for major crop legumes opens new avenues of research and possibilities for tackling agronomic problems that beset these crops. In addition, evolutionary comparisons are possible at a level of resolution that was previously impossible. In this presentation, I will summarize advances in legume genome sequencing and implications for both basic and applied research and the potential impacts for agriculture.



Genomics for Soybean Crop Improvement

Scott A. Jackson
University of Georgia, Athens, GA USA

Soybean is contained in the genus *Glycine* which is approximately 5 Million years old. Soybean (*Glycine max*) is a domesticated form of *Glycine soja* which is found in Asia. Most of the wild perennial relatives are, however, found in Australia, though a few are also found in Asia. We have developed a set of genomic tools consisting of large-insert clone libraries, draft genome sequences, transcriptomes and genetic markers to explore the untapped genetic diversity in the perennial species as well as the annual *Glycine soja*. Genetic diversity within cultivated soybean is extremely low and the wild relatives offer a reservoir of alleles that may have agronomic value. Crossing barriers do exist between the annual and perennial species that complicate introgression, however, the annuals are generally compatible thus enabling breeders/geneticists to explore the genetic potential contained in the undomesticated forms of *G. soja*.



CHALLENGES AND OPPORTUNITIES FROM MAIZE IN BRAZIL: A VIEW FROM THE PUBLIC SECTOR

Sidney NettoParentoni

Associate Director of Research and Development, EMBRAPA-Maize and Sorghum
Research Center – P.O.B 151 - CEP 35701-970 -SeteLagoas, MG, Brazil. E-mail:
chpd@cnpmc.embrapa.br

A review of the world agriculture scenario of the past four decades demonstrates that more and cheaper food has been produced based mainly on productivity gains but only a small increment in expansion of area. This scenario will be challenged in the next decades by a number of factors such as: a) uncertainty of climate change; b) water scarcity for irrigation; c) soil degradation; d) exhaustion of non renewable fertilizer sources; e) land use competition for food, energy and environmental protection; and f) increased consumption due to higher per capita income. The agriculture sector has been able to attend the needs of 7 billion people on the planet but it is not clear if it will be able to maintain the necessary food production growth rates in the future. In this scenario, Brazilian agriculture has achieved remarkable progress in grain production during the past three decades with an increase of 228% in production, a 151% increase in yield and only a 31% increase in area. During the past 12 years Brazil has doubled its grain production (83 million tons in 2000 to 162 million tons in 2012) while expanding the production area by only 14% (44 million ha in 2003 to 50 million ha in 2012). Soybeans and maize have been the major crops responsible for this increase in grain production in Brazil. Maize production increased from 36 million tons in 2002 to 70 million tons in 2012. The major changes in maize production during this period were: a) establishment of a second maize crop growing season ("safrinha") which increased production by a five fold factor (7 to 35 million tons) from 2002 to 2012; b) increased technology adoption, such as single cross hybrid seed (approximately 70%), GMO adoption, mainly for insect control (67% of commercialized seed in 2011), adoption of soil management practices including no till, weed control, higher plant density, better fertilizer management, and better harvest and storage infrastructure; c) internal price regulation by connection to international markets (Brazil exported less than 1 million ton of maize in 2005 while in 2012 this value is expected to be close to 15 million tons). This favorable scenario for maize production in Brazil has been the joint result of appropriate government policies such as credit and minimum price guarantee, but the major driving factor has been the investments in R&D and technology transfer done by both the public and private sectors. Investment in agriculture R&D has increased faster in private sector than in public sector which clearly indicates the need to strengthen public-private partnerships to keep the public sector relevant in the innovation of new technology in this area.



FUNCTIONAL GENOMICS FOR DROUGHT TOLERANCE IN *Phaseolus vulgaris*

Caldas, D.G.G.; Recchia, G.H.; Biazuzo, M.M.A.; Beraldo, A.A.; Konzen, E.R.; Tsai, S.M.

Cell and Molecular Biology Laboratory, CENA- University of São Paulo, Av.
Centenário-303, Piracicaba 13.4160-000, São Paulo, Brazil. E-mail: tsai@cena.usp.br

Although breeding programs are underway, the genetic control of tolerance to drought in *Phaseolus vulgaris* is still unclear, once it is a multigenic character. With the improvement of phenotyping methods, we have now some contrasting varieties to be tested. Thus, the Laboratory of Cellular and Molecular Biology, CENA, USP, Brazil, started in 2009 a project devoted to depict the functional genomics of drought tolerance in *P. vulgaris* aiming at understanding the molecular mechanisms involved in this trait. For this, we constructed a subtractive cDNA library where BAT477 (tolerant genotype) and Carioca 80SH (susceptible genotype) were studied. 1120 differentially expressed ESTs in roots of BAT477 under drought were identified. Then, we used the cDNA-AFLP technique and observed around 3000 differentially expressed TDFs in leaves, stems and roots of both the genotypes. Fifty genes were selected to be studied according spatial and temporal regulation through RT-qPCR and revealed some interesting patterns of gene expression, indicating possible candidate genes for molecular marker and/or genetic transformation. In addition, four DREB genes were cloned, sequenced and characterized; *PvDREB6a* was chosen for a functional study by overexpression in *Arabidopsis thaliana* due to its expression in *P. vulgaris* under drought and to have a transit peptide not yet described. Finally, a proteomic approach was conducted to compare the expressed proteins from roots of BAT477, Carioca 80SH and RAB96 (susceptible genotype) under drought stress. BAT477 presented much more proteins differentially expressed (in % and absolute number) than Carioca 80SH and RAB96, indicating a more active regulatory machinery during water deficit. All these results compiled respond to a series of questions on what are the genes responsible for drought tolerance, where they express in the different plant tissues, when they are activated or repressed and how they work to the plant drought perception, response and adaptation. [CNPq, CAPES, FAPESP]



Cassava Proteome Technologies: approaches and strategies to increase starch yield and nutritional quality varieties

Songbi Chen¹, Kaimian Li¹, Luiz JCB Carvalho²

¹Tropical Crops Genetic Resources, Chinese Academy of Tropical Agricultural Sciences, Danzhou, China;

²Genetic Resources and Biotechnology, Embrapa, Brazil.

Proteomics is a leading technology for the high-throughput analysis of proteins on a genome-wide scale. It has become a major field of functional genomics. In plant it is used to find new genes, validate gene functions, evaluate the roles of transgenic plants and improve the efficiency of molecular breeding by design. Its applications are currently being extended to analyze various functional aspects of proteins such as posttranslational modifications, protein-protein interactions, activities and structures. Cassava is widely grown as a staple food and animal feed in countries of tropics and subtropics. In Asia, cassava products are for multiple uses for multiple markets. Cassava proteome technologies will provide the insight on the improvement of crop integrated breeding for starch yield and nutritional quality varieties.

In this study proteomics provides a broad view of cassava varieties at the level of proteins. It is intended to give an understanding of the technologies behind proteomics and its application to address biological questions regarding source-flux-sink interactions, high starch accumulation, nutritional-quality characteristics and etc. It was used to characterize the proteomes of source, flux and sink organs of cassava varieties. More than 2,000 protein spots in protein-expression images of cassava were analyzed and the identified proteins were classified into 14 functional groups. The results indicated the differential-protein expression and the unique metabolic pathways in starch accumulation and nutritional quality in storage roots. The cross-talking between photosynthetic pathway in leaves, signal transduction in petioles and starch-accumulation pathways in the storage roots were also discussed in the present study. These data involved proteomic evaluation of crosstalk of metabolic pathways would direct provide a guide to the improvement of cassava breeding for high starch yield and nutritional quality varieties. In addition, proteomic approach would be used to identify the cassava mutant and decrease the breeding cycles. This work may pave the way towards to evaluate cassava varieties in global protein levels, and also reveal the biological regulatory networks for cassava proteomics-assisted breeding.

Key words: Cassava, proteome technology, starch accumulation, nutritional quality.



Gene expression associated with soybean resistance to stink bug complex

Steven J. Clough^{1,2}, Michelle da Fonseca Santos³, Mohammad Belaffif², Milene Möller³, Clint Allen⁴, José Baldin Pinheiro³

¹US Department of Agriculture, Agricultural Research Services, Urbana, Illinois, USA

²University of Illinois, Urbana, Illinois, USA

³Universidade de São Paulo, Escola Superior de Agricultura Luiz de Queiroz, Piracicaba, SP, Brazil

⁴US Department of Agriculture, Agricultural Research Services, Stoneville, Mississippi, USA

Stink bugs are emerging as a major pest of soybean throughout the world and their populations are increasing in countries such as the USA and Brazil. Because these insects pierce immature pods to feed on developing seed, the insects are responsible for significant losses of yield and seed quality. To identify genes that might be associated with stink bug resistance in soybean, we looked at gene expression levels from isolated pods that had been fed upon by stink bugs versus expression in control pods. The partially resistant genotype IAC100 was compared to highly susceptible CD215 at 24 hours post-infestation, with and without insects feeding upon them, using plants grown in a field in the state of Mississippi in the USA. Four biological replicates were analyzed for each treatment, paired-end sequenced by an Illumina system (sequencing performed by the High-throughput Sequencing and Genotyping Unit of the Roy J. Carver Biotechnology Center at the University of Illinois, Urbana), processed by the Trinity freeware package (<http://trinityrnaseq.sourceforge.net/>), and the differential expression ratios and *fdr* corrected *p*-values calculated using the RNA-seq analysis software, RSEM (<http://deweylab.biostat.wisc.edu/rsem/>). Of the 166,593 contigs created by Trinity from the IAC100 128,668,640 sequenced RNA fragments, 59.8% hit a known soybean gene (Williams 82 GlymaID), another 37.6% hit elsewhere on the Williams 82 soybean reference genome, and only 2.6% did not align to the reference genome. Of the 194,425 contigs created by Trinity from the CD215 120,959,538 sequenced RNA fragments, 60.3% hit a known soybean gene (Williams 82 GlymaID), another 34.9% hit elsewhere on the Williams 82 soybean reference genome, and only 4.8% did not align to the reference genome. To assign added likelihood that a given gene might be associated with resistance, one approach was to search for genes that were both differentially expressed more so in IAC100 than CD215, as well as located near a mapped stink-bug resistance QTL. Other approaches to identify candidate resistance associated genes will include the analysis of the annotations of differentially expressed genes for a likely role in insect defense, as well as comparisons of the frequencies of expression of each gene between the two cultivars, with or without insect feeding. Preliminary results will be discussed.



CLIMATE CHANGE ADAPTATION STRATEGY FOR CROP IMPROVEMENT EMPLOYING GENOMICS

Suk-Ha Lee

Department of Plant Science and Research Institute for Agriculture and Life Sciences, Seoul National University, Seoul, 151-921, Korea

Plant Genomics and Breeding Research Institute, Seoul National University, Seoul, 151-921, Korea

Global villages confront climate changes that result in the impacts on water resources and crop productions. To evaluate the uncertainty of the impacts on future climate, several scenarios have been developed regarding interactions of climate system, ecosystem, and human activities. From the climate model scenarios, irradiative forcing scenarios and emissions scenarios, we expect the future environment and climate change will affect on crop production seriously. As the adaptation strategy to cope with this danger, we implement genomics to maneuver biotic and abiotic stresses. Responsible genes of QTL for the biotic stress and abiotic stress resistance and flowering and maturity would be the good genetic resources to resist or avoid the environmental changes. To figure out the putative responsible genes for those QTL, we used whole genome sequences of two major crops, rice and soybean. Several QTL regions contained similar gene contents with co-linearity. Especially, in genomic regions of biotic and abiotic stress related QTL in rice, gene contents of chromosomes 1 and 5 were highly conserved, indicating that these genes are putatively related to those traits. Moreover, the population specific QTL and location specific QTL are also important genetic resources because those represent genetic regions for specific environmental condition. In rice populations of indica/indica, several abiotic QTL were not shared with japonica/indica and japonica/japonica populations. These population specific regions might be the candidate regions for adaptation against high temperature. Meanwhile, one population of soybean was grown at different locations and QTL for flowering were mapped to different genomic regions. Interestingly, different regions of QTL showed synteny, which implicate the environmental specific role of syntenic regions. Those approaches using whole genome gene contents and the QTL information are able to develop adaptation-related markers and the recently developed high-throughput genotypers facilitate crop breeding to manage future climate and environmental changes.



Physiological Improvement in Soybean Water Use to Increase Yields

Thomas R. Sinclair
North Carolina State University
Raleigh, NC, USA

Drought often impacts the yields of soybean, and 2012 may be long remembered as year of severe drought that shook global grain markets. Plant trait improvements to increase yield under water-limited conditions could offer substantial benefit to growers and consumers. One trait often voiced for improvement is plant transpiration use efficiency (TUE). However, close analysis shows that TUE has a maximum value in each species, which is very difficult to exceed. This results because both carbon dioxide acquisition and transpiration occur through the same physical pathway, i.e. the stomata. The intrinsic ratio of photosynthesis to transpiration for soybean has a maximum of about 5 Pa. Assuming drought survival is not relevant for commercial production, there are only a few options for improving plant performance under water-limited conditions. One putative trait is a decrease in stomata conductance early in the soil drying cycle. The early decrease results in a slow extraction of water from the soil so that water is available for use in a prolonged drought. Unfortunately, no large variation has yet been identified in soybean for this trait, although large variation has been identified in other crop species. Another trait is the response of plants to high atmospheric vapor pressure deficit (VPD). Under conditions of high VPD such as midday, a restriction on leaf gas exchange results in a lowered 'effective' VPD than would be experienced by the plant if the stomata remained continuously open. An additional benefit of the restricted gas exchange under high VPD is that soil water is conserved for use later in the season when drought may develop. A "slow-wilting" genotype, PI 416937, has been identified that expresses the restriction on transpiration rate at high VPD, i.e. no further increase in transpiration rate above a VPD of about 2 kPa. This behavior has been traced to low hydraulic conductance in the leaf. Also, this genotype appears to have a unique population of aquaporins in the leaf that result in the low hydraulic conductance. This trait has now been linked to four QTLs in soybean.



Photoperception and Photoperiod Genes in Soybean

Vera Quecini¹, Maria I. Zucchi², José B. Pinheiro³, Natal A. Vello³

¹Embrapa Uva e Vinho, Bento Gonçalves, RS, Brazil;

²Agência Paulista de Tecnologia dos Agronegócios (APTA) Polo Centro-Sul, Piracicaba, SP, Brazil;

³Escola Superior de Agricultura "Luiz de Queiroz (ESALQ)/Universidade de São Paulo (USP), Piracicaba, SP, Brazil.

Light is one of the most important environmental factor controlling plant growth and development. It provides energy for growth and biomass production via photosynthesis and temporal and spatial information for developmental control by photoreceptor-mediated signaling networks. Light is the main input to the endogenous time-keeping mechanism, allowing the generation of adaptive responses to daily and seasonal changes in environmental conditions. Photoreceptor genes and signaling partners have been successfully identified in plant species by traditional genetic and molecular approaches, however, the vast majority of the available information is from model plant species. The incorporation of genomic and bioinformatic tools to previously available genetic knowledge has helped us to gain insight into physiological and developmental processes in economically important crops. In soybean, genome-wide analyses of ortholog groups and *in silico* gene expression profiling have helped to identify photoreceptor, light signaling and circadian clock-component genes. Further insight on the molecular function of the identified genes has been gained by phylogenetic and protein-motif investigations. Furthermore, coupling functional information and genome mapping has permitted the attribution of candidate genes to known light and photoperiod-responsive loci in the soybean genome. Comprehensive studies of the natural variation for flowering-time in soybean germplasm have suggested that circadian regulation of photoreceptor gene expression, but not photoreceptor gene sequence, may be associated to photoperiodic flowering. Thus, genomic tools have accelerated soybean research by helping to establish the genetic framework for light- and circadian-controlled processes, associated to economically important traits such as photoperiodic flowering, in soybean. Moreover, knowledge on gene sequences, transcriptional profiles and genome location have helped to clarified the evolutionary relationships between soybean and other crop species. Further genomic investigations may help to elucidate the role of temperature in light and photoperiod controlled-processes in soybean.



Phenotypic plasticity of crop traits

Victor Sadras

South Australian R&D Institute, Waite Campus, Adelaide, Australia

Organisms have two components: the genome and the rest; the rest is phenotype. One genotype can produce different phenotypes in response to environmental conditions. This paper outlines different perspectives on the sources of phenotypic variance. The proposition is made that a focus on phenotypic plasticity contributes biological and agronomic insight. Milestones in the progress of plasticity as a core concept in developmental biology and evolution are summarised, including Woltereck's definition of reaction norms in 1909, Bradshaw's influential article in *Advances in Genetics* (1965) and Reymond and colleagues' unequivocal proof of specific genetic control of trait plasticity (2003). The perspective of phenotypic plasticity is applied to answer agronomic questions and to probe for patterns. Case studies include effects of temperature on stomatal conductance, berry pH and acidity in grapevine, effect of source : sink ratio on water relations of perennial horticultural crops, and the effect of sowing date on the nitrogen economy of maize. The notion of hierarchy of plasticities, first established for seed size and number, is extended to include tillers and components of seed number in an updated model of cereal yield.



Environmental assaying or e-typing as a key component for integrated breeding platform

Yunbi Xu

Institute of Crop Sciences/International Maize and Wheat Improvement Center (CIMMYT), the National Key Facility for Crop Gene Resources and Genetic Improvement, Chinese Academy of Agricultural Sciences, Beijing 100081, China. Email: y.xu@cgiar.org

Breeding for complex traits in crop plants warrants understanding and manipulation of many environmental factors including an array of biotic and abiotic stresses. An efficient integrated breeding platform needs to take into consideration the etyping, a word coined for environmental assaying of a comprehensive set of environmental information (Xu et al 2012, Molecular Breeding 29:833–854). E-typing, together with high-throughput genotyping and precision phenotyping, transforms the concept of plant breeding from a “plane”, determined by genotype and phenotype, to a “space”, measured by all the three dimensions. Basic environmental factors to be considered in etyping include those significantly affecting plants, such as soil, air, light, temperature, water, cropping systems, and accompanying organisms. These factors are being complemented with intentional environmental characterization through improved data collection using advanced systems such as geographic information system (GIS). A large volume of environmental data has been accumulating in multi-environment trials through international breeding programs such as those organized by CGIAR centers and multi-national incorporation. Etypic information should have been well exploited for improving our understanding of plant response to environmental factors in various ways, including precision measurement of environmental factors that affect specific developmental processes or stages, determination of target environments for specific environmental adaptation, understanding of contributing factors to phenotypic variation within a field trial or trial block, dissection of environmental factors involved in genotype by environment interaction into specific components, and breeding for improved response to specific environmental factors and their combinations. The most important factors, which contribute to the large gap existing between the yield achieved in experiments and the yield realized in commercialization, can be identified and addressed to maximize the yield. By the end, an efficient integrated breeding platform can be built up with the 3-D profile projecting genotype, phenotype and environment. For a genotype that has been well-characterized for alleles and their haplotypes at all relevant loci, its phenotype or target product at a specific location with a set of environmental factors defined could be predicted precisely.

Key words · Integrated breeding platform · precision phenotyping · environmental



Program and Abstracts