

# Book of Poster Abstracts

2006  
International Plant Breeding Symposium

Honoring John Dudley



Mexico City, 20-25 August, 2006

Editor: Sophie Higman



IOWA STATE UNIVERSITY  
COLLEGE OF AGRICULTURE



# Book of Poster Abstracts

**2006 International Plant Breeding Symposium**

**Honoring John Dudley**

Mexico City, 20-25 August, 2006

Editor: Sophie Higman



## Contents

Welcome to the 2006 International Plant Breeding Symposium. In this Book of Poster Abstracts you will find the following:

Program	2
IPBS 2006 Honoree and presenters – biographical information	7
Poster Abstracts – Table of contents	19
Plant breeding education abstracts	31
Plant breeding and allelic discovery abstracts	32
Breeding for quality, nutritional and micronutrient traits	53
Molecular breeding	79
Cultivar development methodologies – maize	107
Cultivar development methodologies – wheat	153
Cultivar development methodologies – other crops	174
Cultivar development methodologies – modeling	182
Index of Authors	185
Mexico City Center – local information	195

## Program

- IPBS registration and logistics desk will be in *Salon Doña Sol* from 8:00 a.m. to 6:00 p.m. Monday to Friday, except Wednesday.
- BCD Travel Service staff will be next door to the IPBS desk, open from 7:00 a.m. to 7:00 p.m. throughout the week.

<b>Sunday, August 20</b>		
Arrivals	Airport welcoming committee	Airport/Hotel
14:00-20:00	Conference Registration	Doña Sol Salon
20:00-21:00	Cocktails (nationals drinks, snacks)	Lobby – Salon Don Alberto
<i>Open</i>	<i>Dinner (on your own)</i>	
<b>Monday, August 21</b>		
07:00-08:00	Breakfast	Salon Don Alberto 1
07:30-08:30	Conference Registration	Salon Doña Sol
<b>Session One - Frontiers in Breeding for Complex Traits</b>		
<b>Chair: Rex Bernardo</b>		
08:30-08:40	Welcome and Opening Address	Masaru Iwanaga CIMMYT
08:40-08:50	University of Illinois Comments	Robert A. Easter
08:50-09:00	Iowa State University Comments	Kendall R. Lamkey
09:00-09:40	<u>Keynote Address</u> : History, Contribution, and Future of Quantitative Genetics in Plant Breeding	Arnel R. Hallauer Iowa State University
09:40-10:20	<u>Honoree Address</u> : From Means to QTL: The Illinois Long-term Selection Experiment as a Case Study in Quantitative Genetics	John W. Dudley University of Illinois
10:20-10:40	<i>Coffee Break and Belated Registration</i>	
10:40-11:20	Marker-assisted Selection: Strategies for Identifying and Manipulating Novel and Functionally Important Alleles	Steven J. Knapp University of Georgia
11:20-12:00	At the Interface of Genomics and Quantitative Genetics	William D. Beavis National Center for Genome Resources
12:00-12:30	Customer and Consumer-based Plant Breeding in the 21 <sup>st</sup> Century	Bill Niebur Pioneer Hi-Bred
12:30-14:00	<i>Lunch (on your own)</i>	

<b>Session Two - Plant Breeding Education</b>		
<b>Sponsored by the University of Illinois and Iowa State University</b>		
<b>Chair: Kendall Lamkey</b>		
14:00-14:40	Education and Preparation of Plant Breeders for Careers in Global Crop Improvement	Fred Bliss Seminis Vegetable Seeds and University of California-Davis
14:40-15:20	Plant Breeding and Related Biotechnology Assessment: Strengths and Needs in the Developing World	Elcio Guimarães FAO, Rome
15:20-16:00	NOVA University: Plant Breeding Education in a University Without Walls	Sven B. Andersen The Royal Veterinary and Agricultural University, Denmark
16:00-16:30	Question and Answer Session	
16:30-17:00	<i>Coffee Break</i>	
17:00-20:00	Poster Sessions	Salon Don Alberto 2
<i>Open</i>	<i>Dinner (on your own)</i>	
<b><u>Tuesday, August 22</u></b>		
07:00-08:30	Breakfast	Salon Don Alberto 1
<b>Session Three - Plant Pre-Breeding and Allelic Discovery</b>		
<b>Sponsored by Generation Challenge Program</b>		
<b>Chair: Rodomiro Ortiz</b>		
09:00-09:40	Generation Challenge Programme: Unlocking Genetic Diversity in Crops	Wayne Powell NIAB, UK
09:40-10:20	Evolution of Population Structure and Heterotic Groups in Temperate Maize: Consequences for Association Genetics	Alain Charcosset Institut National de la Recherche Agronomique, France
10:20-10:50	<i>Coffee Break</i>	
10:50-11:30	Maize Anthracnose Resistance: Genetics and Breeding	Sandra Milach Pioneer Hi-Bred, Brazil
11:30-12:10	Pre-breeding and Genetic Diversity in Field Beans	Jorge Acosta-Gallegos INIFAP, Mexico
12:10-12:40	Question and Answer Session	
12:40-14:00	<i>Lunch (on your own)</i>	

<b>Session Four - Breeding for Quality, Nutritional, and Micronutrient Traits</b>		
<b>Sponsored by HarvestPlus Challenge Program</b>		
<b>Chair: Torbert Rocheford</b>		
14:00-14:40	Breeding For Modified Fatty Acid Composition In Soybean	Walter R. Fehr Iowa State University
14:40-15:20	HarvestPlus: Breeding Crops for Better Nutrition	Wolfgang H. Pfeiffer CGIAR Harvest Plus, Colombia
15:20-15:50	<i>Coffee Break</i>	
15:50-16:30	Breeding Progress and Prospects for Provitamin-A and Other Micronutrients in Rice	Gerard Barry IRRI
16:30-17:00	Question and Answer Session	
17:00-18:00	Poster Sessions	Salon Don Alberto 2
<i>Open</i>	<i>Dinner (on your own)</i>	
<b><u>Wednesday, August 23 - CIMMYT Field Day</u></b>		
06:15	Meet in hotel lobby to be led to buses and receive box-breakfast	Hotel lobby
06:30	Bus departure to CIMMYT Headquarters and INIFAP. Participants will be divided into Group A and Group B	
08:00-10:30	Part One of Program – Group A at CIMMYT, Group B at INIFAP	CIMMYT / INIFAP
10:30- 11:00	Groups exchange between CIMMYT and INIFAP	
11:00-13:30	Part Two of Program – Group A at INIFAP, Group B at CIMMYT	CIMMYT / INIFAP
13:30-14:00	Both Groups move to CIMMYT Guest House Gardens	
14:00-15:00	Luncheon	Guest House Gardens
15:00 15:45	Speech by Masa Iwanaga, CIMMYT Director General	
15:45-16:15	Performance of Traditional Mexican Dance	
16:30	Board buses to Mexico City	
17:30	Expected arrival at Hotel Sheraton Centro Historico	
<i>Open</i>	<i>Dinner (on your own)</i>	

<b>Thursday, August 24</b>		
07:00-8:30	Breakfast	Salon Don Alberto 1
<b>Session Five - Molecular Breeding</b>		
<b>Sponsored by Syngenta</b>		
<b>Chair: Sam Eathington</b>		
09:00-09:40	Candidate Gene Approach to the Identification of Genes Underlying Quantitative Traits in Potato and for Diagnostic Marker Development	Christiane Gebhardt Max Planck Institute for Plant Breeding Research, Germany
09:40-10:20	Molecular Breeding Using a Major QTL for Fusarium Head Blight Resistance in Wheat	James A. Anderson University of Minnesota
10:20-10:50	<i>Coffee Break</i>	
10:50-11:30	QTL for Root Architecture and Drought Tolerance in Maize	Roberto Tuberosa University of Bologna
11:30-12:10	Molecular Breeding to Enhance Ethanol Production from Corn and Sorghum Stover	Wilfred Vermerris University of Florida
12:10-12:40	Question and Answer Session	
12:40-14:00	<i>Lunch (on your own)</i>	
<b>Session Six - Cultivar Development Methodologies</b>		
<b>Sponsored By: Renessen</b>		
<b>Chair: Bruno Albrecht</b>		
14:00-14:40	Breeding for Striga Resistance in Sorghum: Exploitation of an Intricate Host-Parasite Biology	Gebisa Ejeta Purdue University
14:40-15:20	Insights and Innovations from Wide Crosses in Plant Breeding	Tom Osborn Seminis Vegetable Seeds
15:20-15:50	<i>Coffee Break</i>	
15:50-16:30	Use of Double Haploids in Recurrent Selection and Hybrid Development in Maize	André Gallais Institut National Agronomique Paris-Grignon, France
16:30-17:00	Question and Answer Session	
17:00-18:00	Poster Sessions	Salon Don Alberto 2
20:00-20:30	Cocktails	Lobby – Salon Don Alberto
20:30	Gala Dinner, sponsored by SAGARPA (MC: John Dodds, CIMMYT). Speakers: Mexican Agriculture Minister (20 min) Robb Fraley - Monsanto (15 min)	Salon Don Alberto 1



<b>Friday, August 25</b>		
07:00-08:30	Breakfast	Salon Don Alberto 1
<b>Session Seven - Cultivar Development Methodologies</b>		
<b>Sponsored By: CIMMYT</b>		
<b>Chair: Bruno Albrecht</b>		
09:00-09:40	Environmental Classification in Plant Breeding	Carlos M. Löffler Pioneer Hi-Bred
09:40-10:20	Breeding for Highly Variable Abiotic Stress Environments	Marianne Banziger CIMMYT, Kenya
10:20-10:50	<i>Coffee Break</i>	
10:50-11:30	Breeding for Abiotic Stress Tolerance in Temperate Maize	Elizabeth A. Lee University of Guelph
11:30-12:10	Use of Crop Physiology to Enhance Breeding for Stress Environments	Matthew Reynolds CIMMYT
12:10-12:40	Question and Answer Session	
12:40-14:00	<i>Lunch (on your own)</i>	
<b>Session Eight - Contributions from Prof. Dudley's Former Students</b>		
<b>Sponsored By: University of Illinois</b>		
<b>Chair: Kendall Lamkey</b>		
14:00-14:30	Practical Uses Of Molecular Markers In A Commercial Breeding Program	Sam Eathington Monsanto Company
14:30-15:00	Backcross Versus Forward Breeding in the Development of Transgenic Maize Hybrids: Theory and Practice	Rita H. Mumm GeneMax Services
15:00-15:30	Apomixis for Cultivar Development in Tropical Forage Grasses	John W. Miles CIAT
15:30-16:00	Question and Answer Session	
16:00-16:30	<i>Coffee Break</i>	
16:30-17:00	Symposium Summary	Rex Bernardo University of Minnesota
17:00-17:30	Closing Ceremony (MC: Ted Crosbie, Monsanto) <ul style="list-style-type: none"> <li>• Closing Comments</li> </ul>	Ted Crosbie and John Schoper
Open	<i>Dinner (on your own)</i>	
<b>Saturday, August 26</b>		
07:00-08:30	Breakfast	Salon Don Alberto 1
Departures		

## **IPBS 2006 Honoree and presenters – biographical information**

### The Honoree

John W. Dudley is an emeritus Professor of Plant Genetics at the University of Illinois. Prior to his retirement he was the inaugural holder of the Renessen Endowed Chair in Corn Quality Trait Breeding and Genetics. Dr. Dudley's breeding career has spanned 49 years and three important crops: maize, alfalfa, and sugar beets. Dr. Dudley is most well known for his research on long-term selection for protein and oil in the classic University of Illinois experiment, selection for the simultaneous improvement of multiple traits, particularly yield and disease resistance, developing methods for choosing parents for use in breeding programs, and the application of biotechnology to plant improvement. Dr. Dudley has been extremely active in academia, has published over 155 papers, served on the editorial board of the esteemed journal *Crop Science* in various capacities from 1964 to 1976, and served as associate head of the Department of Crop Sciences at the University of Illinois. Dr. Dudley is a fellow of the American Society of Agronomy, Crop Science Society of America, and the American Association for the Advancement of Science. He has received the DEKALB Crop Science Distinguished Career Award, the National Commercial Council of Plant Breeders Award, and the Crop Science Research Award (CSSA).

### The Presenters

#### Jorge A. Acosta-Gallegos

Dr. Jorge A. Acosta-Gallegos is a traditional plant breeder that has a passion for exploring the Mexican mountains in search for wild *Phaseolus* beans. As a result of that hobby he has contributed with a few hundred accessions to the germplasm banks of INIFAP and CIAT. After graduating as an agronomist in 1972 he started working at the National Agricultural Research Institute (now INIFAP) on rainfed dry beans of the semiarid highlands of the state of Durango. The main emphases of his breeding efforts in Durango were drought adaptation and disease resistance, mainly to root-rots and anthracnose. After graduating from Michigan State University in 1988, he released several improved cultivars, the most important of which was "Pinto Villa", a cultivar that dominated its commercial seed class in the semiarid highlands of Mexico for over a decade. He has also collaborated in the Latin-American project of the Bean/Cowpea-CRSP for more than twenty years. From 1991 until 2002 he worked in a sub-humid temperate environment in Central Mexico, mostly concentrating on breeding beans with multiple disease resistance. During the last four years he has built a new breeding program in the Bajío region where he now lives. There, he aims to develop bean cultivars belonging to half a dozen commercial seed classes that are adapted to either irrigated or rainfed conditions. During the course of his career, Dr. Acosta has participated in the development of more than twenty improved dry bean cultivars.

### James Anderson

James Anderson is a professor in the Department of Agronomy and Plant Genetics at the University of Minnesota. He obtained his B.S. degree in Agronomy from the University of Minnesota in 1987, M.S. in Crop Science (Plant Breeding) from the University of Kentucky in 1989, and a Ph.D. in Plant Breeding from Cornell University in 1992. His previous positions include Assistant Professor at North Dakota State University and Research Geneticist with the USDA-ARS, Pullman, Washington. Dr. Anderson has been working in the areas of wheat breeding and genetics since 1989. He has contributed to the development of 11 released wheat cultivars and authored/co-authored 61 articles in peer-reviewed journals. His major research effort is the genetic investigations of complexly inherited traits including grain quality and disease resistance. Recent research has focused on Fusarium head blight and leaf rust resistance and incorporating resistance into new cultivars using marker-assisted selection. Dr. Anderson received the Crop Science Society of America's Young Crop Scientist Award in 1998.

### Sven Bode Andersen

Sven Bode Andersen is professor of plant breeding at the Royal Veterinary and Agricultural University, Denmark with a MSc in Horticulture 1980 and a Ph.D. in plant breeding 1983. Research focused on haploid production for breeding of horticultural and agricultural species and the use of molecular markers for diversity evaluation and to speed up breeding programs.

### Marianne Banziger

Marianne Banziger is the Director for CIMMYT's Global Maize Program. She obtained her PhD in crop physiology at the Swiss Institute of Technology (ETH) in Zurich Switzerland in 1992. She joined CIMMYT as a Post-Doctoral Fellow and Scientist, before she moved to southern Africa in 1996. Dr. Banziger's research focuses on the abiotic stress tolerance in maize, in particular drought and low soil fertility, environmental characterization of maize growing environments, and use of molecular markers in drought breeding. In southern Africa, she initiated and led maize germplasm development network targeted at stress-prone environments which involved well over 50 organizations, including NARS, NGOs, the private seed sector, farmer organizations, universities and regional organizations. This partnership developed, evaluated and deployed so far over 45,000 tons of seed of stress tolerant maize varieties to smallholder farmers in Africa.

### Gerard Barry

Dr. Gerard Barry joined the International Rice Research Institute (<http://www.irri.org/>) in November 2003 as the Coordinator of the Golden Rice Network (<http://www.goldenrice.org/>), and is also the HarvestPlus Rice Crop Team Leader (<http://www.harvestplus.org/>), and Head of IRRI's Intellectual Property Management Unit. Prior to joining IRRI, Dr. Barry spent more than 20 years with Monsanto Company in St. Louis, USA, where he had various responsibilities, including co-head of the Rice Business Team, head of the Rice Genome and Rice Genomics

projects, and Director of Research for developing country research cooperation. He received B.Sc. and M Sc. degrees from University College, Cork, Ireland, and his Ph.D. from Columbia University in New York, and he was formerly Charge de Recherche at the Institut Pasteur in Paris. Dr. Barry is co-inventor on 20 patents, co-author of more than 50 research articles, and has been a frequent invited speaker at international conferences.

### William D. Beavis

Most often cited for his discovery of bias in estimates of genetic effects from QTL analyses of segregating populations (the "Beavis Effect"), Dr. Beavis gained extensive experience in the application of statistical genetic methods during his twelve years at Pioneer-Dupont. Since joining NCGR in 1998, Dr. Beavis has been the principal investigator for a variety of bioinformatics projects, including The Arabidopsis Information Resource (TAIR), GeneX and GeneX-Lite gene expression systems, the Legume Information System (LIS), the Legume Information Network (LIN) and the Genome Explorer and Survey of Immunological Response (GEySIR) system. Currently, Dr. Beavis is developing novel methods, based on Bayesian inference, to identify global gene expression patterns associated with genotypes. Dr. Beavis received his Ph.D. degree in Plant Breeding and Statistics from the Iowa State University in Ames, Iowa. He holds an M.S degree in Interdisciplinary Biology-Statistics from New Mexico State University in Las Cruces, NM and a B.S. degree in Range Management from Humboldt State University, Arcata, California. Since 2003, Dr. Beavis is also an Adjunct Professor in the Department of Mathematics and Statistics at University of New Mexico and an adjunct scientist at Lovelace Respiratory Research Institute.

### Rex Bernardo

Rex Bernardo is a professor and endowed chair in corn breeding and genetics in the Department of Agronomy and Plant Genetics, University of Minnesota. He obtained a B.S. degree in agriculture at the Visayas State College of Agriculture in the Philippines in 1984, and a Ph.D. degree plant breeding and genetics at the University of Illinois at Urbana-Champaign in 1988. Dr. Bernardo's research focuses on the use of quantitative genetics theory and molecular markers to improve the efficiency of plant breeding methods, particularly for corn. Dr. Bernardo teaches a graduate course on the application of quantitative genetics to plant breeding and a graduate course on publishing in plant science journals. He is currently director of the Applied Plant Sciences graduate program at the University of Minnesota. Dr. Bernardo has served on the editorial boards of Crop Science and Theoretical and Applied Genetics. He received the Crop Science Society of America (CSSA) Young Crop Scientist Award in 1999, is a Fellow of CSSA and the American Society of Agronomy, and is currently chair of the Crop Breeding and Genetics division of CSSA.

### Fred Bliss

Fred Bliss is Senior Director of R&D Special Projects/NAFTA Commercial Research Coordinator at Seminis Vegetable Seeds; and Professor Emeritus at the University of California, Davis. Dr. Bliss received the B.S. Degree in Agronomy from the University of Nebraska and the Ph.D. Degree in Horticulture-Genetics from the University of Wisconsin-Madison. Prior to joining Seminis in 1998, where he has served in varied capacities including Director of World-wide Breeding and of Support Science and Technology, he was a member of the Department of Horticulture at U.W.-Madison (1966 -1988), and the Department of Pomology (Lester Endowed Chair) at UC Davis (1988-1998). Fred has taught courses on The Principles of Plant Breeding, Advanced Line Breeding, and Vegetable Crops Production and served as Major Professor for some 30 Ph.D. and M.S. students from around the world. He has managed research projects in Africa and Latin America as well as the U.S. where emphasis has been on breeding and genetic improvement of self-pollinated agronomic crops (dry beans and cowpeas), horticultural crops (table beets, garden beans and tomatoes), vine fruits (kiwifruit) and tree fruits (peaches, apricots and rootstocks). He has served as president of the American Society for Horticultural Science and is a Fellow of the ASHS, CSSA, and AAAS.

### Alain Charcosset

Dr. Alain Charcosset is a senior scientist in the Plant Genetics and Breeding department at the Institut National de la Recherche Agronomique (INRA) in Gif-sur-Yvette, France. He studied Agronomy and Plant Breeding at the Institut National Agronomique Paris-Grignon, where he received his Ph.D. degree in 1990. His research focuses on the characterization of genetic diversity and its utilization for quantitative trait improvement, based on genomics information and the use of marker-assisted selection. This research involves theoretical contributions and application to early maize and its adaptation to northern Europe environmental conditions. After having coordinated its maize program since 1993, he is presently vice-head of the Plant Genetics and Breeding department of INRA.

### Sam Eathington

Sam Eathington was raised on a grain and livestock farm in west-central Illinois. He received his B.S. ('90), M.S. ('93), and Ph.D. ('95) from the University of Illinois at Champaign-Urbana. Sam's graduate education focused on genetics, plant breeding (soybeans and corn) and application of molecular markers to plant breeding. Sam spent one year as the Quantitative Traits Project Leader for ICI/Garst Seed Company, where he worked to integrate molecular markers into traditional corn breeding programs. In September of 1996, Sam joined Monsanto as part of Asgrow Seed Company's New Concept corn program. This program focused on trait integration and application of molecular markers. In 1998, Sam accepted the ROW Trait Integration position for Monsanto Global Seed Company. In this role, Sam worked to integrate and develop the trait integration programs for Monsanto's International corn breeding programs. In April of 1999, Sam

became the Team Leader for the Molecular Breeding Informatics and Quantitative Applications Team. This team was responsible for development and implementation of informatic tools that support the analysis of molecular marker information. In January of 2001, Sam also assumed leadership of the Molecular Breeding Project Coordination program, which is responsible for implementing molecular breeding project plans in cooperation with the breeding programs. In September of 2005, Sam became the North America Corn Line Development Director.

### Gebisa Ejeta

Gebisa Ejeta is a professor of plant breeding and genetics in the Department of Agronomy at Purdue University. His research focuses on the improvement of the sorghum crop for resistance to biotic and abiotic stresses as well as for value-added, nutritional quality and end product development. He has full responsibility for teaching the first graduate level course in plant breeding and assists in teaching of a number of other courses at Purdue University. Dr. Ejeta is involved in a variety of programs in international agriculture through Purdue University, international research centers, foundations, and other agencies. He has contributed to agriculture in developing countries through sorghum cultivars and hybrids that he developed, programs that he initiated, and graduates students he has trained. Dr. Ejeta is a member and fellow of the Crop Science Society of America, the American Society of Agronomy, and the American Association for the Advancement of Sciences.

### Walter R. Fehr

Walter Fehr is a Charles R. Curtiss Distinguished Professor in Agriculture and director of the Office of Biotechnology at Iowa State University. He is a soybean breeder in the Department of Agronomy and teaches undergraduate and graduate courses in plant breeding. He obtained his B.S. and M.S. degrees at the University of Minnesota and his Ph. D. in plant breeding and cytogenetics at Iowa State University. His research has emphasized evaluation of breeding methodologies, development of novel traits, genetic and agronomic analysis of novel traits, and cultivar development.

### André Gallais

André Gallais is Professor Emeritus of the “Institut National Agronomique Paris-Grignon” (INAPG, Paris, France) where he was Professor Genetics and Plant Breeding from 1982 to 2005 in charge of a graduate course. He was the head of the research Station of Genetics and Plant Breeding of Le Moulon (Gif/Yvette, France) from 1982 to 1999. Dr Gallais first developed theoretical research on quantitative genetics and the breeding of autopolyploid species, with application to the breeding of two autotetraploids species cocksfoot and alfalfa. Simultaneously he developed theoretical work on the best combination of recurrent selection and variety development. Since 1982 he has been working mainly on corn, where he has developed studies on genetic resources, recurrent selection, marker-assisted selection and more recently on the

genetics and breeding of nitrogen use efficiency. His main interest is the use of quantitative genetics theory and molecular markers to increase the efficiency of breeding methods.

### Christiane Gebhardt

Dr. PD Christiane Gebhardt is a senior scientist and research group leader at the Max-Planck Institute for Plant Breeding Research. In 1978, she obtained a diploma degree in biochemistry from the University of Tübingen, Germany. She did her PhD work at the Friedrich-Miescher Institute in Basel and graduated 1982 from the University of Basel (Switzerland). After postdoctoral positions at CSIRO in Canberra, Australia, and Rothamsted Experimental Station (Harpenden, UK) she took up her current position at the MPI for Plant Breeding Research in 1985. In 1995, she habilitated at the University of Cologne. Her group's research focuses on genome analysis (DNA-based markers, molecular maps, QTL analysis, population genetics) of potato (*Solanum tuberosum*), the world's fourth most important crop. Dr. Gebhardt served six years on the Board of Trustees of CIAT and is associated editor of Theoretical and Applied Genetics.

### Elcio Perpetuo Guimaraes

Elcio Perpetuo Guimaraes received his BSc degree in Agronomy from the “Escola Superior de Agricultura Luiz de Queiroz” in Brazil. His MSc is on Genetics and Plant Breeding from the same University in Brazil. In 1976 he began working as a rice breeder at EMBRAPA. He obtained a PhD degree in 1985 from University of Iowa in USA, also on Genetics and Plant Breeding. From 1989 to 1996 he worked as rice breeder at the International Center for Tropical Agriculture (CIAT), in Cali, Colombia. In 1996 he returned to EMBRAPA where he remained until the end of 2001 when he became a senior officer at FAO. In his career he has been responsible for releasing several rice varieties in Latin America and has published and edited several books and technical articles.

### Arnel R. Hallauer

Dr. Arnel R. Hallauer is a retired C. F. Curtiss Distinguished Professor of Iowa State University, a member of the National Academy of Science, and a member of the US Department of Agriculture Agricultural Research Service's Science Hall of Fame. Hallauer has influenced plant breeders around the world through his teachings, publications, and breeding accomplishments. His book, Quantitative Genetics in Maize Breeding, is considered a standard textbook for corn breeders. He conducted and established full-sib reciprocal recurrent selection as an effective breeding method for maize. Hallauer graduated with a BS degree in 1954 with a major in plant science at Kansas State University. After military service, he entered Iowa State University where he got his MSc in 1958 and his PhD in 1960. Hallauer started his professional career in 1958 with the USDA/ARS. After having completed over 30 years of federal service, Hallauer retired from

USDA and accepted a full-time faculty position at Iowa State. He was named a Charles F. Curtiss Distinguished Professor in Agriculture in 1991. He retired in 2003.

### Steven J. Knapp

Steven J. Knapp is professor and Georgia Research Alliance Eminent Scholar in Plant Breeding and Genomics in the Center for Applied Genetic Technologies at the University of Georgia. He received B.S. and M.S. degrees from the University of Nevada in 1978 and 1980 and a Ph.D. from the University of Nebraska in 1983. He was a faculty member in the Department of Crop and Soil Science at Oregon State University from 1985 to 2004 where he held the Paul C. Berger Endowed Chair and taught Advanced Plant Breeding and Quantitative Genetics, Genetic Mapping, and Quantitative Trait Locus Mapping. His research has focused on the domestication and breeding of industrial oilseeds and molecular breeding and comparative and translational genomics in sunflower. Since moving to UGA, he has initiated molecular breeding and genomics research programs in peanut and watermelon. He has mentored 28 graduate students and 14 postdoctoral scholars and served on the editorial boards of Crop Science, Theoretical and Applied Genetics, and Molecular Breeding. He is a Fellow of the Crop Science Society of America and American Society of Agronomy and was awarded an Alexander Von Humbolt Fellowship in 1992.

### Elizabeth A. Lee

Elizabeth Lee is an associate professor in the Department of Plant Agriculture, University of Guelph. She has a B.Sc. in Agronomy from the University of Minnesota, a MSc. in Plant Breeding and Cytogenetics from Iowa State University, and a Ph.D. in Genetics from the University of Missouri-Columbia. In addition to running an active maize inbred line development and germplasm enhancement program at the University of Guelph, Dr. Lee's research focus is on understanding the mechanisms underlying quantitative traits. Dr. Lee is currently serving as an associate editor for Crop Science, a NSERC GSC03 committee member, and is a member of the Dept. of Plant Agricultural executive and graduate studies committees. Dr. Lee is primarily involved in graduate student teaching, teaching classes in plant genetics, plant breeding, and quantitative genetics.

### Carlos M. Löffler

Carlos M. Löffler is a senior scientist within the Maize Product Development department of Pioneer Hi-Bred Int'l. Born and raised in the Argentine Pampas region, Dr. Löffler obtained his Ingeniero Agrónomo degree at the University of La Plata, Argentina, and his M.S. and Ph.D. degrees in Plant Breeding at the University of Minnesota. After a four-year professorship at the University of Mar del Plata/INTA, Balcarce, Argentina, he joined Pioneer in 1986 to manage the company's Argentine corn breeding program. Dr. Löffler developed corn germplasm adapted to the Argentine Pampas, including the first successful commercial single-cross product in the



Argentine market. He moved to Pioneer's headquarters in Johnston, Iowa, in 1991 to conduct various research projects, including investigations of the causes of genotype by environment interactions in corn. Dr. Löffler currently leads the development of environmental classification systems for crop breeding.

### Sandra Milach

Sandra Milach is a Senior Scientist with Pioneer Hi-Bred Int'l, at its Passo Fundo research center in Brazil. She is currently engaged in breeding corn for southern Brazil market and leads the application of molecular breeding and marker assisted selection technologies for Pioneer in Brazil. Prior to joining Pioneer, she was a Professor at Federal University of Rio Grande do Sul since 1991 where she taught and conducted research on oat breeding, quantitative genetics and molecular breeding applied to cereal crops. She worked for EMBRAPA from 2001 to 2003 where she conducted research on the genetics of aluminum tolerance and resistance to leaf rust in wheat. Dr. Milach received a BS in Agronomy from Pelotas Federal University, a M.S. degree in Plant Breeding from Federal University of Rio Grande do Sul in Brazil, and a Ph.D. in Plant Breeding and Genetics from University of Minnesota.

### John W. Miles

John Miles has been a forage breeder at the International Center for Tropical Agriculture (CIAT) in Cali, Colombia since 1979. He obtained his B.S. in Plant Science from the University of California at Davis in 1968 and his M.S. in Plant Breeding at Cornell University in 1971. After serving in the U.S. Peace Corps in Colombia, he obtained his Ph.D., under the supervision of John Dudley, at the University of Illinois at Urbana-Champaign in 1979. Dr. Miles conducts an applied plant breeding program aimed at developing superior apomictic tropical forage grass cultivars. His major research interest is in developing practical breeding schemes to exploit heterosis in asexually propagated crops. He is currently serving as associate editor of Crop Science.

### Rita H. Mumm

Rita Mumm is a consultant and principal for the firm, GeneMax Services, in Chapel Hill, NC, specializing in applications of biotechnology to crop improvement. She earned an A.S. degree with an emphasis in Agriculture at Joliet Junior College in Joliet, IL in 1987, a B.S. degree in Agricultural Science at the University of Illinois at Urbana-Champaign in 1989, and a Ph.D. in Genetics and Plant Breeding at UIUC, under the supervision of Professor John Dudley, in 1993. Entering the seed industry as transgenic product development was in its infancy, she managed the value-added product development program for DEKALB Genetics Corp., facilitating commercial launch of four value-added traits, one each year from 1995 through 1998. She went on to lead a team in establishing a high-throughput molecular marker system for DEKALB, aimed at providing this technology as a powerful tool for the breeder in the development of corn hybrids

with key performance characteristics and positioning DEKALB as an industry leader in implementing genomic information in seed product development. She led efforts to establish transgenic product development programs for Syngenta in cotton, wheat, barley, rice, and plant-made pharmaceuticals in safflower. She has extensive experience in developing Quality Systems to safeguard transgenic event identity and purity through Research, Development, and Commercialization phases of seed product development. She is a named inventor on three U.S. patents, one of which includes the GA21 source of glyphosate tolerance in corn.

### Tom Osborn

Tom Osborn is Director of Genetic Resources Development at Seminis Vegetable Seeds in Woodland, CA since 2004. Prior to joining Seminis, he was Bascom Professor of Agronomy at the University of Wisconsin, where he taught and conducted research on molecular breeding and genetics of crop plants. He received a B.S. in Horticulture and a Ph.D. in Plant Breeding and Plant Genetics from the University of Wisconsin.

### Wolfgang H. Pfeiffer

Wolfgang H. Pfeiffer is the Plant Breeding Coordinator for HarvestPlus; based at CIAT, Colombia. He obtained his Ph.D. and MSc. degrees in Agricultural Sciences from Stuttgart – Hohenheim University in Germany. Before joining HarvestPlus, Wolf was Head Plant Breeder/project manager (small grains), Intensive Agro-ecosystems Program, at the International Maize and Wheat Improvement Center (CIMMYT) in Mexico and responsible for applied and strategic bread wheat, durum wheat and triticale improvement under CIMMYT's global germplasm development mandate. Wolf has over 20 years' experience in International Agriculture in crop improvement, the development and implementation of research strategies and methods, human resource development, and the coordination of global and regional networks and projects. His expertise is in Crop Improvement and International Agriculture.

### Wayne Powell

Wayne Powell is Director and Chief Executive Officer of the National Institute Agricultural Botany (NIAB), Cambridge UK. Previous appointments include Head of the School of Agriculture and Wine, University Adelaide, Australia; Deputy Director of the SCRI, Dundee, UK; he also worked at the DuPont Company in Wilmington, Delaware, USA. He has reviewed crop science research sponsored by CGIAR in Latin America, Africa and the Near East and has been a member of the external review teams for VIB (Belgium), Rothamsted (UK) and INRA (France). He is Chairman of the Program Advisory Committee for the Generation Challenge Program and Honorary Research Fellow at CIMMYT, Mexico; Member of the JIC Governing Council, Norwich and is an Honorary Professor at Heriot-Watt University, Edinburgh, UK.

Personal research interests are at the interface of plant genetics, genome science, plant breeding and conservation of genetic resources with a strong emphasis on the delivery of ‘public good’ outcomes. He has published over 225-refereed scientific papers, presented numerous invited papers at international meetings and successfully supervised 20 PhD students and numerous visiting workers. He maintains an active research group, continues to write grants to support his research from a diverse range of funding sources and has an extensive international network of collaborators and contacts.

### Matthew Reynolds

Matthew Reynolds is Head of Wheat Physiology at The International Maize and Wheat Improvement Center (CIMMYT). He obtained his bachelors degree in Botany at Oxford University in 1984 and Ph.D. in Horticulture at Cornell University in 1989. He also is Special Professor at Nottingham University and serves on the editorial board of Journal of Agricultural Science. His main professional activity is to develop and transfer wheat breeding technologies to increase productivity in developing countries with a special focus on marginal environments. As Head of the Global Wheat Physiology Program, a principal role is to develop partnerships with investigators worldwide that enable appropriate technologies to be applied to the problems facing resource poor farmers. His work has contributed to the understanding of the fundamental limitations to wheat yield potential in irrigated environments as well as identifying rapid and efficient early generation selection tools such as canopy temperature, which have been adopted in major wheat breeding programs. His work on developing conceptual models of wheat to highlight its genetic limitations under stress are used as decision support tools in strategic breeding, exploration of genetic resources, and QTL mapping of stress adaptive traits. He has also been involved in developing agronomic recommendations for wheat in marginal environments, supervises young scientists in the area of application of crop physiology to breeding, and has organized a number of international workshops addressing strategies to increase wheat production.

### Roberto Tuberosa

Roberto Tuberosa is a professor in Biotechnology Applied to Plant Breeding in the Department of Agroenvironmental Sciences and Technology, University of Bologna, Italy. He obtained a B.S. degree in Botany at the University of Bologna and a M.S. and Ph.D. in Plant Breeding and Genetics at the University of Minnesota. The research of Dr. Tuberosa focuses on the use of genomics approaches to unravel the genetic basis of the response to drought and to improve the sustainability of cereal production, particularly corn and durum wheat. Dr. Tuberosa teaches a number of courses related to the application of biotechnology to plant breeding and is a member of the Editorial Board of Maydica, Molecular Breeding, Plant Biotechnology Journal, and Plant Genetic Resources. Dr. Tuberosa is also a member of the Board of Plant Genomics European Meetings and of the EUCARPIA Maize and Sorghum section.

Wilfred Vermerris

Wilfred Vermerris recently joined the University of Florida Genetics Institute as Associate Professor of Agronomy. He has a Master's degree in Bio-molecular Engineering from Wageningen University in the Netherlands and a Ph.D. in Genetics from North Carolina State University. He was on the faculty at Purdue University from 2001-2006. His research focuses on cell wall biosynthesis in grasses, with an emphasis on maize and sorghum. He is an expert on the brown midrib mutants in these two species. Research on these mutants has been the basis for the development of maize and sorghum lines with improved biomass conversion properties that can be used for the production of fuels and green chemical feedstocks. He has taught Plant Genetics, Physiology and Biochemistry of Crop Improvement, and a lab course on PCR.



## Poster Abstracts – Table of Contents

Plant breeding education	31
1. Sedlák, P. and Vejl, P. Plant breeding – an important part of study programs at the Czech University of Agriculture in Prague	31
Plant pre-breeding and allelic discovery	32
2. Alarcón-Zúñiga, B., Cervantes-Martínez, T. and Sachiko, I. Morphological and molecular characterization of alfalfa populations adapted to Central Valley of Mexico	32
3. Bayuelo-Jiménez, J.S., López-Gomez, R. and Bahena-Betancourt, L. The role of carbohydrate accumulation in osmotic adjustment of salt-stressed <i>Phaseolus</i> species	33
4. Claire Iriarte, T. Compilation, characterization and purification of two native varieties of maize	34
5. Dotlačil, L., Hermuth, J. and Stehno, Z. European winter wheat landraces and obsolete cultivars and their value for breeding	35
6. Dreisigacker, S., Warburton, M., van Ginkel, M., Balfourier, F., Xueyong, Z., Miloudi, N., Thachunk, C. and Crossa, J. Genetic characterization of global wheat genetic resources and their wild species	36
7. El Felah M. and Bettaieb-Ben Kaab L. Barley <i>in situ</i> -conservation: a significant risk	37
8. Fernández, L., Castiñeiras, L., Fundora, Z., Shagardsky, T., Cristóbal, R., García, M., Giraudy, C., Harper, V., Acuña, G., Puldón, G., Pérez, M.F. and Figueroa, M.B. Variability of maize landraces on farm in two rural areas in Cuba	38
9. Gutierrez, L., Jannink, J.-L. and Nason, J. Genetic diversity in cultivated barley and wild barley	39
10. Jones, H., Leigh, F., Mackay, I., Smith, L. and Powell, W. The diversity of European <i>Hordeum vulgare</i> ssp. <i>vulgare</i> landraces for the adaptive trait photoperiod response <i>PPD-H1</i>	40
11. Leigh, F. and Powell, W. Wheat cytoplasmic diversity	41
12. Lorea, R.D.; Delucchi, C.; Eyhéabide, G.H.; López, C.G. Identifying Argentine maize populations as a source of favorable alleles for grain yield	42
13. MacKay, I. and Powell, W. Prospects for association mapping in UK winter wheat	43

14. Magorokosho, C, Bänziger, M, and Betrán J Genetic diversity for abiotic stress tolerance of maize landraces selected for 100 years in southern Africa	44
15. Moreira, P.M., Santos, J.P., Antunes, M., P., Moura, R., Santos, J.P., Vaz Patto, M.C. and Pêgo, S. Pre-breeding on Portuguese maize landraces: biometric and pest evaluation	45
16. Nass, L.L., Fávero, A.P., Bianchetti, L.B. , Ferreira, F.R. and Mendes, R.A. Utilization of autochthonous germplasm in Brazilian pre-breeding programs: <i>Ananas</i> , <i>Arachis</i> , <i>Capsicum</i> and <i>Manihot</i>	46
17. Stehno Z., Dotlačil L., Faberová I., Evaluation of wheat genetic resources in the Czech Republic for their use in breeding	47
18. Taba, S., Chavez-Tovar, V.H., Rivas, M., Rodriguez, M. and Ramirez, M. Maize genetic resources and prebreeding at CIMMYT International	48
19. Vázquez–Carrillo, G., Ortega Corona, A., Vidal Martínez, V.A., Salinas Moreno, Y., Guerrero Herrera, M., Cota Agramont, O. and Palacios Velarde, O. The protein quality of native maize from northwest Mexico	49
20. White, J., Smith, S., Law, J., Powell, W. and Wolters, P. The genetic diversity of UK and US wheat varieties, 1930 – 2005	50
21. Yáñez, C, Franco, J, and Taba, S The core collection of highland Ecuadorian maize genetic resources	51
22. Zencirci, N. and Karagoz, A. Effect of developmental stage length on yield and some quality traits of Turkish durum wheat ( <i>T. turgidum</i> L. Conv. <i>durum</i> (Desf.) M. K.) landraces	52
 Breeding for quality, nutritional and micronutrient traits	 53
23. Ado, S.G., Abdullahi, U.S., Usman, I.S. and Falaki, A.M. Progress in quality protein maize breeding at Samaru, Nigeria	53
24. Bayuelo-Jiménez, J.S., Rivera Alcantar, N., Ochoa, I. Quality attributes of mamey fruit ( <i>Pouteria sapota</i> ) and their potential use in crop improvement	54
25. Burt, A.J., Smid, M.P., Shelp, B.J. and Lee, E.A. High carotenoid maize project: increased accumulation and modified chemical profiles	55
26. Cakmak, I. Using wild wheats to improve zinc nutrition of cultivated wheats	56
27. Castañeda, L. and Graef, G. A national program for quality traits in soybean: effects of environment	57
28. Córdova, H. and Krivanek, A. Yield potential and combining ability of tropical quality protein maize inbred lines	58
29. Cruz Núñez, O. Evaluation of fourteen varieties of high quality protein maize in Honduras	59

30. Ewool, M.B., Sallah, P.Y.K., Nelson-Quartey, F. and Menkir, A. Potentials for improving maize for iron, zinc and beta-carotene content in Ghana	60
31. Fuentes López, M.R. Advances in maize biofortification in Guatemala: achievements and perspectives	61
32. Gevers, H.O. Quality protein maize: a review	62
33. Gregová, E., Šliková, S. and Mihálik, D. Breeding for breadmaking quality in common wheat ( <i>Triticum aestivum</i> L.) in Slovakia	63
34. Kitenge, K.M., Kirubi, D. and Mduruma, Z.O. The status of quality protein maize in Tanzania	64
35. Kocourková Z., Bradová J., Kohutová Z., Křenek P., Slámová L., Vlastníková H., Vejl P. Characterization of high molecular weight glutenin of the gene locus Glu-B1 in common wheat ( <i>Triticum aestivum</i> L.)	65
36. Krivanek, A.F., Córdova, H. and Ramirez, A. Stability and reliability analysis of lowland tropical quality protein maize ( <i>Zea mays</i> ) three-way and single-cross hybrids	66
37. Manirakiza, A., Mbagaye, G. and Barisize, T. Introduction and evaluation of early, stress tolerant and quality protein maize varieties in Burundi	67
38. Menkir, A., White, W., Maziya-Dixon, B. and Rocheford, T. Genetic potential for increasing pro-vitamin A content in tropical maize	68
39. Morgounov, A., Gómez-Becerra, H.F., Abugalieva, A., Massalimov, A., Yessimbekova, M., Muminjanov, H., Zelenskiy, Y., Ozturk, L. and Cakmak, I. Iron and zinc grain density in bread wheat grown in Central Asia	69
40. Nakamura, H. Genetic variation of common wheat <i>Glu-1</i> alleles in the noodle-culture zone compared with the bread-culture zone	70
41. Narro, T.P, Hidalgo E., and Jara W. Adaptation of yellow quality protein maize hybrids in Perú	71
42. Nigussie, M., Diallo, A.O., Mduruma, Z., Gezahegne B. and Lealem T. Status of quality protein maize research in the drought stressed areas of Ethiopia	72
43. Palacios-Rojas, N., Beck, D., Bänziger, M., Rocheford, T. and Pixley, K. Genetic variation for improving micronutrient content in maize	73
44. Reddy, B.V.S., Ramesh, S., Longvah, T., Elangovan, M. and Upadhyaya, H.D. Prospects of breeding micronutrient-dense sorghum	74
45. Shimelis, H., Mashela, P. and Hugo, A. Characterization of vernonia ( <i>Vernonia galamensis</i> var. <i>ethiopica</i> ) as an alternative industrial oil crop in Limpopo Province	75
46. Taboada-Gaytan, O.R., Pollak, L., Johnson, L., Fox, S. and Duvick, S. Wet milling efficiency of hybrids from exotic by adapted inbred lines of corn	76



47. Velu, G., Rai, K.N., Muralidharan, V., Kulkarni, V.N., Longvah, T. and Raveendran, T.S. Iron and zinc content in pearl millet grain: genetic variability and breeding implications	77
48. Son, B.Y., Hyeon-Gui Moon, Tae-Wook Jung, Ja-Hwan Ku, Sun-Lim Kim and Si-Ju Kim Identification of quality protein maize lines by marker assisted selection, differential chemical composition and lysine content analysis	78
 Molecular breeding	 79
49. Abertondo, V. and Lee, M. Phenotypic analysis of intermated B73xMo17 (IBM) populations	79
50. Asea, G., Bigirwa, G., Vivek, B., Lipps, P.E. and Pratt, R.C. Validation and characterization of candidate resistance quantitative trait loci for host-resistance to multiple foliar pathogens of maize	80
51. Bergvinson, D.J. and García-Lara, S. Consensus mapping for field and storage pest resistance in tropical maize	81
52. Novaris, J., Fonseca, R., Grift, T., and Bohn, M. Genetic evaluation of maize root complexity	82
53. Bradová, J. and Šašek, A. Utilisation of genetic protein markers for the prediction of wheat baking quality	83
54. Butruille, D., Diniz Silva, H., Bockelman, D. and Tianxing Zhang Linkage disequilibrium in haploids extracted from old open-pollinated maize varieties and synthetics	84
55. Choe, E. and Rocheford, T. Detection of quality trait loci (QTL) for pericarp thickness and ear inflorescence traits in waxy corn	85
56. Cukadar, B. and Gupta, A. Quantitative trait loci associated with husk traits in maize ( <i>Zea mays</i> , L.)	86
57. Hassan, L. Development of salt tolerant rice varieties using marker assisted selection	87
58. Hauck, A. and Bohn, M. Stem borer resistance in maize – a joint analysis	88
59. Ininda, J., Danson, J., Langat, M., Gichuru, L. and Njuguna, J.G.M. Application of simple sequence repeats to study within and between family variations for resistance to maize streak virus disease	89
60. Kobiljski, B. Use of the TRAP (Trace Relevant Allele Polymorphism) approach in breeding for complex traits – a wheat example	90

61. Kohutová, Z., Kocourková, Z., Slámová, L., Vlastníková, H., Křenek, P., Vejl, P. and Zoufalá, J. Molecular markers for leaf rust resistance genes and genes controlling vernalization in wheat	91
62. Křenek, P., Vlastníková, H., Mazáková, J., Kocourková, Z., Kohutová, Z., Slámová, L., Zouhar, M., Domkářová, J., Škodáček, Z. Development of specific PCR markers for <i>Solanum</i> ssp. late blight resistance genes and detection of their homologues	92
63. Mayor, M.L. and Lee, M. Quantitative trait loci mapping for ear shoot development in maize	93
64. McIntyre, L. Using mating designs to uncover quantitative trait loci and the genetic architecture of complex traits	94
65. Negrão S., Jayamani P., Rocheta M., Maçãs B., Mackill D. and Oliveira M.M. Gene pyramiding to improve rice by marker assisted backcrossing	95
66. Pérez Lara, E., Rodríguez, L., García, H. and Valdez, M. Is it possible to complement the Shiltz scale with biochemical and molecular analysis to evaluate tobacco varieties' ( <i>Nicotiana tabacum</i> L.) resistance to blue mold?	96
67. Poland, J.A., Wisser, R.J., and Nelson, R.J. Recurrent selection mapping in two diverse maize populations selected for northern leaf blight resistance	97
68. Silva, H.S. and Rocheford, T.R. Detection of donor alleles for enhanced starch concentration in maize	98
69. Singh, D., Park, R.F., Bariana, H.S. and Wellings, C.R. Characterization of leaf, stem and stripe rust resistance genes in CIMMYT wheat germplasm	99
70. Singh, D., Park, R.F., Snape, J., Simmonds, J. and Bariana, H.S. Genetic analysis of resistance to leaf rust in European winter wheat cultivars	100
71. Singh, R.K., Gregorio, G.B., Adorada, D., Mendoza, R. and Sajise, A.G. Molecular breeding strategy to combine multiple abiotic stress tolerance in rice	101
72. Slámová, L., Vejl, P., Veškrna, O., Kohutová, Z., Kocourková, Z., Křenek, P. and Vlastníková, H. Detection of the <i>Bdv2</i> gene in some wheat varieties by means of molecular-genetic markers	102
73. Stamati K, Mackay I., Russell J., Booth A., Baum M., Morgante M., Radovic S. and Powell W. <i>Cis</i> -acting regulatory variation in cereals	103
74. Upadyayula, N., Bohn, M., Johnson, R. and Rocheford, T. Enhanced detection of inflorescence architecture QTL in Intermated B73 x Mo17 (IBM) RIL population	104

75. Vejl, P., Melounová, M., Zoufalá, J., Sedlák, P., Blažek, J. and Dandová, M. Application of PCR markers of the <i>Vm</i> and <i>Vf</i> genes controlling apple resistance to <i>Venturia inaequalis</i> in Czech apple breeding	105
76. Vlastníková H. , Křenek P. , Domkářová J. , Kohutová Z. , Kocourková Z. , Slámová Z. and Vejl. P. Estimation of molecular genetic markers used for detection of <i>Phytophthora infestans</i> (Mont.) de Bary in infected plant tissue of some <i>Solanum</i> species	106
 Cultivar development methodologies – maize	 107
77. Acosta Roca, R., Ríos Labrada, H., Martínez Cruz, M., Miranda Lorigados, S., Ortiz, R., Ponce Brito, M. Participatory plant breeding: a maize case study from Cuba	107
78. Aguirre, A., C. and Crisóstomo P., F. Early testing for inbreeding tolerance in four local maize populations from the Peruvian Andes	108
79. Alarcón-Zúñiga, B., Cervantes-Martinez, T. and Warburton, M. Heterosis and combining ability of tropical maize in the Central Valley of Mexico: morphological and molecular characterization for silage	109
80. Arcos, A.L., Medina, S., Narro, L.A. and Salazar, F. Inheritance of callose formation in tropical maize inbreds	110
81. Bucheyeki, T.L. and Simon, S.M. Participatory breeding for maize varieties tolerant to maize streak virus in the western zone of Tanzania	111
82. Cervantes-Martínez, J.E. Combining ability of tropical and temperate maize inbreds	112
83. Cervantes-Martinez, J.E., Betanzos-Mendoza, E., Gomez-Montiel, N. and Coutiño- Estrada, B. Heterotic responses of white tropical maize inbred lines	113
84. Choukan, R. Establishment of heterotic groups within Iranian maize inbred lines	114
85. Coutiño-Estrada, B. and Marquez-Sanchez, F. Advances in cyclic hybridization based on three prolific corn varieties	115
86. Denic, M., Mariote, D., Chauque, P., Fato, P., Senete, C. and Haag, W. Breeding approaches in simultaneous selection for multiple stress tolerance of quality protein maize	116
87. Diallo, A.O., Kanampiu, F., Mugo, S., and Mbogo, P. Combining ability of imidazolinone resistant maize inbred lines and performance of their hybrids under <i>Striga</i> infestation	117

88. Espinosa-Calderón, A., Tadeo-Robledo, M., Gómez-Montiel, N., Sierra-Macías, M., F. Caballero H., A. Palafox C., F. Rodríguez-M., R. Valdivia B., R. Martínez M. Plant breeding, seed production and andro-sterility in normal and quality protein maize (QPM) in Mexico	118
89. Espinosa-Calderón, A., Tadeo-Robledo, M., Gómez-Montiel, N., Sierra-Macías, M., Sandoval, A., Coutiño E.,B., Caballero H.,F., López-Pereira, M., Piña D.V., Martínez M., R. Criss cross and interchange of line order for maize hybrids and seed production in normal and quality protein maize (QPM)	119
90. García-Lara, S. and Bergvinson, D.J. Seed deterioration of tropical maize varieties stored under accelerated aging conditions	120
91. Gethi, J.G. Can we reduce maize postharvest losses through host plant resistance?	121
92. Grudloyma, P. and Prasitwatanaseree, S. Performance of promising tropical late yellow maize hybrids ( <i>Zea mays</i> L.) under water stress conditions in Thailand	122
93. Hyrkas, L. and Lamkey, K.R. Alternative maize cultivar types for sustainable farming systems	123
94. Iriany M., R.N., Takdir M., A., Yasin HG, M. and Mejaya, M.J. Tolerance of sixteen maize genotypes to drought stress	124
95. Islam, A. Maize Research in the Bangladesh Rural Advancement Committee (BRAC)	125
96. Khonje, P., Ngwira, P. and Vivek, B. Managing maize diseases through breeding for resistance in Malawi	126
97. Kirkpatrick, K.M., Lamkey, K.R., Scott, M.P., Moore, K.J., Haney, L.J., Coors, J.G., Lorenz, A.J. Identification and characterization of maize varieties with beneficial traits for biobased industries	127
98. Magulama, E.E., Sillote, C.C. and Madriaga, W.Q. Morphology-based grouping and heterotic pattern analysis in ten white Mindanao maize varieties	128
99. Makumbi, D., Bigirwa, G. and Diallo, A.O. Combining ability and identification of maize three-way cross hybrids adapted to the mid-altitude ecology of Uganda	129
100. Mariote, D., Denic, M., Haag, W., Chauque, P. and Fato, P. Breeding for resistance to Downy Mildew in quality protein maize in Mozambique	130
101. Mashingaidze, K. Farmer-participatory maize ( <i>Zea mays</i> L.) cultivar evaluation and selection in Eastern Cape province of South Africa	131
102. Mduruma, Z., Twumasi-Afriyie, S., Napir, G., Demmisew, A. and Ombakho, G. Collaboration in Eastern and Central Africa bears fruit: increasing the availability of enhanced maize germplasm.	132

103. Moreira, P.M.; Pego, S.; Vaz Patto, C. and Hallauer, A.R. Twenty years of mass selection within the some degree fasciated Portuguese synthetic maize variety ‘Fandango’	133
104. Muasya, W.N.P., and Diallo, A.O. Strategies for developing high yielding maize varieties for the dry mid-altitude ecology of Kenya	134
105. Mugo, S., Gichuki, S.T., Murenga, M., Taracha, C., Songa, J., Bergvinson, D., Hoisington, D. and Pellegrineschi, A. Control of stem borers by Bt maize in confined field trials in Kenya	135
106. Muungani, D., Mhike, X., Kwazira, K., Madamba, R. Evaluation of maize ( <i>Zea mays</i> L.) hybrids and open pollinated varieties for yield stability in Zimbabwe	136
107. Ngaboyisonga, C., Njoroge, K., Kirubi, D. and Githiri, S.M. Effects of low nitrogen and drought on grain yield and endosperm hardness of quality protein maize single cross hybrids	137
108. Nginamau, D., Mwala, M.S. and Bänziger, M. Implications of genotype-by-environment interactions in maize ( <i>Zea mays</i> L.) variety selection using mother and baby trials	138
109. Orquera, E. and Paz, P. ‘Valluno’, an open pollinated maize variety for the Cruceño valleys of Bolivia	139
110. Pascual, C.B., Guzman, P.S. and Salazar, A.M.’ Reaction of maize germplasm to <i>Stenocarpella macrospora</i> (Earle) infection and effect of resistance to disease development	140
111. Pascual, C.B., Salazar, A.M.’ and Guzman, P.S. Development of multiple disease resistant maize populations and inbreds	141
112. Preciado-Ortiz, R., Guerrero, R., Ortega, A., Terrón, A., Crossa, F., Córdova, H., Reyes, C., Aguilar, G., Tut, C., Gómez, N. and Cervantes, E. Superior quality protein maize (QPM) hybrids for different mega-environments in Mexico using the Biplot methodology	142
113. Salazar, F., Narro, L. and Alirio Vallejo, F. General and specific combining ability for phosphorus deficiency in acid soil maize inbreds	143
114. San Vicente, F. and Garcia, P. Inbreeding depression before and after full-sib recurrent selection in tropical maize	144
115. Setimela, P., Vivek, B., Bänziger, M. and Crossa, J. Biplot analysis of early to medium maturing open pollinated maize varieties in southern Africa	145
116. Sharma, D. and Adhikari, K. Diallel analysis of intermediate to late Nepalese maize inbred lines for grain yield	146
117. Takdir M., A., Iriany M., R.N., Isnaeni, M., Mejaya, M.M. and Dahlan, M. Combining ability of CIMMYT maize lines with two Indonesian tester parents	147

118. Takdir M., A., Iriany M., R.N., Mejaya, M.J. and Dahlan, M.M. Hybrid maize adaptations at several locations in Indonesia	148
119. The, C., Mafouasson, A., Calba, H., Menkir, A. and Horst, J.W. Establishment of heterotic patterns of maize ( <i>Zea mays</i> L.) inbred lines with tolerance to acid soils	149
120. Twumasi-Afriyie, S., Nepir, G. and Mduruma, Z. Use of heterotic classification of inbred maize lines to develop hybrids for the highlands of Eastern and Central Africa	150
121. Vanegas Angarita, H., De León, C. and Narro León, L. Inheritance of resistance to <i>Cercospora</i> spp. complex in tropical maize ( <i>Zea mays</i> ) inbred lines	151
122. Worku, M., Abera, W., Tadesse, B., Wolde, L. and Wegary, D. Performance of variety cross hybrids of maize ( <i>Zea mays</i> L.) in the mid-altitude and highland transition areas of Ethiopia	152
 Cultivar development methodologies – wheat	 153
123. Ahmed, K.Z., Allam, H.Z., Moussa, A.M. and Ali, M.S.A. Doubled-haploid studies in elite Egyptian bread wheat ( <i>Triticum aestivum</i> L.) cultivars	153
124. Beshpalova, L.A. Results and prospects of breeding wheat in the South of Russia	154
125. Bhatta, M.R., Ortiz Ferrara, G., Sharma, R.C. Alleviating rural poverty through participatory wheat varietal selection	155
126. Djunusova, M. History of wheat breeding in Kyrgyzstan and current challenges	156
127. Gelalcha, S., Debelo, D., Yaie, B., Girma, B., and Mamo, B. Grain yield stability of bread wheat genotypes in favorable and stressed environments in Ethiopia	157
128. Gharbi, M.S. Durum wheat breeding in Tunisia: new varieties for the post-green revolution.	158
129. Hafsi, M., Hadji, A., Pfeiffer, W.H. and Monneveux, P. Leaf senescence and carbon isotope discrimination in durum wheat ( <i>Triticum durum</i> Desf.)	159
130. Jlibene, M. Breeding drought tolerant wheat in Morocco: an integrated approach for a complex problem	160
131. Kinyua M.G., Njau P.N., Wanyera R and Muchui J. The diversity of reaction of bread wheat ( <i>Triticum aestivum</i> ) germplasm to yellow rust ( <i>Puccinia striiformis</i> ) infection over environments and years in Kenya	161
132. Mamo, B., Gelalcha, S. and Girma, B. Evaluation of bread wheat genotypes in diverse environments of Ethiopia	162

133. Mongi-Henday, R. and Elanga, A.M. Grain yield potential stability and agronomic performance of some wheat genotypes in the Southern Highlands of Tanzania	163
134. Najafian, G., Kafashi, A.K. and Jafar-Nejad, A. AMMI analysis of grain yield stability in hexaploid wheat genotypes grown in temperate regions of Iran	164
135. Najafian, G., Nikooseresht, R., Ghandi, A. and Jafar-Nejad, A. An adapted hexaploid wheat line for late season moisture stress in the temperate zone of Iran	165
136. Osmanzai, M. Wheat productivity improvement in Afghanistan	166
137. Parodi, P.C. Nitrogen efficiency use in wheat breeding	167
138. Piaskowski, J., Murphy, K., Arterburn, M., Dawson, J., Gollnick, M. and Jones, S. Perennial wheat development for sustainable agriculture in the US Pacific Northwest	168
139. Romanenko, A.A. and Bespalova, L.A. Winter wheat seed-growing problems imposed by varietal diversity	169
140. Sharma, R.C., Singh, R.P., Joshi, A.K. and Huerta-Espino, J. New CIMMYT-derived bread wheat germplasm with high yield potential and wide adaptation	170
141. Sikharulidze, Z. and Natsarishvili, K. Virulence spectrum of wheat leaf and yellow rust in the South Caucasus	171
142. Yazdan Sepas, A. and Najafi Mirak, T. Wheat breeding in cold regions of Iran	172
143. Yildirim, M. Heterosis and combining ability in diallel F <sub>1</sub> offspring of six selected bread wheat ( <i>Triticum aestivum</i> L.) cultivars	173
 Cultivar development methodologies – other crops	 174
144. Abdullayev, K. Cereal breeding for the drylands of north-eastern Kazakhstan	174
145. de la Vega, A.J., DeLacy, I.H. and Chapman, S.C. Genetic progress over 20 years of sunflower hybrid release in central Argentina	175
146. Greplová M., Polzerová H., Vlastníková H. , Kopecký D., Švecová R. , Domkářová J. Development of breeding material using somatic hybridization and polyploidization within the <i>Solanum</i> genus	176
147. Perez, P.T., Ortiz-Perez, E., Cianzio, S.R., Wiley, H., Davis, W.H., Horner, H.T., and Palmer, R.G. Evaluation of heterosis in soybean [ <i>Glycine max</i> (L.) Merr.]	177

148. Pržulj, N. and Momčilović, V. Effectiveness of early generation selection in winter barley	178
149. Šliková, S., Vančo, B. and Šudyová, V. Deoxynivalenol content in grain of cereals after artificial inoculation with <i>Fusarium culmorum</i>	179
150. Wessel-Beaver, L., Pérez-Maisonave, R., Pérez-Arocho, J. and Segarra, A. Breeding for melonworm resistance in tropical pumpkin	180
151. Zhang, X.G., Humphries, A. and Auricht, G.C. How many genes might be involved in aluminium stress tolerance in alfalfa ( <i>Medicago sativa</i> L.)?	181
Cultivar development methodologies – modeling	182
152. Bauer, A.M. and León, J. Parental selection in self-pollinating crops using breeding values	182
153. Orellana, M., Edwards, J., Carriquiry, A. and Jannink, J.L. Bayesian modeling of heterogeneous error and genotype by environment interaction variances: model assessment	183
154. Sahagún-Castellanos, J., Rodríguez-Pérez, J.E., Villanueva Verduzco, C. and Peña-Lomelí, A. On the meaning of Busbice's prediction formula	184





---

## Plant breeding education

---

### 1. Plant breeding – an important part of study programs at the Czech University of Agriculture in Prague

Sedlák, P. and Vejl, P.

Department of Genetics and Breeding, Faculty of Agrobiological Sciences, Food and Natural Resources (FAFNr), Czech University of Agriculture in Prague (CUAP), Kamýcká 129, 16521 Prague 6 – Suchbátka, Czech Republic.

Author e-mail: [sedlak@af.czu.cz](mailto:sedlak@af.czu.cz)

Supported by the Ministry of Education, Youth and Sports of the Czech Republic, project number FRVS/1552.

Plant breeding and the creation of new cultivars is worldwide a very important part of agricultural production. The cultivar's characteristics affect both quantity and quality of crop production and are also one of the guarantees of economic profitability. On the other hand, a unilateral way of plant breeding can cause many negative impacts in agro-ecosystems (for example, selection of virulent races of crucial pathogens and subsequent decreases in resistance). Progressive methods of plant breeding, including gene technologies, clearly influence all society events, especially changes in world-view aspects. Consequently, it is necessary to identify correctly all events related to plant genotype exchanges during the breeding process, with the aim of satisfying farmers, agricultural processors and consumers. It is necessary to pass know-how understandably not only to the agricultural community, but also to the general public, reflecting on the processes and results of plant breeding and their direct impacts on the environment. As a consequence, study programs in the FAFNR in CUA Prague give plant breeding considerable attention. Aspects of breeding are included at three different levels. Although only general aspects and theoretical essentials of the plant breeding are included within the scope of BSc. programs, at the level of MSc. study there is an independent plant breeding study program. The third level is intended for postgraduate students. This paper presents the essential objectives, possibilities and forms of education in plant breeding in CUAP-FAFNr.

---

## Plant pre-breeding and allelic discovery

---

### 2. Morphological and molecular characterization of alfalfa populations adapted to Central Valley of Mexico

Alarcón-Zúñiga, B.<sup>1</sup>, Cervantes-Martínez, T.<sup>1</sup> and Sachiko, I.<sup>2</sup>

<sup>1</sup> Animal and Crop Science Departments, Universidad Autónoma Chapingo (UACH), Carretera México-Texcoco km. 38.5, Chapingo, México 56230.

<sup>2</sup> National Agricultural Research Center for Hokkaido Region, Toyohira, Sapporo, Japan

Corresponding author e-mail: b\_alarcon\_zuniga@yahoo.com.mx

Our alfalfa breeding program is interested in identifying and selecting prominent germplasm of cultivars highly adapted to the Central Highlands of Mexico (Mezquital, Central and Toluca Valleys). We established 69 alfalfa populations cultivated worldwide and planted them in a replicated complete block design at the UACH experimental station. Morphological and quality traits were evaluated throughout winter, spring and summer. We also identified and characterized 105 SSR markers obtained from genomic libraries, and EST and BAC sequence data from the *Medicago truncatula* and *Trifolium pratense* genomes, into 24 populations. We included 7 standard cultivars, representing recognized U.S. germplasm sources. 28% of the SSR on the *M. truncatula* genome map amplified polymorphic bands and 10% amplified from the *T. pratense*, suggesting low conserved SSR and transferability of both legumes to the alfalfa populations. The number of alleles per locus ranged from 3 to 6 (average 4.1) and PIC ranged from 0.2 to 0.85 (average 0.71). Mean genetic diversity ( $H_e$ ) within and among populations ranged from 0.37 to 0.825, indicating high among-population diversity. 17 of 69 alfalfa populations showed high biomass accumulation, forage quality, stability and resistance to pests and diseases, and are considered for breeding purposes. A dendrogram of 24 populations based on cluster analysis of GSj (Jaccard coefficient, range 0.32-0.75, mean 0.55) identified four main clusters, representing: 1) fall dormant cultivars; 2) intermediate cultivars; 3) non-dormant cultivars; and 4) others, representing a wide range of populations worldwide. SSRs were transferable and able to discriminate a number of alfalfa populations.

### 3. The role of carbohydrate accumulation in osmotic adjustment of salt-stressed *Phaseolus* species

Bayuelo-Jiménez, J.S.\*, López-Gomez, R. and Bahena-Betancourt, L.

Instituto de Investigaciones Agropecuarias y Forestales, Universidad Michoacana de San Nicolás de Hidalgo, Km 9.5 Carr. Morelia-Zinapécuaro, 58880 Tarímbaro, Michoacán, Mexico

\*Corresponding author e-mail: jsbayuelo2002@aol.com

Tepary bean, *Phaseolus acutifolius* A. Gray and *P. filiformis* Benthams, are adapted to hot, arid and saline conditions and might be a valuable source of genes to improve the drought and salinity tolerance of *P. vulgaris* L. The effects of salinity were examined on two wild (*P. acutifolius*, G40169 and *P. filiformis*, PI535309) and two cultivated (*P. acutifolius*, G40142 and *P. vulgaris*, G04017) *Phaseolus* species. Plants were cultured under greenhouse hydroponic conditions for 20 days. Salinity significantly affected leaf water, osmotic and turgor potentials. Leaf water and osmotic potential declined significantly as stress intensified. However, osmotic adjustment permitted the maintenance of positive turgor throughout the growth period, particularly for wild species. The total content of carbohydrates was higher in leaves than in roots. Tissue levels of glucose (3.31 - 23.3 mg/g fresh weight) and inositol (1.2 – 21.9 mg/g fresh weight) increased significantly during salt stress, to reach high levels in leaves of all species except wild *P. acutifolius* (G40169). Xilose levels were highest in the leaves of cultivated *P. acutifolius* (G40142) (1.1 - 2.7 mg/g fresh weight) and roots of wild *P. acutifolius* (G40169) (2.5 – 3.3 mg/g fresh weight). Accumulation of the sugars glucose and inositol was clearly the major means of protection in the most salt stressed *Phaseolus* plants. The presence of both carbohydrates in the leaves may constitute a major component of osmotic adjustment in stressed *Phaseolus* species.

#### 4. Compilation, characterization and purification of two native varieties of maize

Claire Iriarte, T.

PROINPA Foundation, Consultant for the Project of National Strategic Innovation (PIEN: Proyecto de Innovación Estratégica Nacional) of Maize for the Humid Chaco, Yacuiba, Bolivia.  
E-mail: tclaire@proinpa.org.

In a joint venture with PROMASOR and the Research Center for Tropical Agriculture (CIAT), PROINPA is executing the National Strategic Innovation in Maize Project, with funding from the Agricultural Ministry (MACA); supervised by the Bolivian System of Agricultural Technology (SIBTA); and with scientific assistance from CIMMYT. PROINPA works in the Bolivian Humid Chaco (Tarija) and CIAT works in the Tropical Chaco (Santa Cruz). One project goal is to collect, characterize and purify two native maize varieties selected with local farmers' participation. The other goal is to establish the chemical and physical properties of those maize varieties. The most cultivated native varieties and those with the most interesting characteristics and economic value are the Soft Yellow maize and the Domestic Pearl. The collection includes passport data, descriptors containing the identification, variety, race, location, latitude and some plant and ear characters. For purification, an S<sub>1</sub> line was developed for each variety in every collection, resulting in 175 S<sub>1</sub> lines of Soft Yellow and 155 S<sub>1</sub> lines of Domestic Pearl. To establish physiological and nutritional attributes, grain samples were sent to Tarija University. The two varieties have similar protein quantities: 9.61% in the Soft Yellow and 9.29% in Domestic Pearl. Carbohydrates do not vary substantially, at 71.02% for Soft Yellow and 70.64% for Domestic Pearl. Protein percentages in the native varieties are higher than common maize (9%). The results of this project are very important for the maize processing chain, because processors use information on the nutritional and physiological attributes of the maize.

## 5. European winter wheat landraces and obsolete cultivars and their value for breeding

Dotlačil, L., Hermuth, J. and Stehno, Z.

Research Institute of Crop Production, Drnovská, CZ-161 06, Prague, Czech Republic

E-mail: dotlacil@vurv.cz

Two sets of cultivars (122 and 101 respectively) were studied for 3 years. Old cultivars had on average 2–3% higher crude protein content than modern ones. However, genotypes showing 18% protein content were found (Bergland, Ukrajinka, Sipbachzeller, Innichen Nr. 25001, Barbu du Finistre). Spike productivity characters, except for thousand grain weight (TGW), were negatively correlated with protein content. Donors of earliness and longer grain filling period were also identified. High protein content and relatively good spike productivity and/or long grain filling period or earliness were found in the cultivars Visperterminen 640 E, Hatvan, Szekacz 1242, Berchtesgardener Vogel, Ble du Lot and Barbu du Finistere. High molecular weight (HMW) *Glu*-subunits were identified in 122 landraces and obsolete cultivars. Crude protein content decreased when the subunit at the 1A locus was missing (0). The value of the gluten index was considerably higher (59.2) in cultivars bearing alleles 5+10 at 1D. A range of alleles affected SDS micro-sedimentation test values. Grain yields (tested in 6 environments) of 31 selected landraces and old cultivars were always lower than modern check cultivars. Relatively good yields were provided by the Czech landraces Bila od Dukovan, Vouska z Tremosnice and Zidlochovicka jubilejni osinatka (over 4.3 t.ha<sup>-1</sup>). Also, the higher response of modern cultivars to environment was confirmed. However, some landraces and old cultivars proved comparable in response to modern ones (Bila od Dukovan, Brauner Fuchs, Barbu du Maconnais, Baltischer Winterweizen and Gammel Svensk Landhvedte). Old cultivars had lower yield variability, particularly in less productive environments.

## 6. Genetic characterization of global wheat genetic resources and their wild species

Dreisigacker, S.<sup>1\*</sup>, Warburton, M.<sup>1</sup>, van Ginkel, M.<sup>1</sup>, Balfourier, F.<sup>2</sup>, Xueyong, Z.<sup>3</sup>, Miloudi, N.<sup>4</sup>, Thachunk, C.<sup>1</sup> and Crossa, J.<sup>1</sup>

<sup>1</sup>International Maize and Wheat Improvement Center (CIMMYT), Apdo. Postal 6-641, 06600 Mexico D.F., Mexico

<sup>2</sup>Institut National de la Recherche Agronomique (INRA), Montpellier, France

<sup>3</sup>Z. Xueyong, Crop Science Institute, Chinese Academy of Agricultural Sciences (CAAS), China

<sup>4</sup>N. Miloudi, International Center for Agricultural Research in the Dry Areas (ICARDA), Syria

\*Corresponding author e-mail: [sdreisigacker@cgiar.org](mailto:sdreisigacker@cgiar.org)

Bread wheat was domesticated 12,000 years ago in the Fertile Crescent. Unlike other major cereals, bread wheat is the result of two consecutive hybridizations between species and therefore the size of the founder population of bread wheat was most likely limited causing a domestication bottleneck. CIMMYT's germplasm bank maintains the largest collection of wheat genetic resources in the world, consisting of more than 160,000 accessions of landraces and wild relatives. CIMMYT therefore holds a key position in conserving the genetic diversity of wheat but also in making it available for breeding. Within the Generation Challenge Program, Subprogram 1, our main objective was to examine the genetic variation among and within different species of wheat by characterizing conserved materials from germplasm banks, including related species, recent and older cultivated materials and breeding lines. In total 2500 accessions were genotyped with 44 SSR markers. Associations between *Triticum aestivum* accessions revealed a clear grouping among European cultivars and CIMMYT derived materials. Tetraploid accessions grouped according present species. A core subset of accessions was selected representing maximum diversity.

## 7. Barley *in situ*-conservation: a significant risk

El Felah M.<sup>1</sup> and Bettaieb-Ben Kaab L.<sup>2</sup>

<sup>1</sup>Laboratoire des Grandes Cultures INRAT, Rue Hédi Karray, 2049-Ariana, Tunisia  
E-mail: elifelah.mouldi@iresa.agrinet.tn

<sup>2</sup>Département de Biologie-Faculté des Sciences de Tunis, 2092-El Manar, Tunisia

In Tunisia, barley is grown over half a million hectares, mostly in dry environments. In such areas, barley landraces are subject to various hazards, including genetic erosion and replacement by modern varieties. To safeguard these landraces, 423 barley accessions were collected in 1983 from diverse regions of Tunisia, including the island of Kerkena. Sixty of those accessions, collected from Kerkena (at sites of El Attaya, Mellita, and El Khmara), were evaluated for hordein patterns using SDS-PAGE. Results showed a high polymorphism for B and C hordein bands, with the identification of eighteen distinct barley chemotypes. In 2000, another barley collection mission was undertaken at the same sites, and accessions were evaluated using the same technique. Results showed notable changes in B and C banding patterns, including band shortening, discoloration or total disappearance of a specific storage protein. Since B-hordein is indicative of good grain quality, the modification or disappearance of B-hordein would therefore indicate a reduced grain quality in the barley population at Kerkena during the elapsed period. During the same period (1983-2000), modern barley cultivars have been introduced and adopted by farmers on a large scale. The study shows that *in-situ* conservation of barley landraces by farmers is not a guarantee for their preservation and purity maintenance. To prevent the loss or erosion of valuable genetic resources of barley, it is therefore essential to implement a strict program of genetic resources preservation through cold seed storage in gene banks or through *in-situ* conservation in specially controlled fields.



## 8. Variability of maize landraces on farm in two rural areas in Cuba

Fernández, L.<sup>1</sup>, Castiñeiras, L.<sup>1</sup>, Fundora, Z.<sup>1</sup>, Shagarodsky, T.<sup>1</sup>, Cristóbal, R.<sup>1</sup>, García, M.<sup>2</sup>, Giraudy, C.<sup>3</sup>, Harper, V.<sup>4</sup>, Acuña, G.<sup>1</sup>, Puldón, G.<sup>1</sup>, Pérez, M.F.<sup>1</sup> and Figueroa, M.B.<sup>1</sup>

<sup>1</sup> Institute for Fundamental Investigations of Tropical Agriculture, INIFAT (MINAG), Calle 1, esquina 2, Santiago de las Vegas, Ciudad Habana, CP 17 200, Cuba

<sup>2</sup> Estación Ecológica Sierra del Rosario (CITMA), Pinar del Rio, Cuba

<sup>3</sup> Unidad de Servicios Ambientales de Guantánamo, Guantánamo, Cuba

<sup>4</sup> University of Florida, Gainesville, USA

Corresponding author e-mail: lfernandez@inifat.co.cu

Maize is an important food crop and has potential as a crop of primary economic importance for the people of Cuba. The objectives of this research were: to determine the number of varieties on farm in rural areas of the eastern and western provinces of the island; to identify and characterize the current Cuban landraces of maize, taking into account morphological and agronomic characteristics; and to compare the variability of this crop in the two rural areas. The research was carried out in 28 farms, 14 each in the western and eastern areas. A total of 55 accessions were collected and 25 ears per variety were evaluated and characterized; in addition 10 kernels per variety were analyzed. Sixteen characters (nine quantitative and seven qualitative) were measured directly on the ears and kernels. A frequency study was made of the qualitative characters. The quantitative characters were statistically studied through a principal component analysis and a hierarchical cluster, using the statistical package SPSS version 10.0. This research aims to identify and characterize the Cuban landraces and to develop further strategies for the conservation of maize germplasm in rural household farming systems (*in-situ*), within an overall effort to understand the management of this crop by farmers.

## 9. Genetic diversity in cultivated barley and wild barley

Gutierrez, L.<sup>1-2\*</sup>, Jannink, J.-L.<sup>1</sup> and Nason, J.<sup>2</sup>

<sup>1</sup>Agronomy Department; <sup>2</sup>Ecology and Evolutionary Biology Program, Iowa State University, Ames, IA 50011, USA.

\*Corresponding author e-mail: [luciag@iastate.edu](mailto:luciag@iastate.edu)

Plant genetic diversity of crops and their wild relatives are important sources of variability for breeding purposes. However, the amount and structure of genetic diversity in most crops is yet to be determined. The goal of this study was to study genetic diversity of cultivated barley, and its ancestor, wild barley. Specifically, we estimated genetic diversity within and among populations for molecular markers and quantitative traits. We used 353 advanced inbred lines of barley from 19 breeding programs around the world, and 289 genotypes of wild barley from 23 natural populations of the Middle East. A total of 80 SSR markers and 15 quantitative traits were evaluated in all genotypes. For each species, the level of polymorphism, genetic diversity and among population differentiation was computed. Polymorphism and genetic diversity for barley were 0.34 and 0.34, respectively, while for wild barley they were 0.79 and 0.37, respectively. Among population diversity corresponding to Wright's  $F_{ST}$  was 0.344 (95% C.I.=[0.273,0.418]) for barley and 0.300917 (95% C.I.=[0.270,0.333]) for wild barley. Among population diversity at quantitative traits calculated as Spitze's  $Q_{ST}$  ranged from 0.283 to 0.774 in barley and 0.221 to 0.703 in wild barley. In general, wild barley showed more genetic diversity than cultivated barley, but population differentiation was larger for cultivated barley. Additionally, there is a wide range of  $Q_{ST}$  estimations for both species, indicating that different traits have experienced different selection pressures. The comparison of both species allows for a study of the evolution of barley.

10. The diversity of European *Hordeum vulgare* ssp. *vulgare* landraces for the adaptive trait photoperiod response *PPD-H1*

Jones, H., Leigh, F., Mackay, I., Smith, L. and Powell, W.

National Institute of Agricultural Botany (NIAB), Cambridge, CB3 0LE, UK

Corresponding author e-mail: wayne.powell@niab.com

Barley is one of the original cereals of agriculture, domesticated in the Fertile Crescent and dispersed into Europe in the Neolithic. The dispersal from *Hordeum vulgare* ssp. *vulgare*'s native range required adaptation to novel environments. The ancestral habit of domesticated barley is that of a winter cereal with flowering initiated in response to lengthening days. The organization of the photoperiod response gene *PPD-H1* has been previously described. This paper describes the diversity of the *PPD-H1* gene in a representative set of European barley landraces and the geographic distribution of diversity. This is compared with the diversity of a sample of the wild ancestor *H. vulgare* ssp. *spontaneum*. A latitudinal cline is seen with non-responsive *ppd-h1* predominating in northern Europe. The origins of the non-responsive form (*ppd-h1*), whether in *H. vulgare* ssp. *spontaneum* or in the dispersing population of *H. vulgare* ssp. *vulgare* is discussed.

## 11. Wheat cytoplasmic diversity

Leigh, F. and Powell, W.

Diversity Genomics Group, National Institute of Agricultural Biology (NIAB), Huntingdon Road,  
Cambridge, CB3 0LE, UK

E-mail: [fiona.leigh@niab.com](mailto:fiona.leigh@niab.com)

The genus *Triticum* includes diploid, tetraploid and hexaploid species. The wheat genome has been shaped by major events including polyploidisation and domestication. Studying genetic diversity of wheat species along this continuum provides an opportunity to understand the impact of polyploidisation, domestication and selection on levels of diversity. The sequence of the chloroplast genome of wheat is publicly available. Microsatellites have been identified in the sequence, and have been demonstrated to be useful markers for assessing genetic diversity in wheat. The slow rate of microsatellite mutation and the conserved nature of the wheat chloroplast make it an ideal genome for evaluating diversity fluxes in wheat. Here we use five chloroplast microsatellite markers to evaluate the genetic diversity of wheat chloroplasts in seven wheat species. We demonstrate the impact on diversity of the domestication of tetraploid wheats and the subsequent bottlenecks associated with the formation of hexaploids by polyploidisation.

## 12. Identifying Argentine maize populations as a source of favorable alleles for grain yield

Lorea, R.D.<sup>1\*</sup>; Delucchi, C.<sup>1</sup>; Eyhéabide, G.H.<sup>1</sup>; López, C.G.<sup>2</sup>

<sup>1</sup>National Institute of Agricultural Technology (INTA), Pergamino Agriculture Experimental Station, CC 31 Pergamino 2700, Argentina

<sup>2</sup>University of Lomas de Zamora, Faculty of Engineering and Agricultural Sciences

\*Corresponding author e-mail: rlorea@pergamino.inta.gov.ar

Research was initiated to identify Argentinean maize (*Zea mays* L.) landraces as a potential source of alleles for improving grain yield of three single crosses representing the three major heterotic patterns used in Argentina. Sixteen landraces were crossed to three elite inbred lines (LP612 and LP122-2 (flint kernel type) and Mo17 (dent)). The 48 crosses, the hybrids LP612 x LP122-2, LP612 x Mo17, and LP122-2 x Mo17 and the inbred lines were evaluated in replicated trials. Experiments were conducted in 2004/05 in three locations. Grain yield, kernel weight and number of kernels m<sup>-2</sup> were recorded. Data were analyzed following Dudley's method (1987) for identifying populations as a source of favorable alleles not present in parental inbreds. Most of the landraces would be useful for improving yield of the single crosses. For LP612 x LP122-2, populations, development of new inbreds should require a backcross generation to LP612 or LP122-2. For flint x dent single crosses, backcross to Mo17 would be convenient only for improving LP122-2 x Mo17. These results suggest that breeding populations obtained from crosses of some of these landraces to the elite inbred lines used here would be useful for the development of new inbred lines and hybrids.

### 13. Prospects for association mapping in UK winter wheat

MacKay, I. and Powell, W.

National Institute of Agricultural Botany (NIAB), Cambridge, CB3 0LE, UK

Corresponding author e-mail: wayne.powell@niab.com

In the UK, data from series of integrated trials are used to register new winter wheat varieties for the National List (NL) and Recommended List (RL). Over several decades, these have resulted in the accumulation of data on many varieties for multiple traits, measured at multiple sites, over at least two years. While most of these varieties are no longer grown, remainder seed exist and can be used for genotyping. This has enabled association mapping in this extensively phenotyped collection of varieties. For this process to be implemented most efficiently, information is required on the extent and strength of linkage disequilibrium, the optimum method for integration of historical trait data from different varieties tested in varying numbers of years and sites, and optimum methods of analysis to control for the increased frequency of false positive associations arising from population stratification and unknown pedigree relationships among varieties. In collaboration with breeders and industry, initiatives are underway to genotype this valuable historical data set. Using genotype data collected for other purposes, we have carried out some proof-of-principal analyses to illustrate the problems and opportunities for mapping in this dataset.

## 14. Genetic diversity for abiotic stress tolerance of maize landraces selected for 100 years in southern Africa

Magorokosho, C<sup>1\*</sup>, Bänziger, M<sup>2</sup>, and Betrán J<sup>3</sup>

<sup>1</sup>Maize Program, International Maize and Wheat Improvement Center (CIMMYT), MP163, Mt. Pleasant, Harare, Zimbabwe. \*Corresponding author e-mail: c.magorokosho@cgiar.org

<sup>2</sup>Maize Program, International Maize and Wheat Improvement Center (CIMMYT), P.O. Box 25171, Nairobi, Kenya

<sup>3</sup>Corn Breeding and Genetics Program, Texas A&M University, College Station, TX 77843, USA

Maize is the principal staple crop of southern Africa. Since the original introduction of open-pollinated maize varieties in southern Africa about 100 years ago, new landraces have been created through farmer selection for adaptation to local conditions and hybridization resulting from seed exchange between communities. This selection probably resulted in diverse types with varying levels of adaptation to specific agro-ecologies. Local varieties collected from marginal environments may possess some unique physiological attributes that may not be present in germplasm not exposed to abiotic stress. This study characterizes the genetic diversity among maize landraces, assesses the impact of farmers' selection on adapting maize landraces to specific agro-ecologies in Zimbabwe, Zambia and Malawi, and compares the impact of farmers' selection with progress from formal selection under abiotic stress conditions. This poster details the results of the maize landrace collection mission carried out in the three countries, the morpho-phenological classification of the varieties, the SSR diversity of the varieties, and abiotic stress tolerance of the collected landraces in comparison to the commercially-bred maize varieties available in southern Africa.

## 15. Pre-breeding on Portuguese maize landraces: biometric and pest evaluation

Moreira, P.M.<sup>1\*</sup>, Santos, J.P.<sup>1</sup>, Antunes, M., P.<sup>1</sup>, Moura, R.<sup>1</sup>, Santos, J.P.<sup>1</sup>, Vaz Patto, M.C.<sup>2</sup> and Pêgo, S.<sup>3</sup>

<sup>1</sup>Escola Superior Agrária de Coimbra (ESAC), Departamento de Fitotecnia, Sector de Protecção Vegetal, Bencanta, 3040-316 Coimbra, Portugal.

\*Corresponding author e-mail: pmoreira@esac.pt

<sup>2</sup>Instituto de Tecnologia Química e Biológica, Universidade Nova de Lisboa, Portugal. E-mail: cpatto@itqb.unl.pt

<sup>3</sup>Instituto Nacional de Investigação Agrária, Portugal. E-mail: pego@bragatel.pt

Maize was introduced to Portugal after Columbus' discovery of America (1492). Its quick and broad acceptance gave place to a genetic speciation, where different landraces developed through natural and human selection (topography, microclimate, precocity, polycultural systems, bread making ability, pest and disease resistance, etc). These landraces represent a valuable source of important agronomic traits and the responsible genes have high potential in maize breeding, justifying the existence of a participatory conservation program. With this study a pre-evaluation of 51 maize landraces, collected in the Center North of Portugal, from February to April 2005, took place. The landraces were sowed during May 2005 in the fields of ESAC, and screened with a "HUNTERS" method; five representative ears from each population were also characterized. Data concerning disease and pest attack were recorded too. A certain level of diversity was found in plant and ear morphology and pest resistance but complementary studies will be needed in the future for a complete characterization.



16. Utilization of autochthonous germplasm in Brazilian pre-breeding programs: *Ananas*, *Arachis*, *Capsicum* and *Manihot*

Nass, L.L.<sup>1</sup>, Fávero, A.P.<sup>2</sup>, Bianchetti, L.B.<sup>2</sup>, Ferreira, F.R.<sup>2</sup> and Mendes, R.A.<sup>2</sup>

<sup>1</sup>Embrapa Labex-USA, NCGRP, 1111 S. Mason St., 80521, Fort Collins, CO, USA

E-mail: luciano.nass@ars.usda.gov

<sup>2</sup>Embrapa Genetic Resources and Biotechnology, C.P. 02372, 70770-900, Brasília, DF, Brasil

Pre-breeding programs are being carried out to increase the utilization of Brazilian autochthonous accessions. The main objective is to broaden the genetic basis available for breeding programs by the introgression of genes from wild species using both intra- and inter-specific crosses to transfer desired characteristics. Depending on the species, the specific goals are: i) *Ananas*: Genotype identification and crossability with wild species of *Pseudoananas* with intense color and highly durable peduncle/fruit connection for stronger ornamental plants; ii) *Arachis*: Introgression of resistant genes for fungal diseases from wild species (diploid) using synthetic allotetraploid lines in crosses with a cultivated species; iii) *Capsicum*: Identification and introgression of disease resistant genes from wild and semi-domesticated species; iv) *Manihot*: Crossability studies among *M. esculenta* and wild species for disease and drought resistances. Among the preliminary results, highlights include: i) *Ananas*: Sixteen accessions identified for promising ornamental characteristics in addition to the evaluation of 5,070 plants from various species; ii) *Arachis*: Seven sterile diploid hybrids (genome AB), five synthetic amphidiploids (AABB), four complex hybrids, and 17 distinct hybrid combinations between *A. hypogaea* and wild species (backcrosses 1 and 2); iii) *Capsicum*: Although germination was non-uniform, plantlet establishment was achieved. Incompatibility was noticed in most of the crosses; iv) *Manihot*: Hybrids between *M. esculenta* x *M. glaziovii* were obtained and are being evaluated. These results will be used to evaluate the potential benefits from the utilization of autochthonous Brazilian germplasm in breeding programs.

## 17. Evaluation of wheat genetic resources in the Czech Republic for their use in breeding

Stehno Z., Dotlačil L., Faberová I.,

Research Institute of Crop Production, Drnovská 507, CZ- 161 06, Prague, Czech Republic. E-mail: [stehno@vurv.cz](mailto:stehno@vurv.cz)

Supported by the Ministry of Agriculture of the Czech Republic, Projects No. 0002700602 and 1G57065

Collection and evaluation of wheat genetic resources started in the former Czechoslovakia in the 1950s. Wheat accessions have increased to 10,017 samples, which are currently kept in the Czech gene bank. The wheat collection is divided into two sub-collections, for winter and spring forms separately. Their passport data are available on the internet at

<http://genbank.vurv.cz/genetic/resources/>. Sub-collections are evaluated for morphological characters, phenological data, spike analyses, grain quality characteristics and, in the most important accessions, identification of molecular markers. The results of at least two years' evaluation have been related to long-term check cultivars and transferred into the descriptive part of the database accessible in the gene bank. In addition to two widely utilized species, *T. aestivum* L. and *T. durum* DESF., a further 31 species are presented in the collection. These include *T. spelta* L. and *T. dicoccum* (SCHRANK) SCHUEBL, now being grown by organic farmers in the Czech Republic. In 2001 the spelt wheat cultivar 'Rubiota' was registered and recently the emmer 'Rudico' has obtained legal protection. Other *Triticum* spp. can be used for breeding purposes as donors of valuable properties. For instance, genes for resistance to powdery mildew were transferred from *T. monococcum* L into the registered bread wheat cultivar 'Vlasta'. On the basis of evaluation results, seed samples are available for breeding or research purposes; for example, in 2005 the gene bank provided 574 wheat seed samples. Other information sources include the European Wheat Data Base <http://genbank.vurv.cz/EWDB> and the Wheat Pedigree and Gene Alleles <http://genbank.vurv.cz/wheat/pedigree/>.

## 18. Maize genetic resources and prebreeding at CIMMYT International

Taba, S., Chavez-Tovar, V.H., Rivas, M., Rodriguez, M. and Ramirez, M.

Genetic Resources Unit, International Maize and Wheat Improvement Center (CIMMYT),

Apdo. Postal 6-641, 06600 Mexico D.F., Mexico

Corresponding author e-mail: [staba@cgiar.org](mailto:staba@cgiar.org)

The CIMMYT maize germplasm bank holds large landrace accessions from Latin America, representative accessions from other parts of the world, and accessions of enhanced germplasm from the CIMMYT breeding program. The number of the accessions totals 25,377, including samples of teosintes and tripsacum. The current CIMMYT seed storage facility was renovated in 1996 and this year marks the tenth anniversary of its operation. Since 1993 the bank has received over 11,000 new landrace accessions through cooperative regeneration projects in the Latin America, where the primary maize diversity is found. In the future, additional introductions to the bank are expected, representing the diversity collected in Asia, Africa, and Europe. Improvement of CIMMYT maize gene pools since the early 1970s has produced useful, enhanced germplasms for tropical, subtropical and highland maize growing regions. Germplasm introgression and incorporation, and population improvement schemes have been used to develop the enhanced germplasm. Since 1999, prebreeding work at CIMMYT has comprised of development and improvement of the gene pools, focusing on development of heterotic gene pools. Building on flint and dent gene pools that the CIMMYT Maize Program developed over previous years, an S2-reciprocal recurrent selection scheme has been employed between the flint and dent pools of the same maturity and grain color. Highland and subtropical gene pools have incorporated new sources of germplasm. Tropical gene pools are being improved with little incorporation of new source germplasm. Selected lines from the latest cycles of selection can be shared with the cooperators.

## 19. The protein quality of native maize from northwest Mexico

Vázquez-Carrillo, G.<sup>\*</sup>, Ortega Corona, A.<sup>2</sup>, Vidal Martínez, V.A.<sup>3</sup>, Salinas Moreno, Y.<sup>1</sup>, Guerrero Herrera, M.<sup>2</sup>, Cota Agramont, O.<sup>2</sup> and Palacios Velarde, O.<sup>2</sup>

<sup>1</sup>Laboratorio de Calidad de Maíz del Instituto Nacional de Investigaciones Forestales Agrícolas y Pecuarias (INIFAP), CEVAMEX, Km. 38.5 Carretera Mexico-Veracruz, 56230 Texcoco, Mexico. \*Corresponding author e-mail: vazquez.gricelda@inifap.gob.mx

<sup>2</sup>Centro de Investigación Regional del Noroeste (CIRNO-INIFAP)

<sup>3</sup>Centro de Investigación Regional del Pacífico Centro (CIRPAC-INIFAP)

A diversity of native maize germplasm remains in Mexico, thanks to the efforts of communities that have selected their corn kernels and thereby maintained their preferred maize types. This research contributes to the chemical characterization of 69 accessions from northwest Mexico, analyzing them for protein, lysine and tryptophan content. These accessions were collected in November 2004, mainly from farmers' plots in the states of Nayarit, Sinaloa and Sonora. Analysis at INIFAP's Maize Quality Laboratory revealed differences between accessions in three measurable variables. The accessions with the best quality protein were the Tabloncillo and Blandito races collected in the state of Nayarit. This indicates that quality is associated with a floury endosperm and low protein content. The accessions with the highest tryptophan (0.79 mg/100g protein) and lysine (3.3 mg/100g protein) content, were Tabloncillos from the state of Nayarit, characterized by deep blue-black kernels with a floury texture. This race would contribute 56% and 61% respectively to the tryptophan and lysine contents of preschool children's diets, according to established FAO (1992) requirements. The accessions with the lowest quality protein were also of the Tabloncillo race, though from Sinaloa. Three Blandito race accessions were notable for their high lysine content and low percentage of protein. These had a floury kernel and were spotted purple. The Chapalote race, characterized by small flinty brown-reddish kernels, had the largest percentage of protein (11.9%) and the lowest quality protein. The identification of accessions with good quality protein may expand the genetic base for improvement programs.

## 20. The genetic diversity of UK and US wheat varieties, 1930 – 2005

White, J.<sup>1</sup>, Smith, S.<sup>2</sup>, Law, J.<sup>1</sup>, Powell, W.<sup>1\*</sup> and Wolters, P.<sup>3</sup>

<sup>1</sup>National Institute of Agricultural Botany (NIAB), Cambridge, CB3 0LE, UK

<sup>2</sup>Pioneer Hi-Bred International, Johnston, USA, IA 50131

<sup>3</sup>Dupont, Delaware, USA

\*Corresponding author e-mail: wayne.powell@niab.com

It is often asserted that the genetic diversity of the wheat crop has reduced through the 20<sup>th</sup> century as a consequence of modern plant breeding techniques. This poster presents data from a study of 93 US and 93 UK wheat varieties genotyped using 62 SSR markers and c500 DArT markers. The variety sets represent varieties first commercialized during the period 1930-2005. Diversity is measured both as aggregate genetic distance between contemporaneous groups of varieties in a rolling time series and as areas of convex hulls on a decadal basis. Diversity is shown to rise and fall during the sampling period but the level of diversity in 2005 is similar to the average diversity for the whole sampling period. The USA variety set is shown to be consistently more diverse than the UK set. The major contributor to changing levels of diversity is shown to be the diversity of breeding programs contributing to the variety set at any time. The authors conclude that: 1) It is true that a few popular varieties may represent a very high proportion of the acreage at any time and thus give the appearance of reduced diversity; 2) The regular supersedure of varieties and the presence of a range of competing breeders has, so far, ensured that there has been no reduction in the genetic diversity of varieties available; 3) The key metric may not be diversity *deployed* but rather diversity *available*.

## 21. The core collection of highland Ecuadorian maize genetic resources

Yáñez, C.<sup>1</sup>, Franco, J.<sup>2</sup>, and Taba, S.<sup>3</sup>

<sup>1</sup>Maize Program Leader, Instituto Nacional Autónomo de Investigaciones Agropecuarias, (INIAP), Panamericana Sur Km. 17, Quito, Ecuador. E-mail: maiziniap@accessinter.net

<sup>2</sup>Associate Researcher, International Maize and Wheat Improvement Center (CIMMYT) and Faculty of Agronomy, University of the Republic of Uruguay

<sup>3</sup>Head of Maize Genebank, CIMMYT, Mexico

Ecuador has a great diversity of maize. Of 29 races of maize recognized, 17 belong to the highlands. The varieties cultivated in the provinces depend on farmers' preferences and customs. The core collection constitutes a limited set of accessions, representing much of the genetic variability of the total germplasm collection. For analysis, 13 variables were considered: nine continuous variables (days to female flowering, days to male flowering, number of kernel rows, plant height, ear height, root lodging, stalk lodging, ear length, ear diameter), and four discrete variables (ear quality rating at harvest, ear shape, grain type and grain color). Accessions were grouped according to the multivariate analysis of the Ward-MLM. The number of distinct groups in the Ecuadorian highland collection was determined based on the criteria of Pseudo F, Pseudo  $t^2$ , and profile of verisimilitude. The number of accessions of each group to be included in the core collection was determined according to a logarithmic strategy and the accessions were chosen at random. A total of eight distinct diversity groups in the collection were found with a high probability of 0.98 on average. The accessions were not necessarily grouped by their race classifications. Grain type, grain color and collection site better classify the accessions into the different diversity groups. The 140 accessions of the core collection represent 20% of the original collection. They represent the maize diversity of all the provinces and races of the Ecuadorian highlands in the original collection.

22. Effect of developmental stage length on yield and some quality traits of Turkish durum wheat (*T. turgidum* L. Conv. *durum* (Desf.) M. K.) landraces

Zencirci, N.<sup>1</sup> and Karagoz, A.<sup>2</sup>

<sup>1</sup> Head, Dept. of Project Evaluation & IWWIP Coordinator, Central Research Institute For Field Crops, PO Box: 226 Ulus, Ankara, Turkey. E-mail: nzencirci@yahoo.com

<sup>2</sup> Head, Genetic Resources, Central Research Institute for Field Crops, PO Box: 226 Ulus, Ankara, Turkey. Email: alptekinkaragoz@yahoo.com

This study aimed to explore durum wheat landraces to be utilized in breeding programs. 566 single durum wheat plants, selected from 117 populations collected from 12 provinces, were studied. The selected material was planted in order to characterize some of their qualitative and quantitative traits such as percent vitreousness, pearling index, grain protein content, seed yield and thousand kernel weight; as well as determining the time frame for germination-tillering (G-T), germination-shooting (G-S), germination-heading (G-H), germination-maturity (G-M), tillering-shooting (T-S), tillering-heading (T-H), tillering-maturity (T-M), shooting-heading (S-H), shooting-maturity (S-M), and heading-maturity (H-M). Mean, coefficient of variation (CV), and confidence intervals (0.95) were computed for each of the 12 provinces, for altitudinal origins with 200-meter ranges, and for each of two geographical regions separately. The highest variation existed for number of days between T-H and the lowest for number of days between T-S. The highest variation within developmental stages was observed in samples from Diyarbakir with a CV of 32.96 %; from the 600-799 meter altitudinal range with a CV of 18.86 %; and from Southeast Anatolia with a CV of 20.12 %.

---

## **Breeding for quality, nutritional and micronutrient traits**

---

### 23. Progress in quality protein maize breeding at Samaru, Nigeria

Ado, S.G. \*, Abdullahi, U.S., Usman, I.S. and Falaki, A.M.

Institute for Agricultural Research, Ahmadu Bello University, PMB 1044, Zaria, Nigeria

\*Corresponding author e-mail: shehuga@gmail.com

During the last seven years, the Institute for Agricultural Research (IAR) Samaru has been testing Quality Protein Maize (QPM) germplasm introduced from Ghana and CIMMYT. Inbred lines were tested, characterized and maintained on-station. Results on the performance of the inbred lines show that most of them adapt to the Samaru environment. Mean days to tasseling and silking of the inbred lines were 69 and 72, respectively. The mean plant height recorded was 79cm. In the dry season, the mean days to tasseling and silking were 81 and 85, respectively. Diallel studies to identify good combining inbred lines suitable for hybrid production in our environment is in progress. Open pollinating varieties and hybrids have been extensively tested on farmers' fields resulting in the release of SAMMAZ-14 (Obatanpa) in August, 2005 for production in the short run. Yields of the varieties and hybrids introduced from Ghana and CIMMYT (Mexico and Zimbabwe) fall in the range of 3-8 t/ha which is very similar to adapted normal maize planted by farmers. More QPM varieties will be developed to protect QPM from pests and diseases that might become significant threats to a single variety extensively grown. International QPM germplasm testing in collaboration with CIMMYT continues.



## 24. Quality attributes of mamey fruit (*Pouteria sapota*) and their potential use in crop improvement

Bayuelo-Jiménez, J.S.<sup>1\*</sup>, Rivera Alcantar, N.<sup>1</sup>, Ochoa, I.<sup>2</sup>

<sup>1</sup>Instituto de Investigaciones Agropecuarias y Forestales, Universidad Michoacana de San Nicolás de Hidalgo, Km 9.5 Carr. Morelia-Zinapécuaro, 58880 Tarímbaro, Michoacán, Mexico

\*Corresponding author e-mail: jsbayuelo2002@aol.com

<sup>2</sup> Department of Horticulture, The Pennsylvania State University, University Park, PA 16802, USA

Mexico is rich in botanical biodiversity, particularly in edible fruit species. Most of these species have not been commercially exploited but have fruit production potential for local markets as well as for exportation. The objective of this study was to characterize genotypes of mamey sapote, *Pouteria sapota* [(Jacquin) H.E. Moore & Stearn] of the center-western State of Michoacan, Mexico, based on physical and chemical fruit characteristics. Cluster analysis indicated seven distinct groups with 13, 33, 16, 20, 10, 17 and 19 trees, respectively. Canonical discriminant analysis, along with F and  $\chi^2$  tests, detected the most important variables affecting group differentiation. Those were tree height, trunk diameter, fruit weight, fruit length, fruit width, fruit weight to seed weight ratio, seed weight, seed length, mesocarp thickness, mesocarp weight, titratable acidity (TA), protein, total soluble solids (TSS), TSS to TA ratio, TSS to pH ratio, epicarp weight, fruit shape, and texture. The first and second canonical discriminant functions (CDF1 and CDF2) explained 70.6 and 20.4% of the total variation among groups. Fruit weight, mesocarp thickness, and TSS to TA ratio were dominant in the CDF1 (standardized canonical coefficient CCE1= -2.74, 3.16 and 3.53, respectively). Fruit weight and mesocarp thickness were dominant in the CDF2 (CCE2 = -7.20 and 7.99). Therefore, these morphological variables could be used as the best parameters for selecting mamey trees with uniform fruit quality for either direct consumption or processing.

## 25. High carotenoid maize project: increased accumulation and modified chemical profiles

Burt, A.J., Smid, M.P., Shelp, B.J. and Lee, E.A.

Department of Plant Agriculture, University of Guelph, N1G 2W1 Guelph, ON, Canada.

E-mail: [aburt@uoguelph.ca](mailto:aburt@uoguelph.ca)

New sources of dietary carotenoids are being sought for both humans and livestock as recent investigations indicate that these antioxidants are associated with the prevention of many degenerative and age-related diseases in addition to serving as a source of vitamin A. The University of Guelph maize breeding program has developed a series of high-carotenoid (Hi-C) lines from breeding crosses involving several South American populations and Guelph inbred lines. The 34 Hi-C lines exhibit a deep orange endosperm color and have increased carotenoid accumulation. A previous survey of North American germplasm found total carotenoid contents between 0.15 and 33.11  $\mu\text{g/g}$  (Kurilich & Juvik, 1999. *J. Agric. Food Chem.*, 47: 1948-1955). The total carotenoid accumulation in the Guelph Hi-C lines ranges from 43.6 to 88.3  $\mu\text{g/g}$ . Within the Hi-C lines, there are two major carotenoid profiles: high zeaxanthin or high lutein. Considerable variation can also be found in beta-cryptoxanthin, beta-carotene, and alpha-carotene levels. Correlation analysis reveals that lutein content is strongly and positively correlated to alpha-carotene content, and negatively correlated to zeaxanthin, beta-cryptoxanthin, and beta-carotene contents. This relationship is consistent with expectations, as the carotenoid biosynthetic pathway branches at lycopene into a separate alpha-carotene and lutein branch and a beta-carotene, beta-cryptoxanthin, zeaxanthin path. With the chemical characterization of the Hi-C lines completed, focus will be on elucidating the genetics underlying both the total flux through the carotenoid pathway and the accumulation of the different carotenoid profiles.

## 26. Using wild wheats to improve zinc nutrition of cultivated wheats

Cakmak, I.

Sabanci University, Faculty of Engineering and Natural Sciences, Istanbul, Turkey

Email: cakmak@sabanciuniv.edu

Zinc (Zn) deficiency is a commonly occurring micronutrient deficiency both in humans and crops, resulting in severe economic and health problems, mainly in developing world. One major reason for the widespread occurrence of Zn deficiency in human beings is the extensive consumption of cereal-based foods. Wheat breeding approaches can be used to improve both the Zn concentration in the grain and crop production on Zn deficient soils. The genetic variation for traits is very narrow in modern wheats and not useful for breeding programs. More than 2500 accessions of wild and primitive wheats from the Fertile Crescent region have been screened for micronutrient concentration in the grain. Wild wheats, especially *Triticum dicoccoides*, exhibited substantial variation in concentration of Zn. Several diploid wild wheat accessions were identified showing very significant tolerance to Zn deficiency in calcareous soils. In studies with synthetic wheats produced from wild wheats, the transfer of A or D genomes from wild diploid wheats (e.g., *Triticum monococcum* and *Aegilops tauschii*, respectively) to tetraploid wheat markedly improved growth of plants under Zn deficient conditions. Screening different series of *dicoccoides* substitution lines indicated that the chromosomes 6A, 6B and 5B of *Triticum dicoccoides* carry the genes affecting Zn and Fe concentration in grain. Genes affecting Zn and protein concentrations in *Triticum dicoccoides* are also very closely linked. These results suggest that wild wheats represent a valuable source of genetic diversity for increasing Zn concentration in grains of cultivated wheats and tolerance of modern wheat to Zn deficiency in calcareous soils.

## 27. A national program for quality traits in soybean: effects of environment

Castañeda, L. and Graef, G.

University of Nebraska, Lincoln, NE

E-mail: lcastaneda2@unl.edu

The 2005 soybean Quality Traits Tests were conducted throughout the U.S.A. and Canada in 63 tests at 40 environments for Maturity Groups 0 through V. The objectives of the Quality Traits Test are: (1) Coordinate evaluation of soybean germplasm from breeding programs throughout the USA involved in improving compositional quality of the soybean for both meal and oil traits; and, (2) Interface with Better Bean Initiative (BBI) breeding programs for wide-area testing of promising new lines with improved yield and quality. Entries included soybean lines with a protein/oil ratio that will allow production of a dehulled meal with at least a 50% protein content, lines with saturated fatty acids less than 7%, linolenic acid below 3%, oleic acid content over 50%, and various combinations of these traits. All entries in the Quality Traits Tests are advanced elite lines from breeding programs throughout the USA, and the yield standard is required to be at least 90% of the standard cultivar checks in a test. Analysis of variance indicated no significant genotype x environment interaction effects for any quality traits. However, genotype and environment effects for meal protein, oleic acid, and linolenic acid content were significant. Consequently, minimum specifications for some quality traits may not be met in some environments. This has important implications for choice of production environment and the ability to meet minimum specifications for certain market needs.

## 28. Yield potential and combining ability of tropical quality protein maize inbred lines

Córdova, H. and Krivanek, A.

Maize Program, International Maize and Wheat Improvement Center (CIMMYT), Apdo. Postal 6-641, 06600 Mexico D.F., Mexico. E-mail: h.cordova@cgiar.org

Progress on breeding quality protein maize (QPM) germplasm at CIMMYT has contributed to the release of this type of maize in 21 countries in the developing world. The objective of this study was to estimate the combining ability of 34 new tropical QPM lines crossed to two testers and determine their yield potential in hybrid combinations. Testcrosses were evaluated in eight environments representative of the tropical lowlands. A line x tester model was applied to estimate general and specific combining ability effects. Our results demonstrate new hybrid combinations with outstanding yield potential and stability across sites. The best performing QPM hybrid yielded 7.0 t/ha, across seven sites and 12 t/ha at a Guatemala location, 40% more than the best seed industry check. Ten QPM inbred parents showed significant GCA estimates for yield and ranked from 0.414 to 0.884 t/ha, 2.5 to 4.5 times the standard error for GCA. Each of the 10 lines measured more than double the levels of lysine and tryptophan content of the normal maize checks.

## 29. Evaluation of 14 varieties of improved, high quality protein maize in Honduras

Cruz Núñez, O.

Maize Program Coordinator, Dirección de Ciencia y Tecnología Agropecuaria (DICTA), Honduras. E-mail: [ocruz@sag.gob.hn](mailto:ocruz@sag.gob.hn)

DICTA and CIMMYT evaluated fourteen open pollinated varieties of improved, high quality protein maize (QPM) at nine sites in Honduras in 2005. The objective was to identify QPM varieties that yield as well or better than locally grown varieties and with their higher protein quality ultimately help improve the nutritional levels of the Honduran population. A randomized incomplete block design with 3 repetitions and plot sizes of 8m<sup>2</sup> was used. Traits evaluated were: days to flowering, plant height, ear height, root and stem lodging, and yield. Following the analysis of variance and comparisons based on the least significant difference (LSD), the results indicate that the best yield was obtained with the normal protein reference entry SO3TLW-SCB (RE) (5.0 metric T/Ha), surpassing the two local checks, DICTA-Guayape (4.9 T/Ha) and HB-104 (4.8 T/Ha) by 101% and 104% respectively. Three QPM varieties yielded similarly to the local checks: SO3TLWQ-AB03 with 4.9 T/Ha, SO3TLWQ-AB01 with 4.8 T/Ha, and SO3TLWQ-AB05 with 4.8 T/Ha. In relation to the agronomic characteristics and statistical data, there was no significant difference for plant or ear height, reflecting the similar behavior of the varieties, which are classified as intermediate. The values obtained for root and stem lodging are within commercially acceptable limits; nevertheless, the percentage of ear rot exceeded 12%, the maximum acceptable value. This is due to high precipitation during the crop cycle. It is recommended that the best varieties be validated on resource-poor farmers' fields and in sloping areas, and compared against the best local farmer varieties.

### 30. Potentials for improving maize for iron, zinc and beta-carotene content in Ghana

Ewool, M.B.<sup>1</sup>, Sallah, P.Y.K.<sup>1</sup>, Nelson-Quartey, F.<sup>1</sup> and Menkir, A.<sup>2</sup>

<sup>1</sup>CSIR-Crops Research Institute, P.O. Box 3785, Kumasi, Ghana

<sup>2</sup>International Institute of Tropical Agriculture (IITA), PMB 5320, Ibadan, Nigeria

Corresponding author e-mail: m.ewool@cropsresearch.org

Maize is a major staple consumed in many traditional dishes without adequate micronutrient supplements throughout Sub-Saharan Africa. Iron, zinc and Beta-carotene are the most common micronutrients deficient in infants, young children and mothers. Utilization of maize varieties that have high bio-available micronutrients will be highly desirable. Seed increases of a total of 480 maize genotypes were made at Fumesua in the forest zone of Ghana in the 2004 minor season. Clean ears within each genotype were harvested at physiological maturity, sun-dried and shelled manually. Grain samples were packed into clean envelopes for iron and zinc analyses at the Adelaide University in Australia and for Beta-carotene at IOWA State University, USA. The data showed that 88 genotypes had at least 21-38mg/kg grain iron and 29-50mg/kg grain zinc contents. The best local accession had grain iron content of 38mg/kg and grain zinc of 49mg/kg. The best micronutrient rich quality protein maize (QPM) line had 34mg/kg and 50mg/kg grain iron and zinc, respectively. Mamaba and Obatanpa, which are two QPM commercial varieties grown in Ghana and other countries in the sub-region, had grain iron values of 19mg/kg and 20mg/kg, respectively, and grain zinc values of 22mg/kg and 26mg/kg, respectively. Results also indicated that GH9866SR and GH120DYFP had Pro-vitamin A contents of 2.9µg/g and 3.5µg/g, respectively. Selected genotypes would be further improved for high grain iron, zinc and Beta-carotene contents.

### 31. Advances in maize biofortification in Guatemala: achievements and perspectives

Fuentes López, M.R.

Maize National Program, ICTA, Km. 21.5 hacia Amatitlán, Bárcena, V.N. Guatemala

Email: mfuentes@icta.gob.gt

The Harvest-Plus Project in Guatemala initiated research into maize cultivation in 2004. In this phase the objectives of the project are to quantify the availability of iron (Fe), zinc (Zn) and B carotene in elite lines, commercial varieties and hybrids, and collections of maize originating from farmers in different parts of the country. The principal goal is the identification of germplasm that maximizes availability of these micronutrients, as an important resource of high nutritional value for use in future plant breeding programs. During 2004-2005, trials were carried out to evaluate maize germplasm in three different zones: tropical (0-1500 masl), the transition zone (1500-1800 masl) and the highland zone (>1800 masl). Laboratory samples were taken, according to protocols, of Fe, Zn and B-carotene. 128 samples were analyzed for Fe and Zn (78 white and 50 yellow maize samples). 58 yellow maize samples were analyzed for B-carotene. The results indicate variation between 200 and 2250 ng/g of Trans BC and Alpha-carotene. Iron concentration ranged between 4.6 and 79.9 mg/kg and for Zn the values varied between 3.8 and 39 mg/kg. The laboratory results enabled the identification of a small percentage of germplasm of white and yellow maize that has potential for direct use in plant breeding activities, contributing to achieving the objectives of the project.



## 32. Quality protein maize: a review

Gevers, H.O.

Quality Seed CC., P.O.BOX 100881, Scottsville 3209, South Africa

E-mail: Geversh@ukzn.ac.za

Quality protein maize (QPM) development in South Africa is reviewed, 40 years after the nutrition-related effects of the opaque-2 gene were first announced. Breeding progress has been limited and confined mainly to developing countries while large breeding programs in the United States and those that subsequently followed the US hybrid development pattern, have largely ignored QPM. Reasons for the lack of interest in QPM, which offers quantifiable nutritional benefits to humans and animals, are reviewed historically in the light of physical, agronomic and commercial factors involved in QPM development. Specific attention is paid to progress made in minimizing the adverse physical effects of the opaque-2 mutant on grain yield and kernel hardness as well as evaluating the effects of widely used heterotic groups in commercial maize breeding programs. Lack of progress in QPM development is partly due to the finding that initially the available elite normal inbred lines and other breeding sources were less suitable for conversion to QPM, necessitating the search for new sources and selection procedures. Current research indicates that the development of QPM remains a realistic and realizable aim in large parts of the poorer, developing world. Likewise, indications are that QPM need not remain in the niche market but can potentially enter the larger commercial maize sector by the careful manipulation of breeding material from elite heterotic groupings, which have gradually become usable by sustained selection.

### 33. Breeding for breadmaking quality in common wheat (*Triticum aestivum* L.) in Slovakia

Gregová, E., Šliková, S. and Mihálik, D.

Slovak Agricultural Research Centre, Research Institute of Plant Production,

Bratislavská cesta 122, 92168 Piešťany, Slovak Republic. E-mail: gregova@vurv.sk

Supported by the Agency for Support of Science and Technology of the Slovak Republic, Project No. APVT-27-014504.

The analysis of seed storage proteins is a useful tool for plant breeding, due to their relationship with the technological properties of wheat. The main goal of the present study is to analyze the high molecular weight (HMW) glutenin subunit composition of a collection of Slovak wheats registered in the National List of commercial cultivars between 1976 and 2006. A total of 7 HMW-GS alleles, including 2 at the *Glu-A1*, 3 at the *Glu-B1* and 2 at the *Glu-D1* loci were revealed. The glutenin-based quality scores ranged from 5 to 10. Previous selection methods for quality used rheological properties and the standard SDS-PAGE electrophoretic method. Marker assisted selection (MAS) provides a way to incorporate valuable traits into elite lines that are suitable for cultivar release. The genotype Kotte was used as a donor for new alleles encoding HMW-GS at the *Glu-1B* locus; the Swedish bread wheat line was used as a donor for the 21\* allele at the *Glu-1A* locus; and Noe as a donor for 2+12.3 at the *Glu-1D* locus. We selected desirable HMW subunits such as 5+10 and 2+12.3 (coded by *Glu-D1*), 21\* (coded by *Glu-A1*) and 6\*+8\* (coded by *Glu-B1*) in early generations of breeding material. The unique combination of glutenin alleles was fixed by backcross cycles and unfavorable glutenin alleles were eliminated. Slovak cultivars were used as recurrent parents. Classical breeding methods and new tools like MAS may contribute to the development of genetic resources with novel end-use qualities in future.

## 34. The status of quality protein maize in Tanzania

Kitenge, K.M.<sup>1</sup>, Kirubi, D. and Mduruma, Z.O.<sup>2</sup>

<sup>1</sup>Head, Maize Breeding Program, Ministry of Agriculture – Research and Training, Ari Selian, PO Box 6024, Arush, Tanzania. E-mail: kkitenge@yahoo.com

<sup>2</sup>International Maize and Wheat Improvement Center (CIMMYT), PO Box 5689, Addis Ababa, Region 14, Ethiopia

Maize is a major staple food for over 80% of the population in all 25 regions of Tanzania. Most maize (85%) is produced and consumed by resource poor farmers who have limited access to protein sources such as milk and legumes. This leaves the majority to depend on normal maize, which is deficient in two essential amino acids, lysine and tryptophan, as the main source of protein – leading to malnutrition and protein deficiency. Wider utilization of Quality Protein Maize (QPM), which contains approximately twice as much lysine and tryptophan as normal maize, should substantially improve the nutritional status of these people. QPM was introduced to Tanzania in 1998 with the evaluation of QPM germplasm from CIMMYT and Ghana. Based on their good yield performance, tolerance to diseases and high farmers' ratings, the synthetic S91SIWQ and hybrids CML144/159/179 and CML144/159/Obatanpa were released in 2001 as LISHE-K1, LISHE-H1 and LISHE-H2, respectively. In 2003, the breeding program initiated conversion of widely grown normal maize varieties to QPM; those conversions are now at the BC<sub>2</sub>F<sub>2</sub> level. A regionally coordinated project was initiated in 2004 with CIMMYT, ECAMAW (the Eastern and Central Africa Maize and Wheat Research Network) and NARS breeders in Ethiopia, Tanzania and Kenya, whereby adapted S3 lines are top-crossed to QPM testers, (CML144/CML159) and Obatanpa. The single, 3-way and top-cross hybrids and synthetics will be evaluated extensively and the best will be released for dissemination to farmers who are now demanding QPM, following promotional campaigns in Tanzania of the benefits of QPM.

35. Characterization of high molecular weight glutenin of the gene locus Glu-B1 in common wheat (*Triticum aestivum* L.)

Kocourková Z.<sup>1\*</sup>, Bradová J.<sup>2</sup>, Kohutová Z.<sup>1</sup>, Křenek P.<sup>1</sup>, Slámová L.<sup>1</sup>, Vlastníková H.<sup>1</sup>, Vejl P.<sup>1</sup>

<sup>1</sup> Department of Genetics and Breeding, Faculty of Agrobiological Sciences, Food and Natural Resources, Czech University of Agriculture, Kamycka 957, 165 21 Praha 6 – Suchbátka, Czech Republic

<sup>2</sup> Research Institute of Crop Production, Drnovská 507, 161 06 Praha 6 – Ruzyně, Czech Republic

\*Corresponding author e-mail: kocourkovaz@af.czu.cz

Supported by the Ministry of Agriculture of the Czech Republic, project numbers QF 4190, GACR No. 521/05/H013 and IG of grant agency FAFNR CUA Prague 20/2006.

The main goal of this work was the detection of allelic variation, which encodes high molecular weight glutenin subunits (HMW-GS) lying on the long arm of the chromosome 1B of common wheat (*Triticum aestivum* L.). HMW-GS are important for wheat dough quality and final breadmaking quality. Proteins merit special focus because they are basic factors of wheat quality. The locus encodes two types of high molecular weight glutenin subunits – type x and type y. The PCR method was used for the detection of allelic variation. A set of samples of Czech native and worldwide common wheat varieties was analyzed. These alleles are key markers for wheat breeding programs with high breadmaking quality, allowing selection of required genotypes during early ontogenetic stages.

36. Stability and reliability analysis of lowland tropical quality protein maize (*Zea mays*) three-way and single-cross hybrids

Krivanek, A.F.\*, Córdova, H. and Ramirez, A.

International Maize and Wheat Improvement Center (CIMMYT), Apdo. Postal 6-641, 06600 Mexico, D.F., Mexico

\*Corresponding author e-mail: [a.krivanek@cgiar.org](mailto:a.krivanek@cgiar.org)

Quality protein maize (QPM) contains the opaque-2 mutation, which increases the concentration of lysine and tryptophan in the grain endosperm and roughly doubles the biological value of maize protein, as well as additional modifier genetic systems to maintain tryptophan and lysine content in the endosperm and to make the endosperm vitreous and similar to that of normal maize. Developed by CIMMYT and partners, QPM can improve the diets of the poor in areas where maize is a staple crop and also serves as a low-cost, high-quality animal feed. A primary goal of CIMMYT is to identify maize cultivars that perform well under marginal agronomic environments managed by resource poor farmers, as well as under optimal conditions. Such yield stability can be evaluated by running yield trials at multi-locations. This study was carried out to determine the yield performances and yield stability of 43 white-grained tropical lowland QPM hybrids across 8 locations in the 2004B growing season. Single parameter estimates of stability for individual genotypes and spatial modeling of stability reactions were made using four different analyses including: Shukla's Stability Variance, Eskridge's Reliability estimate, an Additive Main Effect and Multiplicative Interaction (AMMI) model and a sites regression model (SREG).

### 37. Introduction and evaluation of early, stress tolerant and quality protein maize varieties in Burundi

Manirakiza, A., Mbagaye, G. and Barisize, T.

Institut des Sciences Agronomiques du Burundi (ISABU), BP 795 Bujumbura, Burundi

Corresponding author e-mail: manithanase@yahoo.fr

In Burundi, maize is the most important cereal in terms of total food production and area under cultivation. At high altitude, maize is the predominant crop and the staple food. Recently, drought has become a major constraint to production, besides low soil fertility, streak disease and stem borers. Early adapted drought and low nitrogen-tolerant varieties are needed, as well as disease and insect resistant material. There is also a need for quality protein maize (QPM) in Burundi. During 2004, the ISABU maize program, in collaboration with CIMMYT Kenya and Ethiopia, conducted a series of varietal trials aiming at finding solutions to these problems. The trials were planted at Moso research station (1200 masl) in the lowlands and at Gisozi (2150 masl) in the highlands. An alpha lattice design was used with 2 to 3 replications depending on trial type. Plots comprised two five-meter rows (spacing 0.75 x 0.50m, 2 plants per hill after thinning). Ten tons per hectare of farmyard manure were applied, together with chemical fertilizer. Emphasis was put on grain yield; results were analyzed using GENSTAT statistical software. At Moso, the QPM trial with 14 varieties did not show significant differences. The extra early trial, with 20 varieties at Moso, showed highly significant differences between varieties: ECA-EE-21 /NIP25(BC1)F1-# and ECA-EE-54 were the most promising materials. The drought and low nitrogen trial at Moso, with 39 varieties did not show significant differences. At Gisozi, the trial of 14 streak resistant materials plus 2 checks did not show significant differences.

### 38. Genetic potential for increasing pro-vitamin A content in tropical maize

Menkir, A.<sup>1\*</sup>, White, W.<sup>2</sup>, Maziya-Dixon, B.<sup>1</sup> and Rocheford, T.<sup>3</sup>

<sup>1</sup>International Institute of Tropical Agriculture (IITA), PMB 5320, Ibadan, Oyo, Nigeria

<sup>2</sup>Iowa State University, USA

<sup>3</sup>University of Illinois, USA

\*Corresponding author e-mail: a.menkir@cgiar.org

Millions of people in west and central Africa suffer vitamin A deficiency. Maize is a staple food in the sub-region, so improving pro-vitamin A content can contribute to improved supply of vitamin A. Breeding maize for high pro-vitamin A requires adequate genetic variability consistently expressed across environments. A large number of diverse maize inbred lines grown in one location were screened for  $\beta$ -carotene,  $\beta$ -cryptozanthin, other carotenoids, and total pro-vitamin A content. Significant differences were detected in carotenoids among the lines. Means varied from 0.11 to 4.75  $\mu\text{g/g}$  for  $\beta$ -carotene, and 0.26 to 7.75  $\mu\text{g/g}$  for pro-vitamin A. Lines exhibited differing carotenoid profiles. Early- and late-maturing open-pollinated varieties evaluated in multiple locations across seasons did not show significant variety x environment interaction for  $\beta$ -carotene content, suggesting that the varieties had specific  $\beta$ -carotene content consistently maintained in different environments. Promising elite maize inbred lines with relatively high pro-vitamin A (4.5 to 7.75  $\mu\text{g/g}$ ) are being crossed with temperate inbred lines with complimentary carotenoid profiles to develop breeding populations. Elite tropical inbred lines selected for relatively high (2.95 to 5.95  $\mu\text{g/g}$ ) and low (0.83 to 2.20  $\mu\text{g/g}$ ) pro-vitamin A content were used to form hybrids, which were evaluated for carotenoid profile and agronomic traits. The hybrids exhibited significant differences ( $p < 0.001$ ) in pro-vitamin A content, grain yield and other agronomic traits. Five hybrids from this trial produced over 5 tons/ha grain and contained nearly 7  $\mu\text{g/g}$  pro-vitamin A. Combining complementary carotenoid profiles through hybridization should increase these nutrients to levels significant for human nutrition.

### 39. Iron and zinc grain density in bread wheat grown in Central Asia

Morgounov, A.<sup>1</sup>, Gómez-Becerra, H.F.<sup>2\*</sup>, Abugalieva, A.<sup>3</sup>, Massalimov, A.<sup>1</sup>, Yessimbekova, M.<sup>3</sup>, Muminjanov, H.<sup>4</sup>, Zelenskiy, Y.<sup>3</sup>, Ozturk, L.<sup>5</sup> and Cakmak, I.<sup>5</sup>

<sup>1</sup>CIMMYT Regional Office for Central Asia and Caucasus, Almaty, Kazakhstan

<sup>2</sup>Kazakh Research and Production Center for Farming and Crop Sciences, Almalibak, Kazakhstan. \*Corresponding author e-mail: hugoferney2004@yahoo.com

<sup>3</sup>Kazakhstan-Siberia Network for Spring Wheat Improvement (KASIB), Astana, Kazakhstan.

<sup>4</sup>Tajik Agricultural University, Dushanbe, Tajikistan

<sup>5</sup>Sabancı University, Faculty of Engineering and Natural Sciences Istanbul, Turkey

Sixty-six spring and winter bread wheat genotypes from Central Asian breeding programs were evaluated for grain concentrations of iron (Fe) and zinc (Zn). Iron showed large variation among genotypes, ranging from 25 to 56 mg kg<sup>-1</sup> (average 38 mg kg<sup>-1</sup>). Similarly, Zn concentration varied among genotypes, ranging between 20 and 39 mg kg<sup>-1</sup> (average 28 mg kg<sup>-1</sup>). Spring wheat varieties possess higher Fe-grain concentrations than winter wheats. By contrast, winter wheats showed higher Zn-grain concentrations than spring genotypes. Within spring wheat, a strongly significant positive correlation was found between Fe and Zn. Grain protein content is also very significantly (P= 0.001) correlated with grain Zn and Fe content. A strongly significant negative correlation was found between Fe and plant height, and Fe and glutenin content. Similar correlation coefficients were found for Zn. In winter wheat, significant positive correlations were found between Fe and Zn, and between Zn and sulfur (S). Manganese (Mn) and phosphorus (P) were negatively correlated with both Fe and Zn. The AMMI (Additive Main Effects and Multiplicative Interactions) analysis of genotype by environment interactions for grain Fe and Zn concentrations showed that genotype effects largely control Fe concentration, while Zn concentration is almost totally dependent on location effects. Spring wheat genotypes Lutescens 574, and Eritrospermum 78; and winter wheat genotypes Navruz, NA160/HEINEVII/BUC/3/F59.71//GHK, Tacika, DUCULA//VEE/MYNA, and JUP/4/CLLF/3/II14.53/ODIN//CI13431/WA00477, are promising materials for increasing Fe and Zn concentrations in the grain, as well as enhancing the concentration of promoters of Zn bioavailability, such as S-containing amino acids.



#### 40. Genetic variation of common wheat *Glu-1* alleles in the noodle-culture zone compared with the bread-culture zone

Nakamura, H.

Japan International Research Center for Agricultural Sciences (JIRCAS)- CIMMYT, Tsukuba, Ibaraki 305-8686, Japan. E-mail: h.nakamura@cgiar.

It is well known that *Glu-1* alleles directly affect wheat gluten quality. There are several alleles in *Glu-D1* locus. Considering the worldwide distribution of *Glu-D1* alleles, *Glu-D1a* and *Glu-D1d* show high frequency (52.9, 40.8 respectively) while *Glu-D1b*, *Glu-D1-c*, *Glu-D1f*, and some other alleles, generally show low frequency. In relation to bread-making quality, the *Glu-D1d* allele has superior performance over *Glu-D1a*, while the *Glu-D1f* allele has a negative effect. The average *Glu-1* quality scores relating to good bread-making quality are lower in Japan and China than in Australia, Canada and the USA. Japanese Udon-wheat has high frequencies of the *Glu-D1f* allele associated with weak gluten doughs, which has a highly negative effect on bread-making quality. Conversely, Japanese and Chinese wheats differ from average frequencies of *Glu-D1d*, associated with good bread-making quality, as well as the *Glu-D1a* allele. In bread-culture zones (the USA, Canada and Australia), there is a higher frequency of the *Glu-D1d* allele than in Japanese and Chinese wheats in the noodle-culture zones. Similarly, there are three alleles in the *Glu-A1* and *Glu-B1* loci associated with good bread making quality. These are: *Glu-A1a*, *Glu-A1b* and *Glu-B1i*, with average worldwide frequencies of 32.8, 30.9 and 8.8, respectively. Japanese and Chinese wheats have lower frequencies of these *Glu-A1* and *Glu-B1* alleles. This study reveals that the *Glu-1* allele frequencies differ greatly between the noodle-culture zones (Japan and China) and bread-culture zones (U.S.A, Canada, Australia and Europe).

## 41. Adaptation of yellow quality protein maize hybrids in Perú

Narro, T.P, Hidalgo E., and Jara W.

Instituto Nacional de Investigación y Extensión Agraria (INIEA), Av. La Molina, 1981, Lima-Perú. E-mail: [tnarro@inia.gob.pe](mailto:tnarro@inia.gob.pe)

Demand for yellow maize in Peru is 2 million tons annually, which is used mainly for feed in the poultry industry. The poultry industry has increased in the last 40 years. Per capita consumption of chicken has increased from 4 kg/person/year (1970) to 44 kg/person/year (2005). Average yellow maize grain yield in Peru is 3.7 t/ha. The use of quality protein maize (QPM) is one alternative for a more efficient poultry industry. Twenty-three hybrids, including six normal and 17 QPM hybrids, were evaluated in nine locations, seven on the coast and two in the jungle areas of Peru, between 2002 and 2005. No hybrid x location interaction was found and the grain yield varied from 7.2 to 10.7 t/ha. Participatory research was used where strip plots were planted. The experimental hybrid CML161/CML165 was selected as a potential commercial hybrid for Peruvian conditions, not only for its high grain yield in the strip plots (12.9 t/ha) but also for its preference by farmers because of its orange grain color. Protein content for this hybrid is 9.2% and 0.099% of tryptophan. It is expected that this hybrid will be released in 2006.

## 42. Status of quality protein maize research in the drought stressed areas of Ethiopia

Nigussie, M.<sup>1\*</sup>, Diallo, A.O.<sup>2</sup>, Mduruma, Z.<sup>3</sup>, Gezahegne B.<sup>1</sup> and Lealem T.<sup>1</sup>

<sup>1</sup>Ethiopian Institute of Agricultural Research, Melkasa Research Center, P.O. Box 436, Nazareth, Ethiopia. \*Corresponding author e-mail: maize@ethionet.et

<sup>2</sup>International Maize and Wheat Improvement Center (CIMMYT), Nairobi, Kenya

<sup>3</sup>Eastern and Central Africa Maize and Wheat Network (ECAMAW)-Coordinator, P.O. Box 5689, Addis Ababa, Ethiopia

Maize is a staple food for farmers in the drought stressed areas of Ethiopia. With little access to protein sources, millions of people in these areas are protein deficient. Substituting the local normal maize with improved quality protein maize (QPM) would substantially improve the protein status and reduce the malnutrition of resource poor farm families. QPM research was started at Melkasa by introducing and testing CIMMYT materials in the year 2000. Four newly introduced CIMMYT QPM hybrids; the Ghanaian hybrid GH132-28 and an open pollinated variety (OPV – Obatanpa) were evaluated at three locations in the drought stressed areas in 2000. Based on mean grain yield over locations, the single cross CML175 x CML176 revealed the highest grain yield (10.4 t/ha), followed by a three-way hybrid CML144 x CML159 x CML176 (9.5 t/ha). Several other QPM lines, OPVs and hybrids were evaluated; selected materials are at various breeding stages. Intensive breeding work was also started to convert local maize varieties to QPM and develop QPM lines, hybrids and synthetics. Two OPVs are being converted to QPM using two donor parents (CML144 and CML159); at present the breeding populations are at BC<sub>2</sub>F<sub>1</sub> level. Together with regional CIMMYT scientists, several hundred QPM inbred lines are being developed and currently the S<sub>3</sub> lines are planted to be advanced to S<sub>4</sub>. Simultaneously, the S<sub>3</sub> lines are top-crossed to two testers (CML144/CML159 and Obatanpa). The resulting inbred lines, top-crosses and synthetic populations would yield potential materials that could be promoted to end-users in the immediate future.

### 43. Wet milling efficiency of hybrids from exotic by adapted inbred lines of corn

Taboada-Gaytan, O.R.<sup>1</sup>, Pollak, L.<sup>2\*</sup>, Johnson, L.<sup>3</sup>, Fox, S.<sup>3</sup> and Duvick, S.<sup>2</sup>

<sup>1</sup>Iowa State University, Department Of Agronomy, Ames, IA 50010,

<sup>2</sup>USDA-ARS, Iowa State University, Department of Agronomy, Ames, IA 50011-1010

<sup>3</sup>Iowa State University, Department of Food Sciences and Human Nutrition, Ames, IA 50010

Corresponding author e-mail: [toswaldo@iastate.edu](mailto:toswaldo@iastate.edu)

Corn (*Zea mays* L.) is the main crop in the United States and starch is the most important derived product from the corn grain. This study was conducted to determine whether Corn Belt lines introgressed with exotic germplasm from Argentina, Chile, Uruguay, Cuba and Florida have appropriate wet milling characteristics. Ten lines from the Germplasm Enhancement of Maize project were chosen on the basis of starch yield. The highest and the lowest starch-yielding lines for each of the five different germplasm sources were selected. These ten lines were crossed to three testers (LH283, LH283Bt, and IN510) that provided to the progeny different wet-milling efficiency. The compositional characteristics of the lines and the hybrids (moisture, starch, protein, and oil content) were estimated by using the Near-Infrared Transmittance (NIR) technology using a FOSS Infratec 1241 Grain Analyzer. The wet milling characteristics of both the lines and the hybrids were obtained by milling two samples using the 100g modified wet-milling procedure. This procedure yields starch, gluten, fiber, germ, and steepwater fractions. The wet milling efficiency of exotic corn lines and their hybrids was correlated positively with starch content. Statistical differences ( $\text{Alpha}=0.05$ ) were found for yield of the wet milling fractions. Our results indicate that the use of exotic corn germplasm in a wet milling breeding program will enhance available genetic diversity.

#### 44. Genetic variation for improving micronutrient content in maize

Palacios-Rojas, N., Beck, D., Bänziger, M., Rocheford, T. and Pixley, K.

Maize Program, International Maize and Wheat Improvement Center (CIMMYT), Apdo. Postal 6-641, 06600 Mexico D.F., Mexico.

Corresponding author e-mail: [n.palacios@cgiar.org](mailto:n.palacios@cgiar.org)

Iron, zinc and vitamin A deficiencies afflict hundreds of millions of people, particularly women and children. Because cereal grains are staple foods, genetic fortification or biofortification of these cereals with vitamins and/or minerals could contribute to alleviating micronutrient malnutrition. HarvestPlus project partners are working to increase provitamin A carotenoids, iron and zinc concentrations in maize kernels. Grain concentrations of iron and zinc are largely dependent on environmental conditions like soil composition. Analysis of >1,000 genotypes from different environments showed little variation for iron (average  $20 \pm 5$  ppm), and moderate variation for zinc concentration in grain (15-35 ppm). Analyses of genotypes with yellow to dark orange kernels have identified large variation in their content of provitamin A molecules (0.5 to 8.8 ug/g dry weight) and their carotenoid profiles. Furthermore, studies of crosses among lines with contrasting provitamins A concentrations suggest that non-additive effects are important for determining these traits. Thus, our breeding strategy includes: 1) selecting genotypes with high provitamins A content, 2) seeking crosses with favorable specific combining ability for high concentrations of provitamins A, and 3) identifying alleles favorably affecting enzyme activity for key reactions along the carotenoid biosynthetic pathway. Although a substantial breeding effort is needed, genetic variation appears adequate to achieve nutritionally significant concentrations of provitamins A and zinc in maize grain. Efforts to understand and exploit allelic variation for enzymes regulating the carotenoid biosynthetic pathway, or variation in concentration of enhancers or inhibitors of iron and/or zinc bioavailability, may offer new options for breeding biofortified maize.

## 45. Prospects of breeding micronutrient-dense sorghum

Reddy, B.V.S.<sup>1\*</sup>, Ramesh, S.<sup>1</sup>, Longvah, T.<sup>2</sup>, Elangovan, M.<sup>3</sup> and Upadhyaya, H.D.<sup>1</sup>

<sup>1</sup>International Crops Research Institute for Semi-arid Tropics (ICRISAT), Patancheru 502 324, India

<sup>2</sup>National Institute of Nutrition (NIN), Hyderabad, India

<sup>3</sup>National Research Center for Sorghum (NRCS), Hyderabad 500 030 India

\*Corresponding author e-mail: b.reddy@cgiar.org

Malnutrition due to iron, zinc and vitamin A micronutrient deficiency can cause blindness and anemia, especially affecting women and pre-school children of south and Southeast Asia and sub-Saharan Africa. Genetic enhancement of sorghum, a staple in these regions, for these micronutrients maybe cost- and health-effective. Research involving a diverse set of 86 sorghum lines at ICRISAT indicated significant genetic variability and high broad-sense heritability for grain iron, zinc and  $\beta$ -carotene contents. The iron content ranged from 20.1-37.0 ppm with an average of 28 ppm; zinc content ranged from 13.4-30.5 ppm with an average of 19 ppm; and grain  $\beta$ -carotene content ranged from 0.56-1.13 ppm in yellow-endosperm germplasm lines. The variance due to genotype  $\times$  environment [managed soil fertility levels] interaction was non-significant. Significant and fairly higher positive correlation between grain iron and zinc contents and their poor correlation with agronomic traits such as days to 50% flowering, plant height, and grain size and grain hardness indicated the possibility of selecting for higher micronutrients contents with desired maturity and grain traits.

46. Characterization of vernonia (*Vernonia galamensis* var. *ethiopica*) as an alternative industrial oil crop in Limpopo Province

Shimelis, H.<sup>1</sup>, Mashela, P.<sup>1</sup> and Hugo, A.<sup>2</sup>

<sup>1</sup>University of Limpopo, School of Agricultural and Environmental Sciences, Private Bag X1106, Sovenga 0727, South Africa.

<sup>2</sup>Department of Microbial, Biochemical and Food Biotechnology, University of the Free State, P.O. Box 339, Bloemfontein 9300, South Africa.

Corresponding author e-mail: shimelis@ul.ac.za

Vernonia (*Vernonia galamensis*) is a potential, new industrial oil seed crop and a source of natural epoxy fatty acids. The oil content and fatty acid profiles of 36 diverse accessions of *V. galamensis* var. *ethiopica* were analyzed to select potential lines for domestication. Accessions showed varying ranges of oil content (22-29%), vernolic acid (73-77%), linoleic acid (12-14%), oleic acid (3.5-5.5%), palmitic acid (2.4-2.9%) and stearic acid (2.3-2.8%). Accessions collected from southern Ethiopia had higher oil content than those from eastern Ethiopia. Five promising lines, with the highest contents of oil (28-29%) and vernolic acid (75-77%) were identified as best parents for improving the quantity of oil and vernolic acid.

## 47. Iron and zinc content in pearl millet grain: genetic variability and breeding implications

Velu, G.<sup>1</sup>, Rai, K.N.<sup>2</sup>, Muralidharan, V.<sup>1</sup>, Kulkarni, V.N.<sup>2</sup>, Longvah, T.<sup>3</sup> and Raveendran, T.S.<sup>1</sup>

<sup>1</sup>Tamil Nadu Agricultural University, Coimbatore, Tamil Nadu, India,

<sup>2</sup>International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru 502 324, Andhra Pradesh, India. E-mail: k.raai@cgiar.org

<sup>3</sup>National Institute of Nutrition, Jamai Osmania, Hyderabad, 500 007, Andhra Pradesh, India

Iron (Fe) and zinc (Zn) are amongst the few minerals for which widespread micronutrient malnutrition, resulting in numerous health problems, has been reported, especially in the developing world. Development of micronutrient-dense cultivars of major food crops provides a cost-effective approach to this problem. Pearl millet (*Pennisetum glaucum* (L.) R. Br.) is one such major crop, which is grown on 26 million hectares in the arid and semi-arid tropical regions of Asia and Africa. Pearl millet micronutrient enhancement research at the International Crops Research Institute for the Semi-Arid Tropics (ICRISAT) has shown large genetic variability both for iron and zinc. One trial of a diverse range of inbred lines and populations showed 30-76 ppm iron and 25-65 ppm zinc; and another trial of a diverse range of improved populations showed 42-80 ppm iron and 27-50 ppm zinc. Most lines and populations with high iron and zinc contents were predominantly based on early-maturing, large-seeded and high-yielding *iniari* germplasm. There was highly significant and positive correlation between iron and zinc in both trials ( $r=0.84$ ,  $p<0.01$ ). Two released, open-pollinated varieties (AIMP 92901 and GB 8735) had high iron and zinc contents. Selfed progeny evaluation of these showed nearly three-fold within-population variation both for iron (35-104 ppm in AIMP 92901 and 40-105 ppm in GB 8735) and zinc (29-68 ppm in AIMP 92901 and 29-60 ppm in GB 8735). These results indicate good prospects for simultaneous genetic improvement of both iron and zinc contents in pearl millet.



48. Identification of quality protein maize lines by marker assisted selection, differential chemical composition and lysine content analysis

Son, B.Y.<sup>1</sup>, Hyeon-Gui Moon, Tae-Wook Jung, Ja-Hwan Ku, Sun-Lim Kim and Si-Ju Kim

<sup>1</sup>Breeding Resource Development Division, National Institute of Crop Science, 209 Seodun-Dong, 441-857 Suwon, Gweonson-Gu, Republic of Korea. E-mail: sonby@rda.go.kr

Two laboratory procedures were performed at the same time for the analysis of quality protein maize (QPM) and lysine content, with the aim of improving the quality of protein in the maize kernel. Eighty-six lines of the BC<sub>3</sub>F<sub>1</sub> population and sixty BC<sub>1</sub>F<sub>2</sub> lines were analyzed with the *opaque2* specific SSR marker. An *opaque2* specific micro-satellite marker (umc1066) facilitated the differentiation of QPM lines carrying *opaque2* from the non-opaque genotypes. This study demonstrated the effectiveness of the SSR marker in QPM genotype discrimination and could potentially contribute towards the effective utilization of elite QPM lines in Korea's maize breeding program. There was no significant difference in protein content between QPM and non-QPM lines, but significant differences in lipid content, ash, and crude fiber were expressed. An amino acid auto analyzer (Hitachi L-8800) was used to determine amino acid content. QPM lines and non-QPM lines showed no difference in methionine and cystine contents or sulphur-containing amino acids. However, the lysine content of QPM lines was 38% higher than that of non-QPM lines.

---

## Molecular breeding

---

### 49. Phenotypic analysis of intermated B73xMo17 (IBM) populations

Abertondo, V.\* and Lee, M.

Iowa State University, Ames, Iowa, 50010, USA

\*Corresponding author e-mail: [vja@iastate.edu](mailto:vja@iastate.edu)

Random mating within a mapping population creates more opportunities for recombination. Therefore, the probability of observing recombination events between linked loci is increased and more reliable genetic maps may be produced. The intermated B73xMo17 (IBM) population is the most widely used common resource for maize mapping. It was developed by intermating the F2 for four generations before recombinant inbred lines were derived. In order to increase number of recombinants to reach a higher map resolution, a second population of double haploid lines was created after six additional cycles of intermating, and it was termed IBM-10. It is known that intermating was effective in creating a higher frequency of recombinants in IBM-10 than IBM (Jaqueth, 2003). However, there is no information about how intermating affects the phenotypic variation of these populations. IBM and IBM-10 populations are being compared in terms of phenotypic variance, population means and correlation coefficients for a set of traits. The phenotypic variance and correlation coefficients may increase or decrease with repulsion or coupling phase linkage. The presence of new recombinants at the IBM-10 could reveal new epistasis interactions, modifying the effect of the alleles in such recombinants, which might produce a shift in the population mean. Moreover, additional cycles of random mating might cause a change in the allele frequency, which also may affect the population attributes.

## 50. Validation and characterization of candidate resistance quantitative trait loci for host-resistance to multiple foliar pathogens of maize

Asea, G.<sup>1</sup>, Bigirwa, G.<sup>1</sup>, Vivek, B.<sup>2</sup>, Lipps, P.E.<sup>3</sup> and Pratt, R.C.<sup>4</sup>

<sup>1</sup>Namulonge Research Institute, National Agricultural Research Organization, Uganda,

<sup>2</sup>CIMMYT, P.O. Box MP163 Mt. Pleasant, Harare, Zimbabwe,

<sup>3</sup>Department of Plant Pathology, <sup>4</sup>Department of Horticulture and Crop Science, The Ohio State University, Ohio Agricultural Research and Development Center, Wooster, OH 44691, USA.

Corresponding author e-mail: asea@naro-ug.org

Maize (*Zea mays* L.) production in sub-Saharan Africa is threatened by multiple foliar diseases including northern corn leaf blight (NCLB), gray leaf spot (GLS) and maize streak virus (MSV). Most of these diseases are managed using partial resistance conferred by the action of multiple resistance factors. Quantitative trait loci (QTL) conditioning partial resistance to several pathogens have been identified. Validation in new genetic backgrounds of candidate QTL presents marker-assisted selection as a potential strategy for pyramiding resistance to several pathogens. We examined the utility of consensus QTL to determine their effectiveness in improving host-resistance. Genetic gains were calculated for simultaneous improvement of host-resistance following phenotype-based, marker-based, combined phenotype-and marker-based selection (MAS), and a randomly selected control population. Field evaluations and selections were conducted independently for each disease in a population of 410 F<sub>2:3</sub> lines derived from hybridization between inbred line CML202 with known resistance to NCLB and MSV, and a breeding line with known resistance to GLS. Analyses of marker-trait associations in the major QTL positions were highly significant. Estimates of narrow-sense heritability were 0.22, 0.25 and 0.39 for MSV, NCLB and GLS, respectively. Genetic gains varied with traits and selection treatments employed. For all diseases, gains from marker-based selection represented a significant improvement over random selection that ignored QTL information; MAS was the most effective. Our results validated the position and effect of four out of six QTL controlling partial resistance. The lack of confirmation of two QTL highlights the need for validation of resistance loci in new populations.

## 51. Consensus mapping for field and storage pest resistance in tropical maize

Bergvinson, D.J. and García-Lara, S.

Maize Program, International Maize and Wheat Improvement Center (CIMMYT), Apdo. Postal 6-641, 06600 Mexico D.F., Mexico. E-mail: dbergvinson@cgiar.org

Lepidopteran and coleopteran pests cause significant losses to maize production throughout the world. Major constraints in tropical agroecologies are the foliar damage caused by fall armyworm (FAW), southwestern corn borer (SWCB, *Diatraea grandiosella*) and sugarcane borer (SCB, *D. saccharalis*), as well as post-harvest losses due to maize weevil (*Sitophilus zeamais*) and larger grain borer (*Prostephanus truncatus*). The breeding effort at CIMMYT has focused on determining genomic regions involved in insect resistance in maize using molecular markers. Recently, Comparative Map and Trait Viewer (CMTV) was developed to construct consensus maps and compare quantitative trait loci (QTL) data across genomes and experiments. The objective of this study was to develop a consensus map and compare the QTL for field and storage pest resistance and their putative resistance mechanisms in tropical maize. CMTV showed that the major consensus QTL for field pests are located in bins 1.03, 1.06, 1.10, 3.06/08, 6.01, 6.05, 7.02/03/04, 8.03, 8.05, 9.04/05, and 10.04, while for storage pests QTL are situated in bins 1.08, 2.01, 2.09, 3.06/07, 5.03, 6.05, and 10.04/07. Consensus genomic regions associated with both pest complexes are only overlapping in bin 10.04. Cell wall bound phenolics in the leaf and pericarp as well as physical traits overlapped with insect resistance in several consensus areas (1.03, 2.08/09, 3.06/07 and 8.05). These results illustrate the potential of using CMTV to identify candidate genes involved in insect resistance in order to identify target regions for the incorporation of durable and broad-based insect resistance into elite maize lines and varieties.

## 52. Genetic evaluation of maize root complexity

Novaris, J.<sup>2</sup>, Fonseca, R.<sup>2</sup>, Grift, T.<sup>1</sup>, and Bohn, M.<sup>1\*</sup>

<sup>1</sup> University of Illinois, 1102 S. Goodwin Ave. 61801 Urbana, IL, USA

<sup>2</sup> University of Porto, Porto, Portugal

\*Corresponding author: mbohn@uiuc.edu

The development of a healthy root system is an important part of the overall plant development program. Root branching and architecture are tightly linked to plant survival under abiotic (e.g., drought, flooding, nutrient deficiencies) and biotic (e.g., competition among plants, diseases, pests) stress conditions. The objectives of this study were to evaluate a large set of maize recombinant inbred lines (RIL) derived from the four times random mated IBM (Intermated B73×Mo17) population for primary root complexity characteristics, including fractal dimension and entropy estimates and their dynamics, and to map and characterize quantitative trait loci (QTL) affecting the complexity of primary root systems in maize. For each of the 231 RIL, multiple primary root systems were produced applying a replicated incomplete block design. Digital images of each root system were taken at days four and eight after germination. For each root system, its fractal dimension and entropy were determined. Root systems were also evaluated for a comprehensive set of morphological characteristics. Applying composite interval mapping using a set of 1167 molecular markers, a large number of QTL ( $N > 12$  QTL) was found for all traits and their dynamic change in the early phase of root development. All root mutants with known chromosomal position were located in chromosomal BINs carrying QTL for root complexity. The large number of QTL not associated with known root mutants will guide us to additional candidate genes involved in primary root architecture.

### 53. Utilisation of genetic protein markers for the prediction of wheat baking quality

Bradová, J. and Šásek, A.

Research Institute of Crop Production, Drnovska 507, 161 06 Prague, Czech Republic

E-mail: bradova@vurv.cz

Supported by the Ministry of Agriculture of the Czech Republic, Project No. 0002700602.

Genetic protein markers can be used as markers of some commercially important wheat traits, such as baking quality, cold hardiness and resistance to stem rust. Recombinations of suitable gliadin and glutenin parent alleles are helpful in the breeding of new wheat varieties carrying required traits and characters. The composition of gliadins and glutenin subunits was studied in wheat varieties registered in the Czech Republic. We identified particular alleles that are encoded in 6 gliadin loci and 3 glutenin loci. Electrophoretic spectra of gliadins were obtained by the starch gel electrophoresis and the spectra of subunits of high-molecular-weight glutenins were obtained by the polyacrylamide gel electrophoresis with sodium dodecyl sulphate. We evaluated correlations between the wheat baking quality predicted by these signal genes and the actual baking quality expressed by baking and rheological traits of wheat. The Zeleny sedimentation value reliably distinguished the baking quality classes from each other. A significant positive correlation was proved between the value predicted using glutenin markers and the sedimentation value. A significant positive correlation was also found between the total value predicted using gliadin and glutenin markers and the sedimentation value.

## 54. Linkage disequilibrium in haploids extracted from old open-pollinated maize varieties and synthetics

Butruille, D.<sup>1</sup>, Diniz Silva, H.<sup>1,4</sup>, Bockelman, D.<sup>2</sup> and Tianxing Zhang<sup>3</sup>

<sup>1</sup>Monsanto Company, 3320 SE BLV Convenience, Ankeny, IA, 50021 USA

Corresponding author e-mail: david.butuille@monsanto.com

<sup>2</sup>Monmouth Agronomy Center, 1677 80th St, Monmouth, IL 61462, USA

<sup>3</sup>Monsanto Company, 2111 Piilani Highway P.O. Box 645, Kihei, HI 96753, USA

<sup>4</sup>Universidade Federal de Uberlandia, FAMAT-UFU Campus Santa Monica, Av Joao Naves de Avila 1221, 38400-902, Uberlandia-MG, Brazil

Our ability to increase the resolution in quantitative trait loci (QTL) mapping studies is limited by the amount of recombination present in the population being analyzed. Historically, most of the maize marker-QTL associations detected have used segregating populations derived from crosses between two inbred lines. In these populations, the resolution is of the order of 10-20 centiMorgans (cM). More recently, to leverage historical recombination present in the germplasm, several large association studies with a resolution of a few centiMorgans or lower have been proposed or completed. The next stage in the quest of ever-increasing resolution would have to resort to multiple generations of random-mating or using populations that have been intermating for many generations. In the present study, we selected 20 historical open-pollinated varieties and synthetics, derived from these a balanced bulk of haploid kernels, and planted these haploid kernels. Tissue from individual haploid plants was sampled and genotyped at short nucleotide polymorphisms (SNP) loci belonging to clusters of tightly linked markers. The advantage of this type of genotyping is that haplotypes can be identified unambiguously in a haploid progeny (no determination of linkage phase is required). Based on this, we are presenting information on linkage disequilibrium, and heterozygosity of each of these populations.

## 55. Detection of quality trait loci (QTL) for pericarp thickness and ear inflorescence traits in waxy corn

Choe, E. and Rocheford, T.

Department of Crop Sciences, University of Illinois, 1304 E. Mchenry St., Urbana 61801, IL, USA. E-mail: echoe1@uiuc.edu

Due to an increasing Asian-American population and market, breeding and genetic research on waxy corn for U.S. fresh consumption is needed. The objectives of this study were to detect QTL for pericarp thickness, which affects tenderness, and for ear inflorescence architecture traits relevant to consumer preference and yield; and to study genetic relationships among traits using principal components analysis (PCA). Evaluations were performed on 264 (BH20xBH30)F<sub>3</sub> families. BH30 has a thinner pericarp than BH20; both are waxy corn inbreds from South Korea. 100 SSR markers were mapped. Forty-one QTL were detected for five different pericarp thickness traits measured on upper germinal, lower germinal, upper abgerminal, lower abgerminal and crown regions. QTL for pericarp thickness traits explained phenotypic variation ranging from 31.7 to 42.3%. Most alleles for thin pericarp thickness were from BH30. PCA showed the first principal component (PC) explained 87.6% of pericarp trait variation, and eight PC-QTL were detected. Forty-six QTL were detected for ear inflorescence architecture traits measured on cob length, ear and cob diameter, kernel depth, number of kernels per row, number of rows per ear, kernel thickness, ear and cob weight, and kernel weight. QTL for these traits explained phenotypic variation ranging from 8.7 to 32.8%. Four PCs for ear inflorescence architecture traits explaining 81.8% of total phenotypic variation, and 22 PC-QTL were detected. Notably, QTL regions significant for two or more ear inflorescence architecture traits and PC-QTL were detected in bins 1.08(*id1*), 3.04(*ts4*, *lg3*), 4.05(*fea2*), 7.02(*ra1*) and 8.05(*knox5*), which have inflorescence mutants and genes.



56. Quantitative trait loci associated with husk traits in maize (*Zea mays*, L.)

Cukadar, B. and Gupta, A.

Monsanto, PO Box 410, 62567 Stonington, Illinois, USA.

E-mail: belgin.cukadar@monsanto.com

Most semi-tropical and tropical corn lines tend to have very tight and long husk leaves resulting in high ear moisture and slow dry-down rate when introduced into the Corn Belt of the U.S. Hence, breeders typically need to grow very large segregating populations in the field to select against these traits. One  $F_{3:4}$  and two  $F_{2:3}$  populations were evaluated to identify QTL associated with husk traits. This would facilitate marker assisted selection when introducing this germplasm into the temperate U.S. Corn Belt. About 200 families per population were grown as a randomized complete block design with two replications in Rancagua, Chile, during the 2004-05 winter cycle. Phenotypic data on growing degree units to 50% silk and brown husk, ear husk looseness, ear moisture (%), husk cover extension (cm), husk leaf number, ear length (cm), husk width (cm), and husk length (cm) were collected in Chile. Molecular marker data was collected on the  $F_{2:3}$  and  $F_{3:4}$  families and parental lines. Narrow sense heritability values for husk traits were high, ranging from 0.40 to 0.60 for the three populations. In all three populations, husk looseness was highly correlated to 50% brown husk ( $>0.50$ ) and fairly correlated to 50% silk and husk width (about 0.40). Significant QTL ( $p < 0.15$ ) were found for several husk traits, with more QTL being identified in the  $F_{3:4}$  population. Some QTL were consistent across three populations, and based on multiple regression results, these QTL explained 50-80% of the phenotypic variation for husk looseness and 17-40% for husk width.

## 57. Development of salt tolerant rice varieties using marker assisted selection

Hassan, L.

Department of Genetics & Plant Breeding, Bangladesh Agricultural University, Mymensingh-02202, Bangladesh. E-mail: lutfulhassan@yahoo.co.uk

This project aims to develop improved rice genotypes/varieties for the Southern Coastland of Bangladesh. These areas are cultivated by marginal farmers, who are able to grow only one crop of traditional low-yielding rice per year. The traditional rice varieties that are grown here are well adapted to the saline coastal area and are likely to contain genes or Quantitative Trait Loci (QTL) governing adaptability to saline soils. This study attempts to identify molecular markers for salinity. Seedlings of 38 selected rice accessions from the germplasm collection were screened for salt tolerance in a glasshouse using a salt solution of 12 dS/m. They were categorized into tolerant (three varieties), moderately tolerant (20 varieties) and sensitive (15 varieties). Several rice varieties with differing salt tolerance reactions were initially screened for DNA profiles (extracted using a Nucleon PhytoPure DNA extraction kit from 21 day old seedlings) using 30 RAPD primers. Of these, six primers exhibiting polymorphism were used to screen all 38 rice varieties. Primer OPS 3 produced a specific band for salinity tolerance at 510 bp. The band OPS 3 510 was present very distinctly in the three salt tolerant varieties and was absent in all moderately tolerant and sensitive varieties and is considered as unique to tolerant accessions. The development of backcross progenies is underway and may provide improved varieties that can be released after multiplication to be grown in the coastal areas. The identified QTL can also be used to shorten further breeding programs using the traditional rice as donors.

## 58. Stem borer resistance in maize – a joint analysis

Hauck, A. and Bohn, M.

University of Illinois, Crop Sciences, 1102 S. Goodwin Avenue, Urbana, IL, 61801, USA

E-mail: [ahauck@uiuc.edu](mailto:ahauck@uiuc.edu)

The past two decades of plant breeding have resulted in the publication of many studies identifying quantitative trait loci (QTL) using molecular markers. The relatively large effects of environmental variation and small population sizes commonly used in QTL studies limit the power of QTL detection and may explain the difficulty in repeatability of QTL experiments. The purpose of this study was to ascertain the advantages of combining data from multiple QTL studies on common traits for enhanced power of QTL detection. A joint analysis was conducted using genetic and phenotypic data collected from a number of studies examining cell wall strength and insect resistance in maize populations derived from crosses between two inbreds. Parental inbreds adapted to temperate and tropical growing conditions with contrasting levels of insect feeding damage are represented in the combined experimental population, capturing a broad range of the natural genetic variation for this trait in maize. Analysis of variance was performed to associate genotypes within bins with trait expression. The level of significance was determined with a re-sampling strategy. Significant associations between markers and resistance of maize against stem borer larvae leaf feeding and stalk tunneling were summarized by study to link contributions from specific germplasm with resistance. In some cases, bins with no resistance QTL reported in the original studies were found to be significant. A number of significant bins match the genomic locations of candidate genes, such as members of the lignin pathway, and QTL for other correlated traits, like cell wall digestibility.

## 59. Application of simple sequence repeats to study within and between family variations for resistance to maize streak virus disease

Ininda, J.<sup>1</sup>, Danson, J.<sup>2</sup>, Langat, M.<sup>2</sup>, Gichuru, L.<sup>2</sup> and Njuguna, J.G.M.<sup>2</sup>

<sup>1,2</sup>Kenya Agricultural Research Institute, P.O. 30148 Nairobi.

<sup>1</sup>Corresponding author, Email: jininda@todays.co.ke

The objective of this study was to evaluate within and between family variation for resistance to maize streak disease; and assess the relevance of microsatellite markers linked to maize streak disease resistant loci, in discriminating between susceptible and resistant  $S_{4:6}$  lines. A pedigree-breeding program was initiated in 1998 with a cross between a maize streak virus resistant inbred line obtained from CIMMYT, ([MSRXPOOL9]C1F1-205-1[OSU23i]-6-5-3-X-X-1-B), and a susceptible inbred line from Kenya (EM11-133). Selection and generation advance was done at Muguga, Kenya (2093 masl). Lines were screened for maize streak disease resistance at the  $S_1$  generation and three families selected. A final screen for maize streak disease resistance was done on the  $S_{4:6}$  lines in 2004. One hundred and fifteen  $S_{4:6}$  were planted in the field and artificially inoculated with maize streak virus. Genetic analysis was done using 52 Simple Sequence Repeat (SSR) markers in Bin 1.04 and 1.05. There were significant differences between  $S_{4:6}$  lines for maize streak disease expression. Analysis of each  $S_4$  family showed that there were significant differences in disease expression between  $S_{4:6}$  lines in the field. This supported molecular data which showed polymorphism for selected SSR markers between and within families. Thus, selection for resistant lines using molecular data was highly correlated to results from artificial inoculation. The marker umc1676 was the best for discrimination between the lines. We identified 40 individuals with the resistant parent allele, and 23 representing the susceptible parent allele. This agreed well with the field data for artificial inoculation.

## 60. Use of the TRAP (Trace Relevant Allele Polymorphism) approach in breeding for complex traits – a wheat example

Kobiljski, B.

Institute of Field and Vegetable Crops, M.Gorkog 30, 21000 Novi Sad, Serbia

E-mail: kobboris@ifvcns.ns.ac.yu

Despite the fact that in the vast majority of papers published in the last ten years molecular markers have been successfully associated with quantitative trait loci (QTL), they have had very limited usefulness in plant breeding programs. Today, more than ever, it seems that many researchers were right in saying that we urgently need to modify the present “single cross - QTL mapping - validation - use” strategy in order to diminish the huge gap which exists between the potential of modern biotechnology and its application in breeding. In order to narrow this gap the TRAP (Trace Relevant Allele Polymorphism) approach has been proposed and tested in the wheat breeding program in Novi Sad, Serbia. This concept is starting from the top of the pyramid (i.e. grain yield itself) instead from the bottom (major or minor QTLs) and implies searching for certain alleles associated with desirable (undesirable) performance of complex traits. Later, this approach allows us to follow, by molecular markers, the “main route” from a complex trait towards its main components, subcomponents and subunits. There is a risk of a marker-trait association being “false positive”, but still, “real-positive” ones could bring a benefit to breeding programs at a much higher rate than is the case today. The proposed approach is discussed in detail with emphasis placed on the problems and prospects of such an approach in the wheat molecular and breeding context.

## 61. Molecular markers for leaf rust resistance genes and genes controlling vernalization in wheat

Kohutová, Z., Kocourková, Z., Slámová, L., Vlastníková, H., Křenek, P., Vejl, P.\* and Zoufalá, J.  
Czech University of Agriculture, Kamýcká 129, CZ-165 21 Praha 6, Czech Republic  
Corresponding author e-mail: vejl@af.czu.cz

Supported by Ministry of Agriculture of the Czech Republic, project numbers QF 4190, GACR No. 521/05/H013 and IG of grant agency of FAFNR CUA Prague No. 22/2006.

The SCAR and CAPS methods were used for molecular characterization of vernalization and leaf rust resistance genes in thirty-five worldwide lines and two varieties of wheat. Leaf Rust, caused by *Puccinia triticina*, is one of the most important wheat diseases. DNA markers were used to verify the presence of the resistance genes *Lr26*, *Lr25-Lr29*, *Lr37* and *Lr47*. The *Lr26* gene was identified in fourteen genotypes. The identification of both SCAR markers of genes *Lr25* and *Lr29* was accomplished by touchdown multiplex PCR. The *Lr25* gene is present in twelve genotypes; the gene *Lr29* was found only in line P29. Two DNA markers are available to detect the gene *Lr37*, which was identified in the Mexican line 351 from CIMMYT. The gene *Lr47* was detected by CAPS marker only in line P29. Genes *Vrn1* and *Vrn2* are the major genes, which control the process of vernalization. The difference between the dominant and recessive alleles of *Vrn1* is located in the promoter. The recessive allele of *vrn1* was found to be present in thirteen genotypes. The recessive allele of the *vrn2* gene was present in all evaluated genotypes. These results show the usefulness of the markers tested for identifying some resistance genes and the two genes controlling vernalization in wheat.

## 62. Development of specific PCR markers for *Solanum* ssp. late blight resistance genes and detection of their homologues

Křenek, P.<sup>1\*</sup>, Vlastníková, H.<sup>1</sup>, Mazáková, J.<sup>2</sup>, Kocourková, Z.<sup>1</sup>, Kohutová, Z.<sup>1</sup>, Slámová, L.<sup>1</sup>, Zouhar, M.<sup>2</sup>, Domkařová, J.<sup>3</sup>, Škodáček, Z.<sup>1</sup>

<sup>1</sup> Czech University of Agriculture in Prague, Faculty of Agrobiolgy, Food and Natural Resources, Department of Genetic and Breeding, Prague, the Czech Republic.

<sup>2</sup> Czech University of Agriculture in Prague, Faculty of Agrobiolgy, Food and Natural Resources, Department of Plant Protection, Prague, the Czech Republic

<sup>3</sup> Potato Research Institute, Havlickuv Brod, the Czech Republic

\*Corresponding author e-mail: krenek.pavel@seznam.cz, krenek@af.czu.cz

Supported by the Ministry of Agriculture of the Czech Republic, project number QF4107

We report here the development of specific PCR (polymerase chain reaction) markers for routine detection of the RB and R1 genes, the genes conferring resistance to *Phytophthora infestans* in potato, which have recently been cloned from *Solanum bulbocastanum* and *S. tuberosum*. Specific PCR markers for the RB gene and R1 gene were developed using publicly available bioinformatics tools (BLASTN, Primer3). We show that the utility of BLASTN and Primer3 generated specific PCR markers for R genes in marker assisted selection (MAS) is mainly based on a number of homologues known for a particular R gene, the premix setup and the PCR product carry-over prevention system. A simple and low cost PCR-SSCP (single strand conformation polymorphism) protocol was established to confirm the specificity of the PCR markers designated for the detection of R genes. Furthermore we found the PCR-SSCP method to be a great tool for the detection of novel homologues of R genes.

### 63. Quantitative trait loci mapping for ear shoot development in maize

Mayor, M.L. and Lee, M.

Department of Agronomy, Iowa State University, 50011 Ames, Iowa, USA.

E-mail: [mlmayor@iastate.edu](mailto:mlmayor@iastate.edu)

Stable development of ear shoots and prolificacy are important traits in maize production because they provide plasticity in the response to environmental conditions. The objective of this project is to detect Quantitative Trait Loci (QTL) for prolificacy and ear shoot abortion. Ear shoot development is being studied in 2 populations. The first population consists of 218 recombinant inbred lines (RILs) created by mating inbred lines C103 and C103AP. C103 is single-eared and frequently aborts its ear shoots. C103AP, a prolific inbred, was produced by backcrossing a prolific popcorn accession (AP) to C103, the recurrent parent. Genotyping at 656 SSR loci revealed that 76% of the nuclear genomes of C103 and C103AP are identical by descent; hence, the sequences involved in ear development should be located in the remaining 24%. The second population was created by crossing inbreds B104 and 95:2, a prolific popcorn inbred. The F2 and F3 generations of this population have been evaluated to detect QTL with effects for prolificacy. Results from the first year of phenotypic evaluation of the C103xC103AP population showed that C103AP was 30cm taller than C103 and developed 2.94 ears per plant, while C103 had 0.2 ears per plant. The RILs ranged from 0 to 3.5 ears per plant.



## 64. Using mating designs to uncover quantitative trait loci and the genetic architecture of complex traits

McIntyre, L.

Associate Professor, Department of Molecular Genetics, University of Florida, PO Box 100266, 32610 Gainesville, Florida, USA. E-mail: mcintyre@ufl.edu

Quantitative trait loci (QTL) affecting complex traits are often analyzed through single-cross experiments. For most purposes, including breeding, it is desirable to know to what extent findings related to QTL and the overall genetic architecture of the trait can be generalized. Single-cross experiments provide a poor basis for this assessment. Comparison across experiments is hampered by segregation of different allelic combinations among different parents and by context dependent effects of QTL. To overcome this problem, we combined the benefits of QTL analysis (to identify genomic regions affecting trait variation) and classic diallel analysis (to obtain insight into the general inheritance of the trait) by analyzing multiple mapping families that are connected via shared parents. We first provide a theoretical derivation of main (general combining ability (GCA)) and interaction (specific combining ability (SCA)) effects on F<sub>2</sub> family means relative to variance components, in a randomly mating reference population. We then use computer simulations to generate F<sub>2</sub> families derived from 10 inbred parents in different partial-diallel designs. These show that QTL can be detected and that the residual among-family variance can be analyzed. We apply standard diallel analysis methods to reveal the presence and mode of action (in terms of GCA and SCA) of undetected polygenes. We demonstrate that QTL detection and estimation of the genetic architecture of polygenic effects are competing goals. This should be explicitly addressed in experimental design. Our approach provides a general strategy for exploring the genetic architecture, as well as the QTL, underlying variation in quantitative traits.

## 65. Gene pyramiding to improve rice by marker assisted backcrossing

Negrão S.<sup>1</sup>, Jayamani P.<sup>1,2</sup>, Rocheta M.<sup>1</sup>, Maças B.<sup>3</sup>, Mackill D.<sup>4</sup> and Oliveira M.M.<sup>1,5</sup>

<sup>1</sup>Lab.Eng. Genética de Plantas -ITQB/IBET, 2784-505 Oeiras, Portugal

<sup>2</sup>CPBG, Tamil Nadu Agricultural University, Coimbatore 641003, India

<sup>3</sup>ENMP, Apartado 6, 7350-951 Elvas, Portugal

<sup>4</sup>International Rice Research Institute- IRRI- Los Baños- The Philippines

<sup>5</sup>Univ. Lisboa, Fac. Ciências, Dep. Biologia Vegetal, 1749-016 Campo Grande, Portugal

Corresponding author e-mail: [snegrao@itqb.unl.pt](mailto:snegrao@itqb.unl.pt)

Among the European countries Portugal has the highest rice consumption per capita (17.3 kg/capita/year). Portuguese traditional rice varieties are tall, very sensitive to blast, and have low yield, in spite of the good grain quality. Therefore, breeding work was begun to develop dwarf, high yielding varieties, with blast resistance. Our aim was to pyramid a semi-dwarfing gene (*sd 1*) and two blast resistance genes (*Pib* and *Pita-2*) into the cultivars ‘Strella’ and ‘Allorio’ using marker assisted backcrossing (MAB). A total of 165 SSR were used to search for polymorphism among parents. The selected polymorphic SSR were used to track the genome of the recurrent parent and specific markers were used to confirm the presence of genes of interest in the backcross populations. After selection in F<sub>2</sub> progenies with specific markers and SSR, we have recovered the 3 genes of interest in the recipient backgrounds.

66. Is it possible to complement the Shiltz scale with biochemical and molecular analysis to evaluate tobacco varieties' (*Nicotiana tabacum* L.) resistance to blue mold?

Pérez Lara, E.<sup>1</sup>, Rodríguez, L.<sup>2</sup>, García, H.<sup>1</sup> and Valdez, M.<sup>3</sup>

<sup>1</sup>Tobacco Research Institute, Plant Breeding Department, Carretera Tumbadero Km. 8½, San Antonio de Los Baños, La Habana, Cuba. E-mail: enidpl@iitabaco.co.cu

<sup>2</sup>BSc. Biology Student. Biology Faculty, University of Havana, Cuba

<sup>3</sup>Molecular Biology Laboratory, Plant Biology Department, Biology Faculty, University of Havana, Cuba

Seven Cuban tobacco varieties were tested using the Coresta scale described by Shiltz in 1974 to evaluate their resistance to blue mold (*Peronospora hyoscyami* f. sp. *tabacina*). This scale was the only test used in Cuba to evaluate resistance to blue mold and it depends on natural attack by the pathogen. Recently, molecular and biochemical characteristics of plants have been used to study varieties' behavior in the presence of pathogens. Isozymes and total protein electrophoresis are frequently used, as well as ISTR (inverse sequence-tagged reverse) analysis. This work aimed to evaluate the physical behavior of the tobacco varieties under natural attack by blue mold, and to find isozyme bands and ISTR that are probably related to resistance. Leaf samples were collected 25 days after transplant, when the plants begin to show resistance but in the absence of the pathogen. A total extract was done for protein electrophoresis and DNA extraction was carried out. Following a natural attack by blue mold about 35 days after transplant, we evaluated the varieties using the Coresta scale and prepared a second total extract for protein electrophoresis. The varieties showed different levels of stress under attack, according to the Coresta scale. Isozymes and total proteins showed a higher number of band patterns and stronger color resolution of some bands when the plants were under stress than before the attack. Isozymes could be related to the results of the Coresta scale, but ISTR analysis showed low polymorphism, not permitting inferences about the bands involved in resistance.

## 67. Recurrent selection mapping in two diverse maize populations selected for northern leaf blight resistance

Poland, J.A.<sup>1\*</sup>, Wisser, R.J.<sup>1</sup>, and Nelson, R.J.<sup>1,2</sup>

<sup>1</sup>The Institute for Genomic Diversity, Department of Plant Breeding and Genetics, Cornell University, Ithaca, NY, USA.

<sup>2</sup>Department of Plant Pathology, Cornell University, Ithaca, NY, USA.

\*Corresponding author e-mail: [jap226@cornell.edu](mailto:jap226@cornell.edu)

Recurrent selection (RS) is commonly used for trait improvement in crop species. Using RS, the International Maize and Wheat Improvement Center (CIMMYT) achieved significant gains for resistance to northern leaf blight (NLB), a disease of global significance, in eight diverse subtropical maize populations. In two of the populations, putative quantitative trait loci (QTL) for NLB resistance were identified by RS mapping, an approach to locate significant changes in allele frequency in RS populations. We examined the extent to which common loci or chromosomal segments were associated with RS in separate, but similarly selected populations. In the populations, 101 simple sequence repeat (SSR) loci were evaluated. In the two populations, 28 and 25 loci exhibited significant deviations from drift. Of these, nine loci exhibited significant deviations in both populations. However, the alleles which increased in frequency in the two different populations were not the same. The results presented here suggest that there were several common loci associated with NLB selection between these populations but there is little correlation between the SSR allele(s) that increased in frequency.

## 68. Detection of donor alleles for enhanced starch concentration in maize

Silva, H.S. and Rocheford, T.R.

Department of Crop Sciences, University of Illinois, Urbana 61801, USA

E-mail: [ssilva@uiuc.edu](mailto:ssilva@uiuc.edu)

Kernel composition traits in maize and other cereal crops are of great economic importance. There is, therefore, interest in modifying levels and properties of kernel composition traits for specific end uses. An example is breeding for higher levels of starch to enhance fermentation efficiency to produce ethanol. Starch is a major component of mature maize kernels, along with oil and protein. Quantitative trait loci (QTL) associated with kernel composition traits would facilitate the development of maize inbreds and hybrids with desirable properties and levels of components, enabling better and more efficient conversion to secondary products. The Illinois Low Protein cycle 90 (ILP<sup>90</sup>) strain was selected for low protein for 90 generations resulting in an extremely high concentration of starch. Thus, by evaluating kernel composition traits in a (ILP<sup>90</sup>×B73)B73 background we are assessing for donor alleles in the ILP strain that would improve inbreds and likely increase hybrid starch levels. Protein, starch, oil, and kernel weight were measured in grain samples of (ILP<sup>90</sup>×B73) B73 S<sub>1</sub> families using a Near Infrared Reflectance (NIR) instrument. A genetic linkage map with 144 markers was used to map QTL for the individual traits and Principal Components using Composite Interval Mapping. We want to compare QTL identified using the different approaches, as multivariate analysis might be advantageous in detecting QTL on correlated traits. QTL associated with starch concentration did not appear to map to starch structural biosynthetic genes, suggesting that unknown regulatory loci may influence quantitative variation for starch concentration.

## 69. Characterization of leaf, stem and stripe rust resistance genes in CIMMYT wheat germplasm

Singh, D., Park, R.F., Bariana, H.S. and Wellings, C.R.

Plant Breeding Institute, University of Sydney, Private Mail Bag 11, 2570 Camden, NSW, Australia. E-mail: dsingh@camden.usyd.edu.au

In an attempt to characterize wheat germplasm for resistance to leaf rust, stem rust and stripe rust, 143 wheat lines from the CIMMYT international spring wheat screening nursery were tested with respective Australian pathotypes of *Puccinia triticina*, *Puccinia graminis* f. sp. *tritici* and *Puccinia striiformis* f. sp. *tritici* in greenhouse and field experiments. The greenhouse tests identified seven known seedling leaf rust resistance genes (*Lr1*, *Lr3ka*, *Lr13*, *Lr20*, *Lr23*, *Lr26* and *Lr37*), five stripe rust resistance genes (*Yr3*, *Yr7*, *Yr9*, *Yr17* and *Yr27*) and five stem rust resistance genes (*Sr2*, *Sr9g*, *Sr30*, *Sr31* and *Sr38*) with a high frequency of the linked genes *Lr26*, *Sr31* and *Yr9*. Several lines showed a low infection type to all pathotypes tested for each of the rusts. Resistance in these lines may be due to uncharacterized resistance gene(s) or gene combination(s) that could not be identified with the pathotypes used. A high proportion (approximately 80%) of the lines that were susceptible at seedling growth stages expressed high levels of adult plant resistance (APR) to leaf and stripe rust when tested with seedling virulent pathotypes in the field. The unexplained seedling resistances and APR genes identified represent a potentially new pool of rust resistance diversity for Australian germplasm enhancement and breeding programs. The lines will be subjected to detailed tests and genetic studies to permit further utilization.

## 70. Genetic analysis of resistance to leaf rust in European winter wheat cultivars

Singh, D.<sup>1</sup>, Park, R.F.<sup>1</sup>, Snape, J.<sup>2</sup>, Simmonds, J.<sup>2</sup> and Bariana, H.S.<sup>1</sup>

<sup>1</sup>Plant Breeding Institute, University of Sydney, Private Mail Bag 11, 2570 Camden, NSW, Australia. E-mail: dsingh@camden.usyd.edu.au

<sup>2</sup>John Innes Centre, United Kingdom

Genetic studies were conducted on crosses involving two European winter wheat cultivars, Beaver and Rialto, to determine the mode of inheritance of leaf rust resistance at the seedling and adult plant growth stages using two doubled haploid populations (Beaver/Soissons – B/S and Spark/Rialto – S/R). Seedling studies indicated the involvement of *Lr13* and *Lr26* in governing leaf rust resistance in both Beaver and Rialto. An uncharacterized seedling resistance gene (RF Park, unpublished) was also detected in the cultivar Beaver. The population B/S showed monogenic inheritance for this gene when tested with a pathotype recently identified in Australia that is virulent on *Lr13* and *Lr26*. Adult plant resistance (APR) in the field with pathotypes carrying virulence individually for *Lr13* and *Lr26* showed trigenic inheritance for the B/S population, whereas the S/R population segregated for three to four genes. Preliminary quantitative trait loci (QTL) mapping studies on the B/S population identified four QTL on chromosomes 1BL/1RS, 2B, 3B and 4B. In contrast, three significant QTL were identified on chromosomes 3A, 3B and 6A in the S/R population.

## 71. Molecular breeding strategy to combine multiple abiotic stress tolerance in rice

Singh, R.K.<sup>1\*</sup>, Gregorio, G.B.<sup>2</sup>, Adorada, D.<sup>1</sup>, Mendoza, R.<sup>1</sup> and Sajise, A.G.<sup>2</sup>

<sup>1</sup> Plant Breeding Genetics and Biotechnology, International Rice Research Institute (IRRI), DAPO Box 7777, Metro Manila, Manila, Philippines

<sup>2</sup> IRRI Scientist in Africa, WARDA station, IITA, Nigeria

\*Corresponding author e-mail: r.k.singh@cgiar.org

Salinity tolerance is a complex combination of traits, each probably controlled by polygenes. Saline soils are characterized by other soil stresses, in particular zinc deficiency, iron toxicity, phosphorus deficiency and submergence. A “Diallel Selective Mating System” (DSMS) with little modification is employed for the rapid development of multiple, abiotic stress tolerant rice genotypes, with a much wider genetic base, using marker assisted selection (MAS) to support conventional breeding. The objective is to increase the frequency of the desirable alleles in the population; inter-mating of only selected alleles based on MAS and phenotyping to increase the probability of desirable recombinants and improve the inherent adapted/mega rice varieties using the back cross series. Traits like tolerance to salinity, submergence, and zinc deficiency are considered along with semi-dwarf to intermediate height, erect plant type, complete panicle exertion with medium slender, long bold and long slender grain types. The modifications in the original scheme are: MAS is applied to F<sub>2</sub>/F<sub>3</sub> plants for specific traits; an additional backcross series is introduced to convert the mega varieties/adapted varieties with improved tolerance to abiotic stress; and a modified bulk-pedigree method is followed to advance the generations, instead of mass selection. So far MAS based selective mating is followed for seedling stage salinity tolerance and submergence tolerance. However, it could be extended to other traits like reproductive stage tolerance for salinity and iron toxicity when reliable markers are identified. Phenotypic selection is being used for other traits like zinc efficiency, grain quality and other agronomic parameters.



## 72. Detection of the *Bdv2* gene in some wheat varieties by means of molecular-genetic markers

Slámová, L., Vejl, P., Veškrna, O., Kohutová, Z., Kocourková, Z., Křenek, P. and Vlastníková, H.

Department of Genetics and Breeding, Faculty of Agrobiolgy, Food and Natural Resources, Czech University of Agriculture Prague, Kamýcká 129, Praha 6, Suchdol, 165 21 Czech Republic. Corresponding author e-mail: slamova@af.czu.cz

Supported by grant project QF 50073 "Study of tolerance to BYDV in *Triticum*" and GA CR no. 521/05/H013 "Wheat - from genome to quality of production".

Barley Yellow Dwarf Virus (BYDV), vectored by several aphid species, is one of the most economically significant diseases of wheat and other grain cereals. No real resistance has been described in wheat collections except one gene (*Bdv1*) in some wheat cultivars. *Thinopyrum intermedium* Barworth et Bewey, contains at least two genes for resistance to BYDV infection. We used three pairs of primers – *BYAgi*, *SCG-pIU* and *Xgwm* – to prove the presence or absence of the gene *Bdv2*, which is believed to be the major gene for resistance to BYDV. We used 130 wheat varieties, including the potential donors of *Bdv2* and 11 F2 generations. The method of DNA isolation, PCR and the visualization of the electrophoreograms were optimized. The presence of the specific marker was proved in some new breeding lines.

### 73. *Cis*-acting regulatory variation in cereals

Stamati K<sup>1</sup>, Mackay I.<sup>1</sup>, Russell J.<sup>2</sup>, Booth A.<sup>2</sup>, Baum M.<sup>3</sup>, Morgante M.<sup>4</sup>, Radovic S.<sup>4</sup> and Powell W.<sup>1\*</sup>

<sup>1</sup>National Institute of Agricultural Botany (NIAB), Huntingdon road, Cambridge, CB4 2BL, UK.

<sup>2</sup>Scottish Crop Research Institute, Invergowrie, DD2 5DA, Dundee, SCOTLAND, UK

<sup>3</sup>International Center for Agricultural Research in the Dry Areas (ICARDA), P.O. Box 5466, Aleppo, Syria

<sup>4</sup>Dipartimento di Scienze ed Ambientali Universita' di Udine Via delle Scienze 208 I-33100 Udine, Italy

\*Corresponding author e-mail: wayne.powell@niab.com

Heritable differences in gene expression are now considered to be a fundamental mechanism responsible for determining the genetic control of complex, multifactorial traits. It is predicted that such mechanisms are pervasive and control the response of crop plants to stresses such as those induced by limited water, salinity or high temperature. Reliable identification of genetic variants affecting gene regulation and causatively associated with important, complex traits will allow the identification and isolation of mechanistically functional alleles for deployment in breeding programs. Our objective is to develop a method that allows the identification of sequence polymorphisms that are linked in *cis* to regulatory variants and to predict which nucleotide differences are responsible for changes in gene expression. This assay will be exploited to analyze and identify novel alleles for abiotic stress tolerance in barley germplasm. The approach is based on the hypothesis that the relative abundance of allelic transcripts, estimated for individuals in the heterozygous condition, is devoid of *trans*-acting influences and environmental factors. We have established an allelic imbalance assay for barley and scanned 12 genes for putative *cis*-acting variation. One gene, aquaporin (ABC01216), (a class of membrane proteins that facilitate water diffusion across cell membranes, implicated in environmental stimuli as diverse as low temperature, drought, salinity, light (daily rhythm) and nutrient deprivation or supply) has shown a significant imbalance in gene expression. Studies are being extended to include genes involved in stress and nitrogen metabolism to quantify the extent of *cis*-acting regulatory variation in the barley genome.

## 74. Enhanced detection of inflorescence architecture QTL in Intermated B73 x Mo17 (IBM) RIL population

Upadyayula, N., Bohn, M., Johnson, R. and Rocheford, T.

Department of Crop Sciences, University of Illinois, Urbana 61801, Illinois, USA

Corresponding author e-mail: upadyayu@uiuc.edu

Genetic control of maize inflorescence architecture is of interest to developmental and evolutionary biologists as well as crop scientists. A number of maize inflorescence mutants have been identified and genes cloned, providing useful resources for developmental, evolutionary and breeding related studies in maize and across the cereals. QTL (quantitative trait loci) analysis is complementary and is identifying many more loci that influence inflorescence architecture. We summarize a series of QTL studies, two in standard  $F_{2,3}$  or  $BC_1:S_1$  populations and one in a population of recombinant inbred lines (IBM). We measured several traits on tassel and ear, and also calculate traits such as ratio of branch number to spikelet number. In standard QTL mapping populations we detect a couple to several QTL for each trait, with total numbers approximately 30 to 50. In contrast, in the IBM population, depending on permutation generated LOD threshold used, we detect approximately 300 – 500 total QTL for 16 different tassel and ear inflorescence architecture traits. This demonstrates the power of IBM populations. We performed principal components analysis (PCA), and performed QTL analysis on the PC values to detect pleiotropic QTL. We identified QTL that map to relevant mutant loci such as *ts4*, *lg3*, *fea2*, *td1*, *ra1*. However, the vast majority of QTL are not near inflorescence mutants and genes, which provides initial information for new gene discovery approaches. Our results demonstrate enhanced detection of QTL on the higher resolution IBM mapping population, creating mapping information that will become increasingly useful with sequencing of the maize genome.

## 75. Application of PCR markers of the *Vm* and *Vf* genes controlling apple resistance to *Venturia inaequalis* in Czech apple breeding

Vejl, P., Melounová, M., Zoufalá, J., Sedlák, P., Blažek, J. and Dandová, M.

Department of Genetics and Breeding, Faculty of Agrobiological Sciences, Food and Natural Resources, Czech University of Agriculture, Kamýcká 129, CZ-165 21 Praha 6, Czech Republic.

E-mail: vejl@af.czu.cz

Supported by the Ministry of Agriculture of the Czech Republic, project numbers QD1267 and QD1049.

Apple scab is one of the most economically important apple diseases. Donors of *Vf* and *Vm* resistance genes are currently used in Czech apple breeding. Use of DNA markers is the base of Marker Assisted Selection, which is capable of speeding up the breeding process and eliminating mistakes in selection caused by non-genetic modifications. The most widespread resistance genes against apple scab, *Vm* and *Vf*, were detected in a collection of eighteen Czech and worldwide apple varieties and four resistant new breeds, by means of specific PCR markers. The dominant PCR marker of the *Vm* gene was found only in the hybrid OR-45-T-132 that is frequently used for breeding for resistance to apple scab. The allelic constitution of the *Vf* gene was characterized by means of a PCR co-dominant marker. All varieties possessing resistance showed the heterozygous constitution of the *Vf* gene (*Vfvf*); all susceptible varieties had the recessive, homozygous constitution of both genes. DNA markers of the genes studied were also used for evaluation of four F<sub>1</sub> hybrid progenies without infectious pre-selection and three pre-selected F<sub>1</sub> generations. A positive effect of the selection based on infectious tests was proved by means of the  $\chi^2$ -test. A reduction in the occurrence of sensitive plants with the recessive homozygous genotype (*vvf*) was detected in the F<sub>1</sub> progeny. The pyramiding of *Vm* and *Vf* genes was found in only two of the F<sub>1</sub> progenies. The mendelistic heredity of the studied genes was proved by means of a  $\chi^2$ -test.

76. Estimation of molecular genetic markers used for detection of *Phytophthora infestans* (Mont.) de Bary in infected plant tissue of some *Solanum* species

Vlastníková H.<sup>1,2</sup>, Křenek P.<sup>1</sup>, Domkářová J.<sup>2</sup>, Kohutová Z.<sup>1</sup>, Kocourková Z.<sup>1</sup>, Slámová Z.<sup>1</sup> and Vejl. P.<sup>1</sup>

<sup>1</sup> Czech University of Agriculture, Kamýcká 129, CZ-165 21 Praha 6, Czech Republic.

Corresponding author e-mail: vlastnikova@af.czu.cz

<sup>2</sup> Potato Research Institute, Ltd., Dobrovského 2366, CZ-580 01 Havlíčkův Brod, Czech Republic. E-mail: greplova@vubhb.cz

Supported by the Ministry of Agriculture of the Czech Republic, project number NAZV QF 4107.

Late blight, caused by the oomycete pathogen *Phytophthora infestans*, is still the most devastating disease of potato and tomato, causing high losses in the field and storage. Identification of *P. infestans* can be very difficult using methods based only on morphological characteristics, because the symptoms of this pathogen overlap with other species. A rapid and accurate method for specific detection of *P. infestans* is necessary for determination of late blight in infected fruit, leaves and tubers. In this study, the *P. infestans* detection ability of six PCR primer sets based on families of highly repeated DNA and ribosomal DNA (rDNA) and one RAPD (random amplified polymorphic DNA) marker were evaluated. *P. infestans* was successfully detected in most cases of PCR analyses of infected plant tissue (*Solanum tuberosum* – tubers, stems, leaves; *Lycopersicon esculentum* – fruits, stems, leaves). There was no specific amplification in the negative control samples that included healthy plant tissue and isolates of *Cladosporium* ssp., *Aspergillus* ssp., *Penicillium* ssp. and *Mucor* ssp. Rarely primers generated weak, non-specific bands from uninfected tissue of potato and tomato, but they were easily distinguished from the *P. infestans* amplicons by size. Based on this study, the PISP-1 and ITS3 primers were selected as the most reliable tools for detection of *P. infestans* in potatoes and tomatoes. PCR amplification with primers PISP-1 and ITS3 results in an amplicon of approximately 450 bp, which was specific for *P. infestans*.

---

## Cultivar development methodologies – maize

---

### 77. Participatory plant breeding: a maize case study from Cuba

Acosta Roca, R.\*, Ríos Labrada, H., Martínez Cruz, M., Miranda Lorigados, S., Ortiz, R., Ponce Brito, M.

PhD Students, Department of Genetics and Plant Breeding, National Institute of Agricultural Science, La Habana, Cuba

\*Corresponding author e-mail: rosa@inca.edu.cu, rosaar\_cu@yahoo.es

Nowadays, one of the discussions in the field of plant breeding is focused on how to combine the advantages of the formal and informal seed systems with the objective of increasing yield, at the same time as increasing or conserving genetic diversity. In this sense, Participatory Plant Breeding (PPB) is an efficient methodology that involves farmers in breeding varieties and facilitates their participation in the different areas of seed selection and multiplication. There are some reports of the advantages of PPB in terms of increasing genetic diversity and yield in the target environments, as well as increasing farmers' decision-making abilities in the participant communities. However, the relationship between traditional practices and the genetic diversity of a local maize seed system, the genetic advance that farmers obtain through selection in the communities, as well as an estimate of the varietal demand through differential selection in a certain productive system, have rarely been documented. Results, based on farmers' criteria for varietal selection, indicate that the use of only one variety is not sufficient to adapt to specific conditions. In this work we identified farms as units of maize genetic identity, based on farmers' criteria and the GxE interactions in each farm. This could be of significant interest to farmers involved in PPB and in maize breeding systems in Cuba.

## 78. Early testing for inbreeding tolerance in four local maize populations from the Peruvian Andes

Aguirre, A., C.\* and Crisóstomo P., F.

Gensiagro Huancayo-INCAGRO, Pje. Salazar Bondy 315, Urb. Siglo XX, El Tambo, Huancayo, Junín, Perú.

\*Corresponding author e-mail: [caguirre@hotmail.com](mailto:caguirre@hotmail.com)

In 2004, we planted 4 observation plots in the Peruvian highlands (3250 masl) for early evaluation of inbreeding tolerance with populations where selfing was used to generate lines from S1 and S2. We evaluated three early populations (Orcotuna, Jauja and Huacan) with 120 entries each, including 55 S1 lines, 55 S2 lines and 10 S0; and one late population (Cusco) with 120 entries, including 110 S1 lines and 10 S0. Data collected include plant height, ear height, grain yield/plant, cob length, and cob diameter at tip and base; from these last three we generated a Cob Index for each entry. Five plants were evaluated for each line, and the corresponding five ears used to obtain the mean and standard deviation. Inbreeding tolerance was assessed as the lowest inbreeding depression (ID) based on cob index values. Early populations show variable ID; inbreeding tolerance is also expected to vary. Huacan, and Jauja show a small reduction: farmers plant these populations in small plots and retain small seedlots, causing a sample size effect and some inbreeding. They therefore tolerate selfing better. Orcotuna suffers a strong ID in all characters. For Cusco, the ID for plant and ear height is approximately as expected, but not for grain yield/plant. Some of these populations may have greater ID because they carry a higher genetic load. An inbred line recycling process in early generations will eliminate these genes faster. ID for yield is essentially linear with increased homozygosity, accounting for more than 99% of variation for yield.

## 79. Heterosis and combining ability of tropical maize in the Central Valley of Mexico: morphological and molecular characterization for silage

Alarcón-Zúñiga, B.<sup>1</sup>, Cervantes-Martinez, T.<sup>2</sup> and Warburton, M.<sup>3</sup>

<sup>1</sup>Animal and <sup>2</sup>Crop Science Departments, Universidad Autonoma Chapingo (UACH), Carretera México-Texcoco km. 38.5, Chapingo, Mexico 56230.

<sup>3</sup>International Maize and Wheat Improvement Center (CIMMYT), Apdo. Postal 6-641, 06600 Mexico D.F., Mexico

Corresponding author: b\_alarcon\_zuniga@yahoo.com.mx

Heterosis in maize (*Zea mays* L.) is well studied for grain yield, but little is known about silage maize biomass components and forage quality predictors. In conjunction with field trials in a wide range of environments to identify heterotic groups, novel SSR markers can be used to support breeding strategies, classify inbred lines and define heterotic groups. This study aimed to (i) quantify heterosis and combining ability for grain yield, forage biomass components and forage quality; (ii) study genetic diversity and distance for SSR within a set of tropical inbred populations, and (iii) identify correlations between heterosis and genetic distance. Eight maize inbred populations represented in a partial diallel study, were evaluated in three environments in the Central Valley of Mexico. Nineteen SSRs pair primers identified high genetic diversity among inbred populations, with 4.23 alleles/locus and polymorphic information content ranging from 0.37 to 0.91. High-parent heterosis across environments was 120% (stem), 145% (ear biomass), and 112% (grain yield). No heterosis was identified in total biomass, plant height, ear number, and forage quality predictors (crude protein, *in vitro* DM digestibility, NDF, ADF, and soluble carbohydrates). Genetic distance based on SSRs primers classified the inbred populations into three main clusters, and were positively correlated with high-parent heterosis and combining ability in grain yield and ear number; no correlation was found with silage biomass components and forage quality estimators. Results were significantly affected by environment. Polymorphism data within three candidate genes for lignin biosynthesis are presented for the improvement of silage maize digestibility.



## 80. Inheritance of callose formation in tropical maize inbreds

Arcos, A.L., Medina, S., Narro, L.A.\* and Salazar, F.

International Maize and Wheat Improvement Center (CIMMYT), AA 6713, Cali, Colombia

Corresponding author e-mail: l.narro@cgiar.org

Aluminum (Al) toxicity is an important limiting factor of maize production on acid soils in the tropics. Callose formation in root apices is an excellent indicator of Al injury and provides a physiological marker for Al sensitivity. The objective of this work was to study the genetic inheritance of callose using tropical maize inbreds. Fourteen inbreds selected for different reactions to acid soils were chosen and a diallel between them was generated. Seed were put in a growth chamber into filter paper soaked with CaSO<sub>4</sub> solution. After 72 hours, seedlings were transferred to nutrient solution in plastic pots constantly aerated. After 48 hours, 25 µM Al was added to each plastic pot for 12 hours. A check with 0 Al treatment was also included. Three root tips for each cultivar (inbreds and crosses) in each replication were taken and maintained in ethanol 96%. Callose was calculated using water blue as a stain and callose sirofluor complex measured by fluorescence spectrophotometer. The diallel was analyzed as proposed by Hallauer and Miranda (1988). Significant differences were found for parents and crosses but not for parents versus crosses. Average callose content for parents was 139 and 141 for crosses; which means that heterosis was not important for callose content for this set of inbreds. On the other hand, general combining ability (GCA) and specific combining ability (SCA) were highly significant meaning that additive and non-additive gene effects were important for callose inheritance. SCA sum of squares (SS) was 1.5 fold the GCA SS.

## 81. Participatory breeding for maize varieties tolerant to maize streak virus in the western zone of Tanzania

Bucheyeki, T.L. and Simon, S.M.

Agricultural Research Institute (ARI), Tumbi, P.O BOX 306 Tabora, Tanzania.

E-mail: [tlbucheyeki@yahoo.co.uk](mailto:tlbucheyeki@yahoo.co.uk)

This participatory trial was conducted in the Western Zone, Tanzania for three years. The objectives of the experiment were to evaluate maize streak virus tolerant varieties in farmers' fields and to assess farmers' preferences for the varieties. Thirty-two farmers executed the trial. A randomized complete block design was used. Plot size was 10 x 10 m. The harvested area was the six central rows. Five treatments were used: farmers' variety (Local), Kilima-ST, Kilima-ST-MSV, TMV-1 and Tuxpeno (susceptible). The spacing used was 0.9 x 0.5m (two plants per hill). Introduced varieties differed significantly ( $P < 0.001$ ) from Local in the percentage of streaked maize plants per plot for all seasons except year one. Tanzania maize variety (TMV-1) and Kilima-ST-MSV had the lowest percentage of plants infested by streak virus. Local and the susceptible check (Tuxpeno) had the highest percentage of infestation. Maize yields did not differ significantly between treatments ( $P > 0.05$ ). The farmers' assessment revealed that cobs size, maturity, lodging, stalk borer resistance and drought were important criteria for variety selection. In economic analysis, Kilima-ST-MSV had the highest gross field benefits, followed by TMV-1. Local had the lowest gross field benefit. Based on tolerance to maize streak virus, economic returns and farmers' assessment, Kilima-ST-MSV, and TMV-1 were recommended. Following these recommendations, a community based seed production project was initiated in the area. The project is in the first year of execution.

## 82. Combining ability of tropical and temperate maize inbreds

Cervantes-Martínez, J.E.

Maize Breeding Program, Southern Experimental Station, National Research Institute of Forestry, Agriculture and Livestock (INIFAP). Apdo. Postal 31. Altamira, Tamaulipas, Mexico 89610. E-mail: cervantes.ernesto@inifap.gob.mx

The development and adoption of new, high yielding hybrids and open pollinated maize (*Zea mays* L.) varieties would increase farmers' income in Mexico's tropical corn production areas. The breeding program at INIFAP's Southern Tamaulipas Experimental Station in Mexico has developed high-yielding inbreds. Information about how elite inbreds of different origins combine and perform in hybrids will facilitate the selection of parents and breeding strategies for hybrid development. Our objectives were to estimate the general (GCA) and specific combining abilities (SCA) for grain yield and secondary traits among inbreds from different sources, and to identify potential heterotic relationships among them. Nine white inbreds developed from tropical germplasm (LMST-1, LMST-2, LMST-3, LMST-4, LMST-5, LMST-6, LMST-7, LMST-8 and LMST-9) and five yellow inbreds of temperate origin (LMCB-1, LMCB-2, LMCB-3, LMCB-4 and LMCB-5) were evaluated in a diallel experiment with three planting dates (environments) through 2005-2006. The new hybrids showed similar yields to commercial checks. Across environments, GCA effects were highly significant for grain yield and for agronomic traits. On the basis of GCA effects, LMST inbreds had later maturities and shorter plants than most LMCB inbreds. The top ten best-yielding hybrids and highest SCA effects resulted from crosses among inbreds from both sources (Tropical x Tropical and Tropical x Temperate): LMST-9 x LMCB-1, LMST-9 x LMST-2, LMST-9 x LMST-6, LMST-9 x LMST-8, LMST-8 x LMCB-2, and LMCB-2 x LMST-9. Inbreds developed in different regions could represent potential heterotic groups for use in hybrid development and to improve tropical germplasm for breeding purposes.

### 83. Heterotic responses of white tropical maize inbred lines

Cervantes-Martinez, J.E.<sup>1</sup>, Betanzos-Mendoza, E.<sup>2</sup>, Gomez-Montiel, N.<sup>2</sup> and Coutiño-Estrada, B.<sup>3</sup>

<sup>1</sup>Maize Breeding Program, Southern Experimental Station, National Research Institute for Forestry, Agriculture and Livestock (INIFAP). Apdo. Postal 31, Altamira, Tamaulipas, Mexico, 89610.

E-mail: cervantes.ernesto@inifap.gob.mx

<sup>2</sup>Central Chiapas Experimental Station (INIFAP), Km 3 Carr. Ocozocuatla-Citalapa, Chiapas, México, 29140. E-mail: betanzos.esteban@inifap.gob.mx and coutino.bulmaro@inifap.gob.mx

<sup>3</sup>Iguala Experimental Station (INIFAP), Apdo. Postal 29, CP 40000, Iguala, Gro. Mexico.

E-mail: gomez.noel@inifap.gob.mx

Three-line hybrids are the most profitable way for producers to sell maize seed. This study was conducted to identify maize inbred lines for tropical areas that could increase the level of heterosis with the highest yielding single cross at INIFAP's Southern Tamaulipas Experimental Station in Mexico. 303 inbred lines were crossed with the tester CML176 x CML142 (a quality protein maize hybrid). In 2005, the three line crosses were evaluated in five experiments, using a simple 8 x 8 lattice for each one. Four checks, including the tester, were incorporated into each experiment. The evaluation was carried out at Cuauhtemoc, Tamaulipas, Mexico, a tropical location. The analysis of variance showed highly significant differences among entries for grain yield and yield per ear. Thirteen crosses (line x tester) had a greater grain yield than the highest check (A7573), which yielded 6986 kg ha<sup>-1</sup>. The high parent heterosis of the highest yielding lines ranged from -65% to 81%, with the 131 SI-5 V-454-SC-C0-2 and 114-A75SELF-14-6-1 lines emerging as the best. These include a group of ten lines that were selected and will be improved through recurrent selection schemes to increase yield and improve agronomic traits. Moreover, seed will be increased of four or five of these lines in order to make a three-way cross with CML176 x CML142, for extensive further evaluation.

#### 84. Establishment of heterotic groups within Iranian maize inbred lines

Choukan, R.

Maize Program, Seed and Plant Improvement Institute, 31585 Karaj, Shahid Aahmideh, Iran

E-mail: r\_choukan@yahoo.com

Information on the relationships among elite germplasm is essential in crop improvement. The main objective of this study was to establish heterotic groups among maize inbred lines using genetic distance as measured by the SSR markers. Fifty-six late and 36 early maturing Iranian maize inbred lines were fingerprinted with 46 and 43 SSR markers, respectively. UPGMA clustering grouped each maturity group into four clusters, which were consistent with the pedigrees or known information about the source materials. Within the late maturing inbred lines, the highest distance was found between the cluster of Reid Yellow Dent related lines and the cluster of Lancaster Sure Crop related lines. However, in early maturing inbred lines, the highest distance was found between the lines originating from CIMMYT germplasm and the cluster containing the Lancaster Sure Crop related lines. This information can be used by breeders for planning future crosses among these inbred lines.

## 85. Advances in cyclic hybridization based on three prolific corn varieties

Coutiño-Estrada, B.<sup>1</sup> and Marquez-Sanchez, F.<sup>2</sup>

<sup>1</sup>National Institute of Agricultural and Livestock Research (INIFAP), 29140 Ocozocoautla, Chiapas, Mexico. E-Mail: coutino.bulmaro@inifap.gob.mx

<sup>2</sup>Universidad Autónoma Chapingo. Guadalajara, Jalisco, Mexico.  
E-Mail: fidelmqz@hotmail.com

Cyclic hybridization was undertaken simultaneously with three maize prolific populations. In order to establish a broad genetic base breeding population, ten open-pollinated varieties, improved by selection, were crossed under a diallel design. Parental varieties and their diallel crosses were evaluated. Crosses V-531xCABG and V-531xTuxpeño Sequia C8 had high grain yields, and high values of both average mid-parent and high-parent heterosis. In a second step  $S_1$  lines were obtained from these three varieties. The lines were planted each in a single row under low plant density and high nitrogen fertilization in order to promote two ears per plant. In each line the first shoot was used for selfing while the second shoot was used for crossing. In a third step, crosses were tested at three locations in Chiapas State in Mexico under rainfed conditions. Statistical differences were found among grain yield of the crosses and a few showed better performance than a commercial hybrid and the parental variety V-531 used as checks. The best cross, V-531<sub>212</sub> x CABG<sub>211</sub> yielded 39 and 67% more than the checks, and the cross V-531<sub>167</sub> x Tuxpeño Sequia C8<sub>168</sub> yielded 26 and 18% more grain than the checks. The best  $S_2$  selected from the high yielding crosses can be used to continue the next cycle of hybridization.

## 86. Breeding approaches in simultaneous selection for multiple stress tolerance of quality protein maize

Denic, M.<sup>1</sup>, Mariote, D.<sup>1</sup>, Chauque, P.<sup>1</sup>, Fato, P.<sup>1</sup>, Senete, C.<sup>1</sup> and Haag, W.<sup>2</sup>

<sup>1</sup>Institute for Research in Agriculture of Mozambique (IIAM), Maputo, Mozambique, and

<sup>2</sup>SG 2000, Maputo, Mozambique

Corresponding author e-mail: denicm@eunet.yu

Agriculture is the most important sector in the Mozambican economy. Maize is the principal crop and major staple food in many zones of Mozambique. Therefore increased production of high quality protein maize (QPM) is essential for the improvement of the nutritional value of the daily diet. However, maize production faces serious constraints. Among the agro-ecological conditions, the main constraints are: lack of rainfall; low soil fertility; poor weed control; diseases and pests (maize streak virus and downy mildew, borers and storage pests); and stem/cob rots, leaf blights, gray leaf spot and rusts. Among the socio-economic production constraints are: lack of use of improved varieties; a serious shortage of trained manpower; insufficient management expertise and poor cultivation practices. To alleviate many of these constraints, appropriate field-based breeding methodologies to select for multiple stress tolerance were implemented to develop desirable varieties. These approaches are mainly based on: a) Crossing selected genetic resources, developed by the local program, the International Maize and Wheat Improvement Center (CIMMYT) and the International Institute of Tropical Agriculture (IITA), with more desirable stress tolerant traits; b) Using the disease/pest spreader row method, combined with testing and selection of created genotypes (progenies) under strong to intermediate pressure of multiple stress factors in nurseries; and c) Evaluation of the varieties developed in multi-location trials under low and “normal” inputs. Several varieties were developed. Data obtained using these approaches are presented.

## 87. Combining ability of imidazolinone resistant maize inbred lines and performance of their hybrids under *Striga* infestation

Diallo, A.O.<sup>1</sup>, Kanampiu, F.<sup>1</sup>, Mugo, S.<sup>1</sup>, and Mbogo, P.<sup>2</sup>

<sup>1</sup>International Maize and Wheat Improvement Center (CIMMYT), P.O. Box 1041, Village Market-00621, Nairobi, Kenya

<sup>2</sup>Seedco, Kitale, P.O. Box 616, 00621, Nairobi, Kenya

Corresponding author e-mail: a.o.diallo@cgiar.org

The parasitic weed *Striga* is a major limiting factor to maize production in sub-Saharan Africa. A recently developed *Striga* control technology involves coating Imidazolinone-resistant (IR) maize seed with a low-dose of Imazapyr<sup>TM</sup> herbicide (a.i. Imidazolinone, a systemic acetolactate synthase (ALS) inhibitor). The technology delivers a season-long *Striga*-free crop, doubles grain yield, and also depletes the *Striga* seed bank in the soil. In this study, the general (GCA) and specific (SCA) combining abilities of elite, mid-altitude CIMMYT maize lines (CMLs) and their three-way cross (TWC) hybrids, were evaluated. Twenty-six TWC IR hybrids were formed by crossing 13 of the IR CMLs (converted to IR using the backcross method) with IR single-cross testers. Yield performance of the hybrids was assessed under *Striga*-free and infested conditions at 11 sites in eastern and southern Africa. CML445-IR, CML78-IR, and CML312-IR, the parental lines of the five highest-yielding TWC IR hybrids had the highest positive GCA across sites. Under optimum conditions, the grain yields of the TWC IR hybrids were similar to those of the best commercial hybrids (5.1 to 5.6 tons ha<sup>-1</sup>). However, under *Striga* infestation, nine of the TWC IR hybrids gave significantly higher grain yields (14-71%) and lower *Striga* counts (3 vs. 135 *Striga* plants m<sup>-2</sup>) than all commercial checks. The best TWC IR hybrids were announced to collaborators for them to initiate the registration process for commercialization.



## 88. Plant breeding, seed production and andro-sterility in normal and quality protein maize (QPM) in Mexico

Espinosa-Calderón, A.<sup>1\*</sup>, Tadeo-Robledo, M.<sup>2</sup>, Gómez-Montiel, N.<sup>3</sup>, Sierra-Macías, M.<sup>3</sup>, F. Caballero H.<sup>3</sup>, A. Palafox C.<sup>3</sup>, F. Rodríguez-M.<sup>3</sup>, R. Valdivia B.<sup>4</sup>, R. Martínez M.<sup>2</sup>

<sup>1</sup>Seed Production Program, National Research Institute of Forestry, Agriculture and Livestock (INIFAP), Campo Experimental Valle de Mexico, Km 18.5 Carretera Los Reyes-Lecheria, 56230 Mexico. \*Corresponding author e-mail: espinoale@yahoo.com.mx

<sup>2</sup>National Autonomous University of Mexico (UNAM), Mexico.

E-mail: tadeorobledo@yahoo.com

<sup>3</sup>Maize Program, National Research Institute of Forestry, Agriculture and Livestock (INIFAP), Mexico.

<sup>4</sup>Autonomous University of Nayarit

In Mexico, since 1998 INIFAP has been working with CIMMYT (International Maize and Wheat Improvement Center) researchers to obtain quality protein maize (QPM) varieties and hybrids. As a result, some high-yielding materials with good agronomic characteristics have been developed, but it has proven difficult to convince farmers to use the seed of the new materials. In 1999, INIFAP released 26 hybrids and varieties, but only a few of these are used (H-519 C, H-553 C). One possibility for increasing the seed adoption rate of QPM hybrids is to use andro-sterility. INIFAP researchers have been working for many years with the normal parents of the hybrids. Three new andro-sterile hybrids are now ready for release (H-48 AE, H-50 AE, H-153 AE). The new andro-sterile version of those hybrids has better grain yield (10-15%) than the original hybrids. Work is currently under way to achieve the complete andro-sterile scheme, as well as to identify and develop inbred lines that have fertility restoring capacity. In the case of QPM hybrids, work started in 1999, by introducing andro-sterility to the basic lines, and by trying to identify restoring lines. Progress has been achieved, and now the program has second and third generation inbreds on the way to achieving quality protein in elite lines. Restoring lines have also been identified, for use as restoring donors to the QPM lines.

## 89. Criss cross and interchange of line order for maize hybrids and seed production in normal and quality protein maize (QPM)

Espinosa-Calderón, A.<sup>1\*</sup>, Tadeo-Robledo, M.<sup>2</sup>, Gómez-Montiel, N.<sup>3</sup>, Sierra-Macías, M.<sup>3</sup>, Sandoval, A.<sup>3</sup>, Coutiño E.,B.<sup>3</sup>, Caballero H.,F.<sup>3</sup>, López-Pereira, M.<sup>4</sup>, Piña D.V.<sup>5</sup>, Martínez M., R.<sup>2</sup>

<sup>1</sup>Seed Production Program, National Research Institute of Forestry, Agriculture and Livestock (INIFAP), Campo Experimental Valle de Mexico, Km 18.5 Carretera Los Reyes-Lecheria, 56230 Mexico. \*Corresponding author e-mail: espinoale@yahoo.com.mx

<sup>2</sup>National University Autonomous of México (UNAM, México) tadeorobledo@yahoo.com

<sup>3</sup>Maize Program, National Researches Institute of Forestry, Agriculture and Livestock (INIFAP), Mexico

<sup>4</sup>Mexico Economy Program, International Maize and Wheat Improvement Center (CIMMYT), Mexico, until 1993.

<sup>5</sup>Plant Breeder of CERES Seed Enterprises.

The choice and sequence of parents for each maize hybrid is generally defined in the breeding process by plant breeders. However, in some cases it is necessary to change the parental sequence. The factors influencing changes to the line order are good performance in female and male aspects in: 1) seed productivity, 2) seed quality, 3) flowering synchrony from female to male, and 4) seed availability. In single crosses the changes are not complicated because there are only two parents, but in Mexico this kind of hybrid is not common. Three way hybrids are now more common for INIFAP in Mexico. Double crosses were very popular for three decades from 1950 until 1987. Many Quality Protein Maize (QPM) hybrids, three way and single cross hybrids, were evaluated from 1997 until 2001. Some of the three way hybrids had higher yield than the check but it can be difficult to obtain certified seed. We have evidence that this will improve when the sequence of the parents is changed. In the case of the single crosses it is necessary to develop technology and seed production in order to increase the yield of the parents; the lowest acceptable seed yield must be 2.5 tons per hectare. This paper shows some results with the criss cross method (ie. interchange of line order) in normal and QPM hybrids. We confirm that the parents of some hybrids need to be changed even after release, in order to improve the seed production process.

## 90. Seed deterioration of tropical maize varieties stored under accelerated aging conditions

García-Lara, S. and Bergvinson, D.J.

Maize Program, International Maize and Wheat Improvement Center (CIMMYT), Apdo. Postal 6-641, 06600 Mexico D.F., Mexico. E-mail: [sgarcia@cgiar.org](mailto:sgarcia@cgiar.org)

Reducing the rate of seed deterioration is an important trait for seed producers and farmers who store maize from one year to the next. However, small-scale, resource poor farmers cannot afford appropriate storage structures to achieve ideal seed storage conditions. While all seeds undergo deterioration in storage, the rate is dependent on storage conditions (e.g. temperature and humidity) and the seed (seed moisture and genotype). This study was conducted to evaluate the response of quality protein maize (QPM) varieties to deterioration under accelerated seed ageing conditions ( $30 \pm 2$  °C and >90% relative humidity) for six months to observe genotype differences and to quantify biochemical changes associated with seed deterioration. Physiological (germination and vigor), biophysical (hardness and seed moisture), and biochemical (peroxidase, total carbohydrates and protein) characteristics were determined. Variation among 36 genotypes for physiological, biophysical and biochemical traits were significantly different. Seed viability decreased, together with vigor and seed harness, while seed moisture increased progressively over time. Seed viability was correlated with a reduction in total carbohydrate content and peroxidase activity. Significant change was also observed for total protein content. QPM varieties that retained the highest seed viability were: P62 C3 QPM-F2, P65 C6 QPM-F2, and Ac7740-F2. A breeding scheme has been developed for both maize and wheat to select for seed tolerant to deterioration under stress storage conditions that are often found in tropical agroecologies.

91. Can we reduce maize postharvest losses through host plant resistance?

Gethi, J.G.

Kenya Agricultural Research Institute, KARI-Katumani, P.O. Box-90100, Machakos, Kenya

E-mail: jgethi@wananchi.com

Twenty-three single cross maize hybrids, 13 parent inbreds, three commercial varieties, and a landrace were evaluated for resistance to common weevil (*Sitophilus zeamais* Mot.). Grain damage, number of F1 weevils retrieved, grain weight changes, Dobie's index, F1 progeny per adult, and weight changes per adult were measured. Significant differences existed for all the parameters studied. Some inbred lines such as MUG-4 had a very high Dobie's index, showing they were quite susceptible. The CML inbred line series had lower Dobie's index values, suggesting they were more resistant to the weevil. Inbred line Diplo-3 had the lowest Dobie's index and thus the highest level of resistance. The commercial composite supported fewer weevils than other genotypes. Damaged grain and total weevils produced had significant correlation coefficients of 0.82 and 0.80 with Dobie's index ( $p=0.001$ ), implying the-simpler-to-measure parameters can be used to estimate weevil resistance. Significant variation existed among the single crosses tested that can be exploited in development of weevil resistant maize. Inbred lines Diplo-3, CML-373, and CML-395 can be exploited as sources of resistance to the common weevil as they had low Dobie's index, which was lacking in the other materials.

92. Performance of promising tropical late yellow maize hybrids (*Zea mays* L.) under water stress conditions in Thailand

Grudloyma, P. and Prasitwatanaseree, S.

Nakhon Sawan Field Crops Research Center ,Takfa ,Nakhon Sawan ,60190,Thailand

E-mail: pgrudloyma@yahoo.com

Drought is a limiting factor for maize production in Thailand. Annually it damages an estimated 3 to 22% of the planted area, resulting in yield losses of approximately 129,000 to 858,000 metric tons. During the rain-free summer season (December-April) of 2003/04 at Takfa, Nakhon Sawan Field Crops Research Center, 36 tropical late yellow maize hybrids (*Zea mays* L.) were evaluated in separate trials under water stress and non-stress conditions. A randomized complete block design was used with three replications. Water stress was managed by irrigation withdrawal, achieving severe drought stress during the flowering stage. The non-stress condition received weekly irrigation. The objectives were to compare the performance of the hybrids and identify superior germplasm for further development. Analyses of variance showed significant differences ( $P \leq 0.5$ ) due to genotype for all traits measured. Grain yield (GY) averaged 3,837 kg ha<sup>-1</sup> under water stress compared to 8,141 kg ha<sup>-1</sup> under non-stress conditions, a yield reduction of 52.8%. Anthesis – silking interval (ASI) ranged from 0 to 6.3 days. GY correlated positively with ears plant<sup>-1</sup> (EPP), chlorophyll content (CHE), seeds row<sup>-1</sup> (SPR) and seed weight (SW). Increased GY under water stress was associated with increased EPP, CHE, SPR and SW. ASI and leaf rolling (LRO) correlated negatively with GY, suggesting that an increase in GY was associated with a reduction in ASI and LRO. Several hybrids showed good performance under water stress conditions. NSX 022018 had the highest yield (5,513 kg ha<sup>-1</sup>), with an ASI of 0.3 days and EPP of 0.7 ears plant<sup>-1</sup>.

### 93. Alternative maize cultivar types for sustainable farming systems

Hyrkas, L. and Lamkey, K.R.

Agronomy Department, Iowa State University, 3213 Frederiksen Court, 50010 Ames, Iowa, USA

E-mail: lhyrkas@iastate.edu

Organic and sustainable farmers want to minimize inputs while maximizing profits by selling a specialized product. They are not always looking for the highest yielding maize cultivar. This study was conducted to evaluate various cultivar types in maize for their potential use in developing specialized products for organic and sustainable farmers. These cultivar types include singles crosses (both commercial and public hybrids), population crosses, synthetic cultivars, and open-pollinated varieties. Yield and agronomic traits were measured on these five types of maize (*Zea mays*) cultivars throughout Iowa from 2000 to 2003. Cultivar types ranked as expected for yield: commercial hybrid, public hybrid, population cross, synthetic, and open-pollinated variety. Commercial hybrids yielded approximately 2.4 times more than open-pollinated varieties. Commercial hybrids also had greater resistance to lodging, though synthetics and population crosses had decent standability. The open-pollinated varieties had nearly two percent more protein than the commercial hybrids. The improved synthetic and the population crosses also had significantly more protein than the commercial or public hybrids but less than the open-pollinated varieties. There is potential for the use of alternative cultivar types in maize if the loss in yield can be offset by the increased profits for the specialized product.

#### 94. Tolerance of sixteen maize genotypes to drought stress

Iriany M., R.N., Takdir M., A., Yasin HG, M. and Mejaya, M.J.

Indonesian Cereal Research Institute (ICERI), Jl. Dr. Ratulangi No. 274, Maros 90514  
South Sulawesi, Indonesia.

E-mail: balitsereal@plasa.com, balitser@yahoo.com

Drought stress tolerance is an essential issue in the development of maize varieties. It is therefore important to understand the tolerance of maize varieties to drought stress. This study was conducted to observe the drought tolerance of 16 maize genotypes included two varieties check (Pulut and Bayu). Each genotype was planted in three different irrigation conditions: normal condition (plants were irrigated every two weeks until physiological maturity); intermediate drought stress (the plants were irrigated every two weeks, irrigation terminated two weeks before flowering and restarted two weeks after flowering); and severe drought stress (plants were irrigated every two weeks, irrigation terminated two weeks before flowering and no water was applied until harvest). The experiment was conducted at Bajeng, South Sulawesi during the dry season (June-September), using a nested design with three replications. Each plot consisted of two 5m-long rows with a planting distance of 0.75 x 0.20m. The highest drought tolerance indices were shown by the genotypes Across 8763 (tolerance index 0.79), S98TLWQ (F/D) (tolerance index 0.76) and Poza Rica 8762 (tolerance index 0.71). Five varieties showed the highest tolerance index at severe drought stress, namely S00TLWQ-B, POZA RICA 8563, S98 TLWQ (F/D), Pop 62 C6 QPM TLWF, and BAYU.

## 95. Maize Research in the Bangladesh Rural Advancement Committee (BRAC)

Islam, A.

Sr. Manager (Maize research), Bangladesh Rural Advancement Committee (BRAC), Vill-Gopinathpur, Post-Beltail Upazilla, 00075 District-Sirajgonj, Shahzadpur, Bangladesh.

E-mail: [sudhir.cn@brac.net](mailto:sudhir.cn@brac.net)

BRAC is one of the world's largest non-governmental development organizations working in almost all sectors of life with a long-term goal of poverty alleviation and empowerment of the poor. Maize Research is one of the core programs of BRAC agriculture. BRAC is the largest hybrid maize seed producer and distributor in Bangladesh; it produces 600-700 metric tons per year, an increasing trend. BRAC has produced hybrid maize seed since 1998 using parent material from the Pacific Seed Company. With increasing demand for hybrid maize seed, BRAC strengthened its maize research and development activities in 2000 and sought collaboration with national and international organizations. CIMMYT helped BRAC by providing maize genetic materials and technical training to agronomists. Most of the materials received were CIMMYT Maize Lines, as well as other advanced lines. Our vision is to increase farmers' yields and income by supplying them with superior maize hybrids. To achieve this, BRAC undertakes two kinds of activities: firstly, development of hybrids using elite inbred lines and secondly, implementation of international hybrid trials to identify better hybrids. Over the last few years we have implemented a number of international trials such as TAMNET trials and CIMMYT hybrid trials, both tropical and subtropical. Most involved yellow maize, with some white materials of normal and QPM hybrids. Some selected hybrids from those trials are now on the way to commercialization. Using our own germplasm collected from CIMMYT, a single cross hybrid, Uttaran, was released in 2005-2006. Other promising hybrid combinations are now in the pipeline.



## 96. Managing maize diseases through breeding for resistance in Malawi

Khonje, P.<sup>1</sup>, Ngwira, P.<sup>2</sup> and Vivek, B.<sup>3</sup>

<sup>1</sup>Chief Agricultural Research Scientist (Plant Pathologist/Breeder) and Maize Team Leader, Chitedze Research Station, P.O. Box 158, Lilongwe, Malawi.

E-mail: maizepathology@malawi.net

<sup>2</sup>Former Principal Maize Pathologist (Plant Pathologist/Breeder), Chitedze Research Station, P.O. Box 158, Lilongwe, Malawi.

<sup>3</sup>International Maize and Wheat Improvement Center (CIMMYT) Maize Breeder, P.O. Box MP 163, Mt. Pleasant, Harare, Zimbabwe.

Malawi relies on maize as a main food crop. Failure of the maize crop due to biotic and abiotic stresses spells disaster for the country. Managing maize diseases, such as gray leaf spot (*Cercospora zea-maydis*), *Turcicum* leaf blight (*Excerohilum turcicum*) and Maize Streak Virus, has become important for increased maize productivity. Incorporating genetic resistance into maize is a long lasting and sustainable solution to managing diseases. A study was initiated during the 1998/1999 cropping season to develop maize varieties with multiple disease resistance characteristics, while maintaining other preferred farmer traits. A total of 322 S<sub>4</sub> inbred and advanced lines, and 66 varieties from various sources were screened and evaluated against gray leaf spot, *Turcicum* leaf blight and Maize Streak Virus diseases. A total of 71 lines were identified as having multiple disease resistant genes. During the process, several hybrid varieties were developed and selected for their tolerance to the three major diseases of concern in Malawi. In November 2002, the Agricultural Technology Clearing Committee (ATCC) approved and released three varieties, i.e. one 3-way cross hybrid (CZR 8) and two double cross hybrids (CZR 3 and CZR 4), for use by farmers in Malawi. These are currently being multiplied, popularized and will soon be commercially available on the market. A further three new varieties, with similar characteristics as the first ones, are due for release from this Rockefeller funded project with collaboration from CIMMYT, during the 2005/2006 season.

## 97. Identification and characterization of maize varieties with beneficial traits for biobased industries

Kirkpatrick, K.M.<sup>1\*</sup>, Lamkey, K.R.<sup>1</sup>, Scott, M.P.<sup>1</sup>, Moore, K.J.<sup>1</sup>, Haney, L.J.<sup>1</sup>, Coors, J.G.<sup>2</sup>, Lorenz, A.J.<sup>2</sup>

<sup>1</sup>1301 Agronomy Hall, Iowa State University, Ames, IA 50011, USA

<sup>2</sup>Department of Agronomy, 1575 Linden Drive, University of Wisconsin-Madison, Madison, WI 53706, USA

\*Corresponding author e-mail: [kkirkpat@iastate.edu](mailto:kkirkpat@iastate.edu)

Corn stover is recognized as one of the most promising high volume, low cost lignocellulosic feedstocks on which to base a range of biobased industries for the next several decades. This study was conducted to determine the variation among a set of corn genotypes and to evaluate these genotypes for potential use in ethanol production. Fifty genotypes were evaluated for lignin, fiber, silica and biomass conversion properties in plot trials at two Iowa locations. Agronomic, as well as stover composition data, were collected for all plots. Near Infrared Reflectance (NIR) stover composition predictions were made at the National Renewable Energy Laboratory and used to predict ethanol potential (ethanol yield per stover mass). Ethanol yield per acre was calculated by multiplying ethanol potential by stover yield. A significant amount of variation was found among genotypes for stover yield. Stover yield appears to be related to maturity, being higher for later maturing hybrids. Stover yield averaged 2.6 dry tons/acre and ranged from 1.9 to 3.9 tons/acre. Ethanol potential ranged from 92-104 gallons/ton. Ethanol yield per acre ranged from 187 to 392 gallons/acre. The correlation between ethanol yield per acre and stover yield was 0.99. Therefore, selecting for stover yield should be an effective method for improving ethanol yield per acre.

## 98. Morphology-based grouping and heterotic pattern analysis in ten white Mindanao maize varieties

Magulama, E.E.<sup>1</sup>, Sillote, C.C. and Madriaga, W.Q.

<sup>1</sup>Dept. of Plant Breeding and Genetics, University of Southern Mindanao, Kabacan, Cotabato, Philippines

E-mail: emagulama@yahoo.com

This study aimed to (a) assess the genetic diversity of 10 white maize open pollinated varieties (b) evaluate the use of qualitative morphological traits in grouping and establishing heterotic patterns, (c) compare the efficiency of design II and diallel mating in identifying productive crosses, and (d) identify specific variety crosses as potential sources of inbred lines for heterosis breeding. Ten maize varieties from two sources (5 in each germplasm source, Central Mindanao University (CMU) and University of Southern Mindanao (USM)) were diallel crossed to form 45 variety crosses. The parents and crosses, plus a check variety, were evaluated for two growing seasons. Cluster and principal coordinate analyses, using 20 qualitative morphological traits, classified the 10 varieties into two major groups (5 varieties each cluster) according to the germplasm sources. Average genetic distance (GD) of the germplasm was 0.64. GD of breeding populations of USM and CMU sources were similar (0.56 and 0.57); intervarietal group crosses produced a higher GD (0.70). Factorial crosses based on grouping appeared more efficient (88%) than the usual diallel mating (49%) in finding productive crosses. Variety diallel analysis showed that variability in crosses was mainly due to heterosis effects. Four pair crosses with significant positive specific heterosis effects ( $s_{ij}$ ) were identified, with yield potentials of 6.23 to 6.53 t/ha. These were derived from intervarietal group crosses and could be used as parental sources in developing inbred lines for heterosis breeding. Morphology-based grouping can help in designing diallel or factorial crosses in order to establish consistent heterotic groups among maize germplasm.

## 99. Combining ability and identification of maize three-way cross hybrids adapted to the mid-altitude ecology of Uganda

Makumbi, D.<sup>1</sup>, Bigirwa, G.<sup>1</sup> and Diallo, A.O.<sup>2</sup>

<sup>1</sup>National Agricultural Research Organization (NARO), P.O. Box 7084, Kampala, Uganda

<sup>2</sup>International Maize and Wheat Improvement Center (CIMMYT), P.O. Box 1041, Nairobi, Kenya

Corresponding author e-mail: dmakumbi@neo.tamu.edu

Farmers in Uganda need high yielding hybrids to increase maize production and improve food security. This work aimed to: (i) identify three-way cross hybrids adapted to mid-altitude ecology; (ii) estimate combining abilities of new inbred lines; and (iii) classify inbred lines into potential heterotic groups based on grain yield. Seventy-four maize inbred lines were crossed to two single cross testers generating 148 three-way cross hybrids. The testcrosses, three commercial hybrids and a double cross hybrid were evaluated at three eastern African locations. Significant differences were detected among hybrids for grain yield at all locations. General (GCA) and specific (SCA) combining ability effects for grain yield were significant at all locations and across locations. Significant GCA x environment and SCA x environment interactions were observed for grain yield. The variability due to GCA and SCA accounted for 55% and 44% of variation among hybrids across locations, respectively, suggesting the importance of both additive and non-additive genetic effects in determining grain yield. The best hybrid yielded 8.07 Mg ha<sup>-1</sup> across locations. Inbred lines 5 and 73 had the highest significant GCA effect for grain yield across locations (3.88\*\* and 3.00\*\* Mg ha<sup>-1</sup>, respectively) and produced some of the superior hybrids. Based on SCA effects, 18 inbred lines were classified into two heterotic groups, A and B. Twenty hybrids yielding over 6.5 Mg ha<sup>-1</sup> will be advanced to national performance trials; outstanding hybrids will be recommended for release. Inbred lines showing good GCA will be used to predict three-way and double cross performance.

## 100. Breeding for resistance to Downy Mildew in quality protein maize in Mozambique

Mariote, D. <sup>1\*</sup>, Denic, M. <sup>1</sup>, Haag, W. <sup>2</sup>, Chauque, P. <sup>1</sup> and Fato, P. <sup>1</sup>

<sup>1</sup>-INIA-Instituto Nacional de Investigação Agronómica, C.P 3658, Av. FPLM, No 2696, Mavalane, Maputo, Mozambique

<sup>2</sup>-SG 2000- Sasakawa Global 2000, C.P. 4247, Maputo, Mozambique

\*Corresponding author e-mail: mariotedavid@hotmail.com

Maize is the staple food in most African countries. However, the poor quality of protein in normal maize is a serious problem causing malnutrition. Quality protein maize (QPM) can help alleviate human malnutrition, because it contains the opaque-2 mutation, which results in increased lysine and tryptophan concentrations and a higher biological value as a food than normal maize.

Diseases cause great losses in maize production. Downy mildew (DM) is one of the serious constraints to maize production in the southern and central parts of Mozambique. Therefore development of QPM germplasm with stable yield and resistance to major diseases has become an important objective. This might be achieved through: a) Using the Recurrent Selection method, to improve the three QPM populations created by the INIA Maize Program, and b) Determining grain yield potential and yield stability in DM-prone environments. This research started in 2003 using S<sub>2</sub> lines of Sussuma, FS families of [ZM 521/SW 8075 DMR//QSDMR]F<sub>3</sub> and Pop 62 SR C1 seed bulk. These materials were planted in nurseries and evaluated in Umbeluzi using the DM spreader rows method. The results of the first cycle of selection for DM resistance show that, in the case of Sussuma S<sub>2</sub> only 4.7 % of lines had strong to good resistance, but 81.6 % were susceptible to very susceptible to the disease. Susceptibility of Pop 62 SR bulk was 76.4% while the mean of [ZM 521/SW 8075DMR//QSRDMR]F<sub>3</sub> susceptibility was 49.9 %.

## 101. Farmer-participatory maize (*Zea mays* L.) cultivar evaluation and selection in Eastern Cape province of South Africa

Mashingaidze, K.

Breeding Section, Hendrik Schoeman Building, Agricultural Research Council Grain Crops Institute (ARC-GCI), P. Bag X 1251, Potchefstroom 2520, South Africa

E-mail: MashingaidzeK@arc.agric.za

Maize is the most important crop grown by smallholder farmers in South Africa. These farmers are resource-poor and struggle to buy hybrid seed. They mostly grow old open-pollinated varieties (OPVs) and recycled seed of unknown origin. To address this challenge, the ARC-GCI, in collaboration with CIMMYT-Zimbabwe and maize breeders in other SADC countries, is developing OPVs as an alternative to hybrids. Elite OPVs developed by both the ARC-GCI and CIMMYT-Zimbabwe are evaluated in farmer-participatory maize variety trials, in Mother-baby and VEVO (variety evaluation, verification and observation) trials. This enables farmers to evaluate them under their own management practices and make informed decisions about varieties suited to their conditions and preferences, and to quicken release and adoption. The trials also serve as training platforms for farmers to learn good agronomic practices (spacing, fertilization, weed control, stalk borer control, etc). Sixteen maize cultivars (twelve OPVs and four hybrids) were evaluated in Eastern Cape province (South Africa) during 2005/06 summer season. Ten mother trials were planted by lead farmers and were managed following the researcher's guidelines. Forty-seven baby trials (four varieties each) were planted by farmers near the mother trials. Each baby trial was managed in the same way as the farmer's crop. Farmers were consulted during field visits, information days, harvesting and processing. Farmers preferred OPVs to hybrids. Their major selection criteria were drought tolerance, cob size, high yield, grain hardness and grain size. Unwanted traits included small cobs, cob rot, poorly filled cobs, poor husk cover and low yield.

102. Collaboration in Eastern and Central Africa bears fruit: increasing the availability of enhanced maize germplasm.

Mduruma, Z.<sup>1</sup>, Twumasi-Afriyie, S., Napir, G., Demmisew, A. and Ombakho, G.

<sup>1</sup> Global Maize Program, International Maize and Wheat Improvement Center (CIMMYT), PO Box 5689, Addis Ababa, Ethiopia. E-mail: z.mduruma@cgiar.org

In 1997, a collaborative regional project in Eastern and Central Africa (ECA) was initiated to infuse and develop heterotically responsive highland maize germplasm. About 4000 S<sub>1</sub>-S<sub>3</sub> lines introduced from CIMMYT were screened for tolerance to *Exserohilum turcicum*, *Puccinia sorghi*, *Cercospora zea-maydis* and general adaptation to the highland ecology at the Ambo Research Center, Ethiopia (2,250masl). Heterotic groups of the selected elite lines were determined using three population testers, Kitale Syn 11, Ecuador 573 and Pool 9A. Five synthetic varieties were formed from lines with good general combining ability. Extensive evaluation of the synthetics and topcross hybrids on-station and on farmers' fields in Ethiopia resulted in the release of one synthetic (HORA) and one topcross hybrid (AMH800). The best four synthetics are now being evaluated in the highland ecologies of Tanzania, Burundi, Rwanda and Uganda for possible release. Single, 3-way and double-cross hybrids formed from elite lines with good specific combining ability were evaluated across countries in 2004-05 through the ECA Maize and Wheat Research Network. Several of the best performing hybrids are now available to breeders for final evaluation and possible release. This collaborative project has once again shown that region-wide germplasm development and testing in a range of environments helps to guarantee the robustness and sustainability of technology development. Useful germplasm and information products are shared among several countries, allowing the less advanced national research programs or private seed companies access to technologies they cannot develop themselves.

103. Twenty years of mass selection within the some degree fasciated Portuguese synthetic maize variety 'Fandango'

Moreira, P.M.<sup>1\*</sup>; Pego, S.<sup>2</sup>; Vaz Patto, C.<sup>3</sup> and Hallauer, A.R.<sup>4</sup>

<sup>1</sup>Escola Superior Agrária de Coimbra (ESAC), Departamento de Fitotecnia, Sector de Protecção Vegetal, Bencanta, 3040-316 Coimbra, Portugal.

\*Corresponding author e-mail: pmoreira@esac.pt

<sup>2</sup>Instituto Nacional de Investigação Agrária, Portugal. E-mail: pego@bragatel.pt

<sup>3</sup>Instituto de Tecnologia Química e Biológica, Universidade Nova de Lisboa, Portugal. E-mail: cpatto@itqb.unl.pt

<sup>4</sup>Maize breeder and Distinguished Professor in Agronomy, Iowa State University, 1505 Agronomy Hall, Ames, IA 50010, USA. E-mail: hallauer@iastate.edu

During 20 years of participatory plant breeding (PPB) at Sousa Valley, mass selection was used in 'Fandango' a maize open pollinated variety (OPV). To increase our knowledge of the genetic potential of this OPV, an evaluation of the yield gain and plant performance was conducted in Portugal (3 locations) and in the USA (4 locations). ANOVA comparison between cycles of selection and regression analyses on the rate of direct response to selection are presented.



## 104. Strategies for developing high yielding maize varieties for the dry mid-altitude ecology of Kenya

Muasya, W.N.P.<sup>1</sup>, and Diallo, A.O.<sup>2</sup>

<sup>1</sup> Kenya Agricultural Research Institute, Kiboko Sub-Center P.O Box 12, Makindu, Kenya

<sup>2</sup> International Maize and Wheat Improvement Center (CIMMYT ), P.O Box 25171, Nairobi, Kenya

Corresponding author e-mail: a.o.diallo@cgiar.org

Maize (*Zea mays* L.) is the most important staple crop in Kenya grown on about 1.6 million hectares. Improved open pollinated varieties (OPVs) occupy 11% of the area, most of which is in the dry mid-altitude ecology. Hybrids (conventional and non-conventional) occupy 74% of the area and the remaining 15% is planted with local land races. Low soil fertility and frequent drought are the main constraints to maize production in this area. Existing maize varieties are not very productive under moisture stress and low soil fertility. With increasing settlement in marginal areas, increased maize production will require better varieties, probably non-conventional hybrids like varietal hybrids, to meet the challenges of a growing population, declining soil fertility and land holding size. Heterosis as expressed in varietal hybrids has been responsible for much of the yield gains in maize. Varietal hybrids are more stress tolerant than OPVs and are suitable for stressed environments. Varietal hybrid seed is less expensive to produce. Furthermore, where farmers recycle seed from the previous season, the loss will not be drastic as this will be, in effect, an OPV. Therefore, availability of early stress varietal hybrids will enhance the farmers' ability to increase maize production in the dry mid-altitude ecology of Kenya. Seventy early varieties including 29 varietal hybrids, 30 open pollinated parents, six newly released OPVs and five checks were evaluated at 12 sites in Eastern Africa under stressed and unstressed conditions. Three of these hybrids have been nominated for National Performance Trials in Kenya.

## 105. Control of stem borers by Bt maize in confined field trials in Kenya

Mugo, S.<sup>1\*</sup>, Gichuki, S.T.<sup>2</sup>, Murenga, M.<sup>2</sup>, Taracha, C.<sup>2</sup>, Songa, J.<sup>2</sup>, Bergvinson, D.<sup>1</sup>, Hoisington, D.<sup>3</sup> and Pellegrineschi, A.<sup>4</sup>

<sup>1</sup>International Maize and Wheat Improvement Center (CIMMYT), PO Box 1041, 00621 Village Market, Nairobi, Kenya

<sup>2</sup>Kenya Agricultural Research Institute (KARI)

<sup>3</sup>International Crops Research Institute for Semi-Arid Tropics (ICRISAT)

<sup>4</sup>Pioneer Hi-Bred.

\*Corresponding author e-mail: s.mugo@cgiar.org

In Kenya, stem borers destroy an estimated 400,000 metric tons or 13.5% of farmers' annual harvest of maize costing over US\$72 million. Bt maize, developed using modified genes from the soil bacterium *Bacillus thuringiensis*, controls stem borers without harming humans, livestock or the environment, and is now sown to 90m ha globally. Our objective was to test nine public events of Bt maize in confined field trials (CFTs) for the control of four major Kenyan stem borer species. The Bt maize contained *cryIAb::ubi*, *cryIAb::act* and *cryIBa::ubi* genes. Leaf damage scores in the field showed that Bt maize effectively controlled the spotted stem borer (*Chilo partellus*) with mean scores of 1.2 compared to 2.7 for the non-Bt, CML216 control. Laboratory bioassays using leaves from the CFT showed that control was achieved for the sugarcane borer (*Eldana saccharina* Walker) and the pink stem borer (*Sesamia calamistis*), with mean larval mortality of 64% and 92%, respectively. However, complete control was not observed for the African stem borer (*Busseola fusca*) as the larval mortality rate was equal to that of the control. The tests showed that Bt maize will control three of the four major stem borers in Kenya. Backcrossing the lead events into adapted maize inbred lines is now underway to develop insect resistant Bt maize varieties for Kenya and other African countries.

106. Evaluation of maize (*Zea mays* L.) hybrids and open pollinated varieties for yield stability in Zimbabwe

Muongani, D.<sup>1</sup>, Mhike, X.<sup>1</sup>, Kwazira, K.<sup>2</sup>, Madamba, R.<sup>1</sup>

<sup>1</sup>Crop Breeding Institute, P. O. Box CY550, Causeway, Harare, Zimbabwe

<sup>2</sup>Crops Branch, P. O. Box CY550, Causeway, Harare, Zimbabwe

Corresponding author e-mail: deanmuungani@yahoo.com.uk

Seven hybrids and two open pollinated varieties of maize were evaluated for yield performance under two management levels: farmer managed and researcher managed, at 27 sites in different agro-ecological zones using the Mother/ Baby concept in 2003/04 and 2004/05. The design was an alpha lattice design replicated three times. The objective was to determine stability in yield performance of commercial hybrids and open pollinated varieties on-farm. Analysis of variance was done using ASREML and genotypes x environment interactions were analyzed using additive main effects and multiplicative interaction (AMMI) with principal component analysis using Biplot 1.1. Environment was found to play a major role in determining the grain yield across seasons and sites. Sites within agro-ecological zones showed contrasting mean yields across and within seasons. Varieties differed in their performance across sites and seasons. Hybrids PHB30G97 and PHB30R73 had positive deviations from the origin indicating that they were high yielding across environments. Genotypes CZH01021, SC513 and AC31 were close to the origin indicating stable performance across sites. It is therefore recommended that evaluation and selection of maize cultivars should be done in the targeted environments.

## 107. Effects of low nitrogen and drought on grain yield and endosperm hardness of quality protein maize single cross hybrids

Ngaboyisonga, C.<sup>1</sup>, Njoroge, K.<sup>1</sup>, Kirubi, D.<sup>2</sup> and Githiri, S.M.<sup>1</sup>

<sup>1</sup>University of Nairobi, Faculty of Agriculture, Department of Plant Science and Crop Protection, P.O. Box 29053-00625 Nairobi, Kenya

<sup>2</sup>CIMMYT-Kenya, P.O. Box 25171 Nairobi, Kenya

Corresponding author e-mail: cngaboyisonga@hotmail.com, c\_ngaboyisonga@yahoo.com

QPM (Quality Protein Maize) is *opaque-2* maize in which the soft and opaque endosperm has been converted into a hard and translucent type by genetic modifiers, which suppress several pleiotropic effects of the mutant. To study how grain-yield and endosperm hardness of QPM single cross hybrids and the combining abilities of the lines are affected by low nitrogen and drought, 30 single cross hybrids including reciprocals were generated from six inbred lines in a 6 x 6 diallel. The hybrids were then evaluated in three environments: low nitrogen, drought and optimal environment at Kiboko in Kenya and in an optimal environment at Rubona in Rwanda, during the season March-August 2005. Compared to the optimal conditions, low nitrogen reduced grain yield by 57% and drought by 48%. Drought adversely shifted endosperm hardness from a suitable hard and vitreous endosperm under the optimal environment to an unsuitable soft and opaque endosperm. General combining ability (GCA) and specific combining ability (SCA) effects were highly significant for both grain yield and endosperm hardness across environments while reciprocal effects were not significant. Moreover, GCA x Environment and SCA x Environment interactions were highly significant for yield only, whereas Reciprocal Effects x Environment interactions were not significant. Although low nitrogen and drought affect endosperm hardness and grain-yield of QPM, it may be possible to identify QPM cultivars that are less sensitive to these stresses, as some QPM single cross hybrids exhibited heterosis and were less affected by the two environmental constraints.

## 108. Implications of genotype-by-environment interactions in maize (*Zea mays L.*) variety selection using mother and baby trials

Nginamau, D.<sup>1</sup>, Mwala, M.S.<sup>2</sup> and Bänziger, M.<sup>3</sup>

<sup>1</sup>Maize Breeder, Instituto de Investigação Agronómica P.O. Box 2104, Luanda, Angola

E-mail: dibangina@yahoo.fr or dnginamau@yahoo.com

<sup>2</sup>Senior Lecturer, Crop Science Department, University of Zambia, P.O. Box 32379, Lusaka, Zambia

<sup>3</sup>Director, African Livelihoods Program, CIMMYT, P.O. Box 25171, Nairobi, Kenya

Maize cultivar development in most plant breeding programs in the SADC region has used managed stress environments, while conditions in farmers' fields are characterized by random stress. This raises the question: what are the most appropriate selection environments when breeding for such target environments? National Agricultural Research Systems have collaborated with CIMMYT in developing appropriate maize cultivars for farmers' conditions through Mother and Baby Trials (MBTs). Maize varieties are tested in environments where they will be deployed, addressing the concerns about genotype x environment (GxE) interactions. Data from trials in Zimbabwe between 2000 and 2004 were available. This study aimed to characterize environments on the basis of tested maize genotypes and identify repeatable GxE interactions across years, as well as provide clues on improving the strategy in terms of testing environments. Sequential retrospective pattern analysis was applied to data from 33 environments with 40 maize genotypes, including hybrids and open pollinated varieties (OPVs). The environments were classified into four groups based on their similarities. Differences among the clusters were mainly due to soil water holding capacity, evapotranspiration and soil depth. Sixteen environments representing eight locations were identified as critical in evaluating maize in Zimbabwe. Cultivars were grouped into four clusters with variety type and development method underpinning the differences among the groups. OPVs developed for stress conditions (ZM421, ZM521 and ZM523) were in the same cluster. Varying soil nitrogen in the MBTs was effective for introducing environments representative of farmers' growing conditions and enabled discrimination of genotypes for target environments.

109. 'Valluno', an open pollinated maize variety for the Cruceño valleys of Bolivia

Orquera, E. and Paz, P.

Centro de Investigación Agrícola Tropical (CIAT), Casilla 247, Santa Cruz de la Sierra, Bolivia

E-mail: [ppaz@ciatbo.org](mailto:ppaz@ciatbo.org)

CIAT (the Bolivian Agricultural Research Center) has released 15 white and yellow, flint and semi-dent open pollinated maize varieties (OPVs) adapted to altitudes from 300 to 1800 masl. All the released OPVs have a CIMMYT (International Maize and Wheat Improvement Center) background. After testing CIMMYT materials, chosen OPVs pass through a selection and improvement process before release. The most important OPVs in farmers' hands are Cubano Amarillo, Suwan Saavedra, Chiriguano-36, Mairana-45, Kaipepe-18, Chiquitano-28 and Valluno. Valluno was selected from a cross between Suwan Saavedra and Mairana-45. The background of Suwan Saavedra is from Thailand and that of Mairana-45 is from CIMMYT Population 45. The main characteristics of Valluno are high average grain yield (5 t/ha on farmers' fields), 2.20 m plant height, 1.10 m ear height, 60 days to female flowering, flint to semi-flint grain texture and yellow-reddish color. Valluno has shown good tolerance to drought.

110. Reaction of maize germplasm to *Stenocarpella macrospora* (Earle) infection and effect of resistance to disease development

Pascual, C.B.<sup>1</sup>, Guzman, P.S.<sup>2</sup> and Salazar, A.M.<sup>1,3</sup>

<sup>1</sup>University Researcher, Institute of Plant Breeding, University of the Philippines Los Baños (UPLB), Philippines

<sup>2</sup>Formerly Associate Professor, Agronomy Department, UPLB, now at Monsanto, USA and Research Professor at UPLB

<sup>3</sup>Team Leader, Corn RDE Network, Department of Agriculture, Philippines

Corresponding author e-mail: cbpascual22@yahoo.com

Source of resistance to important diseases is an integral component of breeding for high yield and stability. Resistant germplasm is also the most effective and environmentally safe measure to manage plant diseases. In some cases, the use of genotypes with a moderate level of resistance can be integrated with other control measures to provide sufficient disease control. The objectives of this study were to identify sources of resistance to maize leaf blight and ear rot caused by *Stenocarpella macrospora* and to determine the effect of different levels of resistance to disease development. In 2002, out of more than 300 maize accessions evaluated using artificial inoculations for leaf blight and ear rot, six inbreds were found to be resistant to leaf blight and 12 to ear rot (including the six leaf blight resistant lines). To accurately determine the degree of host plant resistance, the resistant inbreds were evaluated for disease reaction continuously for three years. During seasons of frequent rains and cold weather, they became moderately susceptible, except CML 425 which showed relatively stable resistance to leaf blight and ear rot. Results of the study on leaf blight progress of 12 corn inbreds with varying levels of resistance to the disease showed that CML 425 gave the lowest lesion size, 17.58 mm<sup>2</sup> at 15 days after inoculation (DAI) and lowest Area Under Disease Progress Curve (AUDPC) value of 19.84 while AMATLCOHS 115 exhibited the biggest lesion (159.86 mm<sup>2</sup> DAI), highest AUDPC value (204.61) and more susceptible reaction than the susceptible control.

## 111. Development of multiple disease resistant maize populations and inbreds

Pascual, C.B.<sup>1</sup>, Salazar, A.M.<sup>1,3</sup> and Guzman, P.S.<sup>2</sup>

<sup>1</sup>University Researcher, Institute of Plant Breeding, University of the Philippines Los Baños (UPLB), Philippines

<sup>2</sup>Formerly Associate Professor, Agronomy Department, UPLB, now at Monsanto, USA and Research Professor at UPLB

<sup>3</sup>Team Leader, Corn RDE Network, Department of Agriculture, Philippines

Corresponding author e-mail: cbpascual22@yahoo.com

A continuing search for new and more effective genes for resistance to important maize pathogens and transfer of these to breeding populations are vital components of a serious and futuristic breeding program. The objectives of this study were to find sources of resistance to downy mildew, banded leaf and sheath blight and bacterial stalk rot in the available breeding materials and germplasm, and to develop special source populations and inbreds with multiple resistance to these diseases. A total of 735 lines (S3 to S6) and 75 foreign accessions were evaluated for resistance to *Peronosclerospora philippinensis* by spreader row technique during seedling stage. The surviving plants were inoculated with virulent *Rhizoctonia solani* AG1-IA isolate at mid vegetative stage and by *Pectobacterium chrysanthemi* pv *zear* at tasseling. After evaluation for resistance to the different pathogens, selected plants with resistance to one or more diseases were subsequently selfed and advanced for the next generation. They were crossed in a factorial manner and random-mated twice. Twenty double crosses resistant to at least two diseases were recombined. One inbred, Nei 9008 showed resistant reaction to both downy mildew and bacterial stalk rot and has moderate resistance to banded leaf and sheath blight. Another inbred, Tupi 56-3-B, exhibited moderate resistance to the three diseases but was also found to have high starch content. It is currently one of the important components in breeding for high starch in the Institute.



## 112. Superior quality protein maize (QPM) hybrids for different mega-environments in Mexico using the Biplot methodology

Preciado-Ortiz, R.<sup>1\*</sup>, Guerrero, R.<sup>2</sup>, Ortega, A.<sup>1</sup>, Terrón, A.<sup>1</sup>, Crossa, F.<sup>3</sup>, Córdova, H.<sup>3</sup>, Reyes, C.<sup>1</sup>, Aguilar, G.<sup>1</sup>, Tut, C.<sup>1</sup>, Gómez, N.<sup>1</sup> and Cervantes, E.<sup>1</sup>

<sup>1</sup> Maize Breeders of the National Institute of Forestry, Livestock and Agricultural Research, (INIFAP) from different regions of Mexico

<sup>2</sup> Maize research fellow at INIFAP Bajío experiment station

<sup>3</sup> International Maize and Wheat Improvement Center (CIMMYT) Biometrics and Maize staff, Apdo. Postal 6-641, 06600 Mexico D.F., Mexico.

\*Corresponding author e-mail: [repreciado@yahoo.com](mailto:repreciado@yahoo.com)

Because of their higher lysine and tryptophan content, QPM hybrids, are options to improve nutrition of monogastric organisms. In developing countries where maize is a staple food, this is a very important issue. To contribute towards this effort, CIMMYT and INIFAP working together, developed, identified and promoted QPM hybrids in different regions of Mexico. Perhaps the main objective in any breeding project is to develop hybrids that respond well in different environments, this goal requires multiple year-locations trials. The utilization of site regression models (SREG) on multilocation testing allows the detection of significant differences in the genotype x environment interaction, even though these may not be detected by the analysis of variance (ANOVA). Results can be graphically displayed using the Biplot technique, revealing the additive effects on genotypes and genotype x environment interaction across years. A total of 66 uniform field trials conducted by INIFAP's maize breeders in tropical and subtropical environments were grouped in five sets of experiments. The objectives of this work were to identify mega-environments, superior hybrids for each environment and mega-environment, stable hybrids with good performance across environments, and the most suitable environments for evaluation as well. An individual SREG analysis for each set of experiments and their combined analysis were conducted to assist in the graphic representation by the Biplot methodology. Results revealed that the constructed Biplots, graphically allowed the identification of superior hybrids, and the proper environments to conduct hybrid evaluation trials; however, it was not a reliable option for grouping test-sites in mega-environments.

### 113. General and specific combining ability for phosphorus deficiency in acid soil maize inbreds

Salazar, F.<sup>1</sup>, Narro, L.<sup>1</sup> and Alirio Vallejo, F.<sup>2</sup>

<sup>1</sup>International Maize and Wheat Improvement Center (CIMMYT), Colombia, CIMMYT/CIAT, Km 17 recta Cali Palmira. AA 6713.

<sup>2</sup>Universidad Nacional de Colombia, Sede Palmira, Colombia.

Corresponding author e-mail: f.salazar@cgiar.org

High aluminum (Al) and low phosphorus (P) are important limiting factors for maize production in 917 million hectares of tropical acid soils available in South America. The objective of this work was to study the inheritance of P using maize inbreds tolerant to acid soils. Twelve parents with contrasting responses to P absorption and utilization were chosen. A complete diallel was formed; parents and crosses were evaluated on two acid soil locations with 55% Al saturation and two levels of P (low = 4 ppm and high = 15 ppm). The experimental design was an  $\alpha$  lattice with 3 replications. Genetic analysis was performed as proposed by Hallauer and Miranda. Highly significant differences for grain yield were found for parents, crosses, and parents vs. crosses both on low and high P levels. Parents vs. crosses sum of squares (SS) were 58% and 66% of genotypes SS meaning that heterosis was important in both P levels. General combining ability (GCA) and specific combining ability (SCA) were highly significant on low and high P levels. SCA SS was 3 fold the GCA SS, meaning that non additive gene effects for grain yield in P deficient soils are more important than additive gene effects.

## 114. Inbreeding depression before and after full-sib recurrent selection in tropical maize

San Vicente, F. and Garcia, P.

Maize Program, Instituto Nacional de Investigaciones Agrícolas (INIA), Zona Universitaria Via El Limon Edif. 8, 06600 Maracay, San Vicente, Venezuela

E-mail: fsanvicente@inia.gob.ve

Full-sib recurrent selection (FSRS) was conducted in six tropical maize populations (Suwan-1, Foremaiz-2, La Maquina, Compuesto Thai-1, Tuxpeño RC and Agua Blanca). The original populations (Co), their improved cycles (Cn), and the S1 generation of both original and improved populations were evaluated in five locations in Venezuela. Recurrent selection, if conducted properly, should result in an increase in the frequency of favorable alleles with a subsequent reduction in inbreeding depression. The objective of the study was to estimate inbreeding depression in the populations, before and after FSRS. Grain yield (GY), plant height (PH), ear height (EH), and days to silk (FF) were the traits used to estimate inbreeding depression. Inbreeding resulted in a significant reduction in GY, PH and EH and a significant increase in FF, in both original and improved populations. For GY and PH, inbreeding depression was significantly higher for the improved than for the original populations; whereas for EH and FF inbreeding depression rate and percentage were similar in both populations (Cn and Co). Results suggest that for GY and PH dominance effects were more favored than for EH and FF. In general, Foremaiz-2 and La Máquina populations showed the highest inbreeding depression, while Agua Blanca showed the lowest. This suggests a greater accumulation of favorable alleles in the Agua Blanca population due to selection.

## 115. Biplot analysis of early to medium maturing open pollinated maize varieties in southern Africa

Setimela, P.<sup>1</sup>, Vivek, B.<sup>1</sup>, Bänziger, M.<sup>1</sup> and Crossa, J.<sup>2</sup>

<sup>1</sup>Maize Program, International Maize and Wheat Improvement Center (CIMMYT), PO Box MP 163, Harare, Zimbabwe

<sup>2</sup>CIMMYT, Apdo. Postal 6-641, 06600 Mexico D.F., Mexico

Corresponding author e-mail: [psetimela@cgiar.org](mailto:psetimela@cgiar.org)

Analysis of multi-environment trials (METs) of maize genotypes (G) and genotype by environment (GE) interactions for yield performance across environments, and selection of the best genotypes is an important routine in maize breeding. Analysis and interpretation of METs have been limited to analysis of variance and mean comparison among genotypes. This type of analysis has not been effective in exploiting GE interaction encountered in METs data. The objective of this study was to exploit analysis of G plus GE interaction (GGE), its magnitude and significance using biplot analysis methodology, which graphically displays the relationship among environments, genotypes and GE interactions. Grain yield data of 20 early to medium maturing open pollinated maize varieties (OPVs) from five seasons (1999 - 2003) and 55 locations in southern Africa were analyzed. Those OPVs that were evaluated for only one season and the locations that were used as testing sites for only one season were discarded from final the analysis. Through GGE biplots, the results showed the ideal test environments that discriminate well performing genotypes from poor ones, the performance of each genotype in specific environments, the grouping of similar environments or mega-environments, and stable genotypes relative to the environments.

## 116. Diallel analysis of intermediate to late Nepalese maize inbred lines for grain yield

Sharma, D.<sup>1</sup> and Adhikari, K.<sup>2</sup>

<sup>1</sup>Senior Scientist, National Maize Research Program, Rampur, Nepal

E-mail: surath@mos.com.np

<sup>2</sup>National Maize Coordinator, National Maize Research Program, Rampur, Nepal

Maize is the major crop for food and animal feed in Nepal. It is grown in summer in the hills and both summer and winter in the terai and inner-terai of Nepal. Open pollinated varieties (OPVs) are commonly grown and national average yield is low (1.9 t/ha). There is high potential for hybrid maize production in the winter season in terai and inner-terai. A half diallel cross among eight Nepalese intermediate to late maize inbred lines was made at the National Maize Research Program (NMRP) Rampur during the summer season of 2004. The 28  $f_1$ s were evaluated at Rampur and Parwanipur during the winter season of 2005. The objective was to study general (GCA) and specific (SCA) combining ability of those lines and use the information in the development of hybrids and synthetics in Nepal. The diallel progenies ( $f_1$ s) were evaluated in an RCB design with two replications in two locations. The data were analyzed using Gardner and Eberhart's 1966 (Analysis III) model. The result revealed that location MS and hybrid MS were highly significant for grain yield. The hybrid MS was partitioned into GCA and SCA. The GCA effect for grain yield was significant at  $p < 0.05$  significance level, whereas SCA was non-significant. The lines RL-30, RL-35, and RML-8 manifested the highest additive effects confirming them as better general combiners. There was no significant interaction between hybrids and locations for grain yield.

## 117. Combining ability of CIMMYT maize lines with two Indonesian tester parents

Takdir M., A., Iriany M., R.N., Isnaeni, M., Mejaya, M.M. and Dahlan, M.  
Indonesian Cereal Research Institute (ICERI), Jl. Dr. Ratulangi No. 274, Maros 90514  
South Sulawesi, Indonesia.  
E-mails: balitsereal@plasa.com; balitser@yahoo.com; atakdir@plasa.com.

The critical phase in line evaluation for combining ability is choosing the tester parents. If the heterotic patterns of the lines or base populations are known, tester selection is not difficult. The objective of this study was to select CIMMYT lines which had good combining ability with Indonesian lines Mr-4 and Mr-14. A total of 53 lines were crossed with Mr-4 and Mr-14 at Maros, South Sulawesi, Indonesia, early in the dry season of 2003. Testcrosses of each tester and three varietal checks (Semar-10, Bima-1 and Bisi-2) were evaluated in Bontonompo, South Sulawesi and Muneng, East Java using an 8 x 7 alpha lattice with two replicates. Data were analyzed using a covariance factorial randomized block design. The results of the experiment indicated significant interactions between line by tester, testcross by location, and line by tester by location. Thirteen and 20 lines showed good combining ability with Mr-4 and Mr-14, respectively, suggesting these two lines (Mr4 and Mr14) were considered particularly good combiners. The testcrosses developed from these two lines were significantly higher in grain yield than Bisi-2 at two locations namely Bontonompo and Muneng. Four testcrosses showed significantly higher yield than Semar-10 at each location.

## 118. Hybrid maize adaptations at several locations in Indonesia

Takdir M., A., Iriany M., R.N., Mejaya, M.J. and Dahlan, M.M.

Indonesian Cereal Research Institute (ICERI), Jl. Dr. Ratulangi No. 274, Maros 90514  
South Sulawesi, Indonesia.

E-mails: balitsereal@plasa.com; balitser@yahoo.com; atakdir@plasa.com

The interaction between genotype and environment is important for the process of selection in a breeding program. The genotype by environment interaction provides information about how the response of a genotype changes according to the environment. The interaction phenomenon can be used to support the development of varieties adapted to specific conditions or to a broad conditions. The objective of this research was to select hybrids expected to have good adaptation to one particular location or a wide range locations. Fourteen hybrids and two varietal checks (Bima 1 and Bisi 2) were evaluated in Perigi (West Nusa Tenggara), Malang and Muneng (East Java), Blora (Central Java), Bajeng and Lanrang (South Sulawesi), Tenilo (Gorontalo), Metro and Natar (Lampung) during the dry season, between August and December 2004. The experiment used a 4 x 4 alpha lattice design with four replications, two rows per genotype (5 m long), and a planting distance 0.75 m x 0.20 m. The results indicated that B11-209/Mr14, Nei92008/ Mr14, G180/Mr14, B11-157/ Mr14, CML431/ Mr14, G193/ Mr14, B11-136/ Mr14, and B11-126/ Mr14 have a 2-19 % higher average yield potential in nine tested locations, compared to Bima 1 and Bisi 2.

## 119. Establishment of heterotic patterns of maize (*Zea mays* L.) inbred lines with tolerance to acid soils

The, C.<sup>1\*</sup>, Mafouasson, A.<sup>1</sup>, Calba, H.<sup>2</sup>, Menkir, A.<sup>3</sup> and Horst, J.W.<sup>4</sup>

<sup>1</sup>Institute of Agricultural Research for Development (IRAD), P.O. Box 2067, Yaoundé, Cameroon. \*Corresponding author e-mail: charlesthe@hotmail.com

<sup>2</sup>CIRAD CA/01, Avenue d'Agropolis, 34398 Montpellier, France. E-mail: henri-calba@cirad.fr

<sup>3</sup>IITA, Oyo Road, PMB 5320 Ibadan, Nigeria. E-mail: a.menkir@cigiar.org

<sup>4</sup>University of Hannover, Hassenhaeuser Str. 2D 30419 Hannover, Germany.

Maize is grown on eight million hectares of acidic soils in tropical Africa. Knowledge of the heterotic pattern of acid soil tolerant inbred lines can facilitate development of tolerant hybrids. Nineteen tropical inbred lines were crossed to 2 testers representing the Tuxpeño and ETO heterotic patterns. The resulting 38 testcrosses were evaluated at Ebolowa (Aluminium toxicity) and Nkolbisson (Manganese toxicity) in Cameroon for two years. Two blocks were planted at each site: one on native acid soil, and another corrected with 2 tons ha<sup>-1</sup> of dolomitic lime and 4 tons ha<sup>-1</sup> of poultry manure. Results showed significant reduction in grain yield; inhibition of seminal root elongation; longer period from planting to silking, and anthesis-silking interval. Differences among hybrids were significant ( $p < 0.01$ ) for all parameters except grain yield at Ebolowa. Effects due to testers and line x tester interaction were highly significant on acid soils and corrected soils. Grain yield under Aluminium toxicity was predominantly (76%) influenced by non-additive gene action; seminal root length was predominantly (65%) influenced by additive gene action. Under Manganese toxicity, yield was mainly controlled by additive gene action (69%) and seminal root length by additive and non-additive gene action. Seminal root length was effective in predicting genotypes' performances on Aluminium soil, but not Manganese soil. Different mechanisms were involved in conditioning tolerance to the two soil types. Two heterotic pools were formed for each acid soil type, following the Tuxpeño/ETO heterotic patterns on Aluminium toxic soil, but with no known pattern on Manganese toxic soil.



## 120. Use of heterotic classification of inbred maize lines to develop hybrids for the highlands of Eastern and Central Africa

Twumasi-Afriyie, S., Nepir, G. and Mduruma, Z.

Global Maize Program, International Maize and Wheat Improvement Center (CIMMYT), P.O. Box 5689, Addis Ababa, Ethiopia. E-mail: s.twumasi@cgiar.org

The highlands of eastern Africa have a high potential for agricultural production because of the generally long rainfall duration and suitable soils. However, constraints to improving maize productivity in the zone include low yield potential due to the ever-narrowing genetic base of germplasm deployed since the 1980s. The biotic constraints include *Exerohilium turcicum*, *Puccinia sorghi*, lodging and stalk borers. In 1998, CIMMYT commenced a project in collaboration with scientists in the region to enhance the maize germplasm in the zone. A regional maize nursery was established at Ambo, Ethiopia (2250masl). The source germplasm included about 4000 S<sub>1</sub>-S<sub>3</sub> white-grained, mid-altitude inbred lines from CIMMYT-Zimbabwe. Adapted S<sub>2</sub>-S<sub>4</sub> lines were topcrossed to three broad-based population testers: Kitale Syn II and Ecuador 573, belonging to the two well-known heterotic groups in the region, and CIMMYT Pool 9A. The topcrosses were evaluated at highland sites in six participating countries between 1999 and 2001. While general combining ability (GCA) performance was used to develop synthetics, specific combining ability (SCA) responses were used to classify the lines into three heterotic groups. To test the effectiveness of the heterotic classifications, single-cross hybrids were formed from heterotic pairs and evaluated in the region. The lines largely fell into two distinct groups (Kitale and Ecuador) as well as a third group, which belonged to Pool 9A but had heterotic affiliations with either Kitale or Ecuador. Performance of the hybrids showed that the heterotic classifications were effective and could form the basis for developing hybrids for the African highlands.

121. Inheritance of resistance to *Cercospora* spp. complex in tropical maize (*Zea mays*) inbred lines

Vanegas Angarita, H.<sup>1</sup>, De León, C.<sup>2</sup> and Narro León, L.<sup>3</sup>

<sup>1</sup>FENALCE (Colombia), Unidad de Investigación, Regional Valle, CI 35 No. 25-57 Palmira, Colombia. Corresponding author e-mail: vanegashe@uniweb.net.co

<sup>2</sup>Colegio de Postgraduados, Campus Montecillo, México. E-mail: cdeleon@colpos.mx

<sup>3</sup>International Maize and Wheat Improvement Center/ International Center for Tropical Agriculture (CIMMYT/CIAT), Apartado Aéreo 6713 Cali, Colombia. E-mail: l.narro@cgiar.org

Inheritance of resistance to the fungi *Cercospora* spp., causal agents of gray leaf spot in tropical maize, has not been previously reported. Inheritance of resistance was studied by generating and evaluating a diallel mating 1 model (Griffing model I), using ten maize inbred lines with contrasting levels of disease reaction. Parental lines and their crosses, both direct and reciprocal, were evaluated in three environments using conservation tillage and artificial inoculation using gray leaf spot-infected leaves from farmers' fields. Analysis of variance for the variable disease index (scale, 1: resistant; 5: highly susceptible) was performed as suggested by Hallauer and Miranda (1988). In the combined analysis, highly significant differences were found for parents, crosses (direct), general combining ability (GCA) and specific combining ability (SCA); no significant differences were found for parent vs. crosses or direct vs. reciprocal crosses. Consequently, heterosis was not important in the *Cercospora* index (mean for parents was 2.97 and for crosses, 3.03). No maternal effects were observed for this set of lines (mean for both direct and reciprocal crosses was 3.03). GCA sum of squares (SS) was three times the SCA SS, meaning additive gene effects were more important than non-additive effects. No parent x location interaction was observed, allowing identification of the most tolerant and most susceptible parents for the generation mean analysis, the next phase of our study. Interaction of location with crosses, GCA and SCA were highly significant; however, the different performance of crosses across locations does not change the results.

122. Performance of variety cross hybrids of maize (*Zea mays* L.) in the mid-altitude and highland transition areas of Ethiopia

Worku, M., Abera, W., Tadesse, B., Wolde, L. and Wegary, D.

Maize Breeders, National Maize Research Project, Bako Agricultural Research Center, P.O. Box 03, Bako, West Shoa, Oromia, Ethiopia

E-mail: mosisaw@yahoo.com

Improved open-pollinated varieties (OPVs) have been developed and released for commercial production in maize growing areas of Ethiopia. However, the dissemination of these improved varieties is limited because of low interest from seed producers in the production and marketing of OPV seed. The dissemination of broad-based improved varieties can be increased by development and release of adapted commercial, high yielding variety cross hybrids. This study was conducted in 2002 at seven locations in the mid-altitude (1000 – 1800 meters above sea level, masl) and highland transition areas (1800 – 2000 masl) of Ethiopia to evaluate the performance of variety cross hybrids. Twenty-nine variety cross hybrids and nine parental OPVs/populations with another two checks were tested in a randomized complete block design with three replications at each location. Analysis of variance revealed a significant difference ( $P < 0.01$ ) among the entries. The mean grain yield ranged from 3.9 to 8.3 t ha<sup>-1</sup>. Some variety cross hybrids had better performance than the improved OPVs. Kuleni (Pool-9A) x Abo-Bako outyielded the high parent (Kuleni) by 29.7% and Gibe-1 x Kuleni outyielded the best OPV and high parent (Gibe-1) by 14.7%. Gibe-1 x Kuleni also had more stable performance across the testing locations than the parental OPVs. This implied that moving from OPVs to variety cross hybrids, particularly under small scale farmers' conditions, will increase the productivity of maize. The cheap seed price for variety cross hybrids, as compared to conventional hybrids, will be another advantage for resource poor farmers.

---

## Cultivar development methodologies – wheat

---

123. Doubled-haploid studies in elite Egyptian bread wheat (*Triticum aestivum* L.) cultivars

Ahmed, K.Z., Allam, H.Z., Moussa, A.M.<sup>1</sup> and Ali, M.S.A.

Department of Genetics, Faculty of Agriculture, Minia University, El-Minia, ET- 61517, Egypt

<sup>1</sup> Sids Res. Station, Field Crops Res. Inst., Agric. Res. Center, Sids, Bani Suwayf, Egypt

Corresponding author e-mail: ahmed.kz@link.net

This study screened 13 elite Egyptian wheat (*Triticum aestivum* L.) cultivars for anther culture ability. Five agar-solidified media were used. Greatly differing frequencies of calli and green plants were obtained from different cultivars and media. The callus initiation frequency varied from 0.3% to 18.9%. Modified P-4S medium containing 1.5 mg/l 2,4-D, 0.5 mg/l Kinetin and 0.26M sucrose, was most effective. Regeneration frequency varied from zero to 139.9% on the 190-2 medium. The green plant percentage varied from 18.2% to 86.3%. A highly significant genotype x medium interaction was observed on all traits. Mitotic investigations of primary calli revealed considerable variation in chromosome number (7 to >42), and the haploid chromosome number 21 was the most frequent. The genotype, as well as the type of anther culture medium, had a profound effect on chromosomal variation. With long-term subculturing of anther calli, haploid cells decreased from 64.4% to 30.6%, and regeneration ability also decreased. Cytological analysis of anther-derived plants revealed that 79% of the regenerated green plants were haploid. They were treated with colchicine for chromosome doubling, and 53.5% survived the treatment. Genetic differences appear to affect the sensitivity to colchicine, which is why the treated plants varied in their ability to withstand the treatment, to diploidize, and/or to be fertile. The viability of the pollen grains of mature plants ranged from 41.3% to 95.9%. Plants with low pollen viability (below 54%) were completely sterile. Plants with spontaneous chromosome doubling had higher pollen viability and fertility, compared to the colchicine-treated plants.

## 124. Results and prospects of breeding wheat in the South of Russia

Bespalova, L.A.

Wheat Breeding Department, Krasnodar Lukyanenko Research Institute of Agriculture, 350012  
KNIISH, Krasnodar, Russia

E-mail: bespalova\_l\_a@rambler.ru

Significant progress has been achieved in breeding winter wheat. Introgression of plant height reducing genes Rht8, Rht9 (Bezostaya 1, Rannaya 12, Bezostaya 2) and more recently Rht1 (Yuna, Ofelia, Nika Kubani, Nota) and Rht11 from Krasnodarskij karlik 1 (Polukarlikovaya 49, Spartanka, Skifyanka, Pobeda 50, PalPich) has caused the redistribution of a greater part of the biomass into the grain, improving the crop's yield and processing properties. Introduction of 1B/1R translocation into Krasnodarskaya 39 through Saratovskaya 3 has led to an increase in drought resistance and frost-hardiness. Use of 1B/1R translocation from Neuzucht (Kavkaz, Avrora) and more recently B/R translocation through a "triticale bridge" (Polovchanka, Knyazhna, Krasota) has increased overall biomass of the plant and its grain yield. The combination, in one genotype, of B/R translocation and dwarfing genes Rht8+Rht11 in the course of the breeding process has allowed yield potential to be increased to more than 12 t ha<sup>-1</sup> (Tanya) with a harvest index of 45-48%. Potential yield of overall biomass reached 26 t ha<sup>-1</sup>. For further increase of biomass yield, legula-free (lg) wheats with a reduced leaf (RL) are of great interest. Crosses with the plants of this morphological type produce transgressive genotypes. Introgression of semi-lethal genes for hybrid dwarfness might help to improve the economic properties of the plant. Targeted use of amphidiploids as genetic bridges in breeding for disease resistance has allowed introgression of genes for resistance to leaf, yellow and stem rusts, powdery mildew and Hessian fly.

## 125. Alleviating rural poverty through participatory wheat varietal selection

Bhatta, M.R.<sup>1\*</sup>, Ortiz Ferrara, G., Sharma, R.C.<sup>2</sup>

<sup>1</sup> National Wheat Research Program, Bhairahawa, NARC, Nepal

<sup>2</sup> International Maize and Wheat Improvement Center (CIMMYT), Apdo. Postal 6-641, 06600 Mexico D.F., Mexico

\*Corresponding author e-mail: nwrp@nec.com.np

Millions of resource poor farmers in Nepal derive their livelihoods from wheat cultivation. Participatory variety selection (PVS) offers an opportunity to identify and deploy farmer preferred wheat varieties, with rapid adoption of preferred cultivars. Two villages, Semarahana and Mahilbar in the Rupandehi district of western Nepal were selected for wheat PVS activities from 2003 to 2005. The major constraints to wheat production were low seed replacement, slow variety dissemination, and the use of farmers' poor quality, homegrown seed. Fourteen wheat genotypes, including two checks, were evaluated through farmer managed participatory research over a 3-year period, to identify farmers' preferred varieties, speed up varietal adoption, increase varietal diversity and grain yield, and enhance food security in the area. The mother-baby system of varietal evaluation was adopted. Each year, four mother trials per village, consisting of 6 to 8 genotypes, were planted using farmers' inputs and management practices. Each genotype was replicated in five farmers' fields as a baby set for comparison with the farmers' local variety. Farmers, researchers and extension workers jointly evaluated the trials. Seed of the farmer-selected variety was produced and disseminated by participating farmers. Farmers identified BL 1887 and BL 2217 as the most desirable genotypes. Consequently, the national variety system released BL 1887 as 'Gautam'; BL 2217 is in the release process. There has been a 31% net increase in grain yield and 78% increase in variety diffusion rate in the project area. The food sufficiency level has increased by 6% over the three-year period.

## 126. History of wheat breeding in Kyrgyzstan and current challenges

Dzhunusova, M.

Kyrgyz National University, 7, Uch-Tereksky pereulok, 720027 Kyrgyz, Bishkek, Kyrgyzstan

E-mail: kumira@yandex.ru

Wheat production in the Kyrgyz Republic started in the late 18th century along the rivers in irrigated valleys. Initially the local populations were grown, which originated from the land races grown in Persia and Turkmenistan. In the 1920s the first efforts were made to select from the land races and to grow enhanced varieties. This work was done at breeding stations near Bishkek and in the Fergana Valley. In the 1930s, vast new irrigated areas were brought into cultivation, which were devoted mainly to cotton. Wheat occupied little space under irrigation and was grown more in the rainfed mountains. In the 1950s and 1960s, breeding was concentrated at the Kyrgyz Research Institute of Agriculture based on crosses between local wheat and the best adapted wheats from Russia. The variety Bezostaya 1 from Krasnodar played a major role in production and in breeding, being used as parents in many important varieties. The current dominant variety, Intensivnaya, originated from a cross with Bezostaya. New varieties developed in the 1990s and 2000s possess high yield potential combined with disease resistance. The diversity of the germplasm was broadened through germplasm exchanges with ICARDA and CIMMYT. The current tendency of wheat growers is to convert to spring planted facultative wheat due to the constraints of fall planting. This requires varieties that are well adapted to both spring and winter planting. Disease resistance (yellow and leaf rust) remains a constant priority. Enhancement of grain quality to suit the requirements of the local bread is very important.

## 127. Grain yield stability of bread wheat genotypes in favorable and stressed environments in Ethiopia

Gelalcha, S.\*, Debelo, D., Yaie, B., Girma, B., and Mamo, B.

\*Ethiopian Institute of Agricultural Research (EIAR), Kulumsa R. C., P. O. Box 489, Asella, Ethiopia

Corresponding author e-mail: [sgelalcha@yahoo.com](mailto:sgelalcha@yahoo.com)

A multilocation trial consisting of 18 bread wheat genotypes, along with standard and local checks, was conducted in 40 environments from 1999 to 2001 in diverse wheat agro-ecologies of Ethiopia. The yield stability of the genotypes was assessed in high potential, low moisture stress and waterlogged growing environments using the AMMI (Additive Main Effects and Multiplicative Interaction) model. The results showed highly significant genotypic and G x E interaction differences in all three environmental categories. Genotypes FH 8-2, HAR 3354 and ETBWC 037 showed low positive interactions. HAR 3116 and FH 6-1-7 showed low negative IPCA (Interaction Principal Component Axis) axis 1 scores, indicating their stable performance in the climatically and edaphically high potential wheat growing areas. In the low moisture areas FH 8-1, ETBWC026, HAR 3224 and HAR 2870 showed low positive IPCA axis 1 scores. Among these genotypes, HAR 2818 gave the highest mean grain yield and a low stress susceptibility index; it is thus an ideal variety for low moisture stress areas. The analysis for waterlogged areas showed that HAR 3354, FH 4-2-11 and ETBWC037 had a high mean grain yield performance and showed low G x E interaction. From the results we concluded that FH 8-2, HAR 3354, ETBWC 037, HAR 3116 and FH 6-1-7 are widely adaptable; FH 8-1, ETBWC026, HAR 3224 and HAR 2870 perform better in the low moisture stress areas, while FH 4-2-11 and ETBWC037 are tolerant to naturally waterlogged vertisols.



## 128. Durum wheat breeding in Tunisia: new varieties for the post-green revolution

Gharbi, M.S.

Field Crop Laboratory, National Research Institute of Tunisia, Rue Hedi Karray 2049, Ariana, Tunisia

E-mail: gharbi.medsalah@iresa.agrinet.tn

Durum wheat is grown on approximately 800,000 hectares in Tunisia. It accounts for around 65% of the total area covered annually by cereals. The introduction of the semi-dwarf durum varieties in the 1960s, the use of fertilizer inputs and advances in weed control have brought about a significant increase in durum wheat production during the last three decades. Average durum wheat yield has increased from 3.5 q/ha between 1910 and 1970, to 7.5 q/ha between 1971 and 1985; and then to 12 q/ha during the period 1986-2005. Recent data from the national durum-breeding program show that consolidation of yield potential through enhanced resistance to biotic and abiotic stresses helped in re-boosting the genetic gain in durum wheat grain yield. Wide cultivation in their respective target environments of the newly released varieties Nasr, which is tolerant to septoria; Mâali, a drought tolerant variety; and BD2347 which has combined resistance to septoria and leaf rust, will certainly raise durum yield and render durum cultivation more profitable for farmers by simultaneously increasing yield and reducing production costs through lower chemical inputs for disease control.

129. Leaf senescence and carbon isotope discrimination in durum wheat (*Triticum durum* Desf.)

Hafsi, M.<sup>1\*</sup>, Hadji, A.<sup>1</sup>, Pfeiffer, W.H.<sup>2</sup> and Monneveux, P.<sup>2</sup>

<sup>1</sup>Université Ferhat Abbas, Sétif, Département de Biologie, Algeria

<sup>2</sup> International Maize and Wheat Improvement Center (CIMMYT), Apdo. Postal 6-641, 06600 Mexico D.F., Mexico

\*Corresponding author e-mail: hafsimiloud@yahoo.com

Studies were conducted to examine the relationships between leaf senescence, carbon isotope discrimination and yield performance in durum wheat (*Triticum durum* Desf.) in the high plains of Setif, eastern Algeria. Ten CIMMYT high-yielding cultivars were grown during two cropping seasons characterized by low rainfall (217 and 162 mm, respectively), freezing temperatures at heading stage and terminal heat stress. Senescence was assessed at 300°C the day after anthesis using numerical image analysis (NIA). Carbon isotope discrimination was analyzed in flag leaves at anthesis and grain at maturity. Senescence was significantly negatively correlated to grain yield in season 1, but not in season 2. There was no relationship between carbon isotope discrimination ( $\Delta$ ) and grain yield in either season. The absence of an association between carbon isotope discrimination and grain yield is likely to be due a strong contribution of pre-anthesis assimilates to yield together with a sink limitation of yield. The results of this study showed that the association between senescence and yield in wheat is highly dependent on environmental conditions. They also allowed definition of the limits of carbon isotope discrimination as a yield predictor.

### 130. Breeding drought tolerant wheat in Morocco: an integrated approach for a complex problem

Jlibene, M.

Wheat breeder, INRA-Morocco, B. P. 578, Meknes, 50000, Morocco

E-mail: jlibene@yahoo.com

Annual rainfall variation and its erratic distribution within the season impose severe challenges to wheat breeding in Morocco, in terms of abiotic stresses (drought and heat) and weather associated biotic stresses (Hessian fly, yellow rust, leaf rust, *Septoria tritici*). Drought occurs in nine seasons out of ten, and may be early, mid-season, late or terminal, or a combination of these. Breeding for mid-season drought is the focus of this paper. Disease and insect resistance, and drought and heat tolerance, are major components of the breeding program. Resistance to *Septoria* and yellow rust were included to insure high productivity under rainy conditions. A natural selection environment (Meknes) was modified to include biotic and abiotic stresses. Naturally, mid-season and late season droughts, as well as terminal heat, occur frequently. Major modifications include continuous cropping, which increases biotic stresses, minimum fertilization for mineral stress, and late planting to amplify abiotic stresses, Hessian fly and rusts. Selection was applied in the field for resistance to biotic and abiotic stresses and agronomic performance, and in the laboratory for grain quality and plumpness. This strategy has yielded positive results. Drought resistant cultivars have survived the worst drought of the century in 2000, on only 73 mm of available effective moisture, and maintained high productivity under favorable environments. However, required stresses do not occur when needed for selection. In particular, *Septoria* may not be present during the five or six cycles of selection in segregating generations. Molecular marker assisted selection for *Septoria* may help in this regard.

131. The diversity of reaction of bread wheat (*Triticum aestivum*) germplasm to yellow rust (*Puccinia striiformis*) infection over environments and years in Kenya

Kinyua M.G., Njau P.N., Wanyera R and Muchui J.

National plant Breeding Research Centre, KARI- Njoro, Private bag 20107, Njoro, Kenya

Corresponding author e-mail: mgkinyua@africaonline.co.ke

Infection of bread wheat by yellow rust is widespread in the wheat growing areas in Kenya. Severe epidemics of yellow rust occur annually on both commercial bread wheat and introductions, being erratic over years and sites. In the past, resistance for most released cultivars became ineffective in less than six years and now even the latest cultivar releases have succumbed to yellow rust infection. A study was carried out countrywide over four years (2001, 2002, 2004 and 2005) in six sites to evaluate the reaction of existing wheat varieties to rust disease under natural infection in the country. The main entries were the commercial cultivars and CIMMYT germplasm. The disease is widespread in all the wheat growing areas in the country being more severe in the high altitude areas. Yellow rust is still a serious threat to all the wheat commercial cultivars grown in Kenya because most of the cultivars are susceptible. However, wheat cultivars such as Africa Mayo, Kenya Kudu, K. Leopard, K. Plume, Frontach and Trophy, released in the sixties, appear to retain their resistance for a longer time. Data on the wheat rust revealed that the disease is on the increase in Kenya and all wheat growing areas are prone to the disease. There were significant differences in the resistance reactions of the varieties tested. There was also a site by variety difference. Commercial cultivars and some of the old varieties, which have remained resistant/ moderately resistant to yellow rust can be utilized in the breeding program.

## 132. Evaluation of bread wheat genotypes in diverse environments of Ethiopia

Mamo, B., Gelalcha, S. and Girma, B.

Kulumsa Agricultural Research Center, P.O.Box 489, Arsi, Assela, Ethiopia

Corresponding author e-mail: bandargemamo@yahoo.co.uk

Genotype evaluation was conducted to assess bread wheat genotypes' adaptation to, and interaction with, their growing environments. The experiment comprised 20 bread wheat genotypes including standard and local checks in 12 locations for 3 years (a total of 33 environments). A randomized complete block design with 4 replications was used at all locations. Additive main effect and multiplicative interaction (AMMI) and Classification analysis indicate that there were significant ( $P < 0.001$ ) differences among the tested genotypes and locations. Classification analysis grouped the tested genotypes into four different groups and the environments into seven cluster groups. The classification of environments effectively identified trials that experienced similar environments. Nine principal components (PC) extracted 89.4% of the entire variation of the genotypes. 28.42% of the total variance was explained by the first PC. Overall, the study confirmed that the wheat growing locations of Ethiopia are subject to environmental variation not only on a geographical basis but also from year to year. Special consideration should be given to locations with high year-to-year variation; this variation offers a chance for testing the genotypes under different environmental conditions. Genotype adaptation varied significantly between different environmental groups; this offers ample opportunity for improvement through breeding.

### 133. Grain yield potential stability and agronomic performance of some wheat genotypes in the Southern Highlands of Tanzania

Mongi-Henday, R. and Elanga, A.M.

The Uyole Agricultural Research Institute, P. O. Box 400, Mbeya, Tanzania

E-Mail: rhmongi@yahoo.com

Wheat (*Triticum aestivum* L.) cultivars differ primarily in grain yield potential, stability and agronomic performance when grown in diverse environments. Evidence of enhanced yield potential, combined with enhanced yield stability would facilitate wider acceptance of improved wheats by farmers. In this study eight genetically diverse advanced lines of spring wheat and three widely grown wheat cultivars in the Southern Highlands of Tanzania (SHT), were evaluated for their yield potential, agronomic performance and stability at four different locations representing diverse environments of the SHT. The experiments were conducted over three years and involved four replications of a randomized complete block design. Combined analysis of variance showed that genotypes were significantly different in grain yield potential, kernel weight, plant height, days to heading and days to maturity. Genotype x environment variance was significant for grain yield and other agronomic traits evaluated, indicating differences across environments, where grain yield advantage increased with increased environmental potential. Genotype mean yields were regressed on an environmental index based on location means. Deviation from the regression was significantly lower for three genotypes. Stability analysis identified four advanced lines, UW88078, UW86041, UW86085 and UW90028 as stable for yield across environments. UW90028 showed the highest yields and was released as an improved cultivar to wheat farmers in Tanzania.

## 134. AMMI analysis of grain yield stability in hexaploid wheat genotypes grown in temperate regions of Iran

Najafian, G.<sup>1</sup>, Kafashi, A.K.<sup>2</sup> and Jafar-Nejad, A.<sup>3</sup>

<sup>1</sup>Cereals Research Dept., Blvd. Shahid Fahmideh, SPII, Karaj, Iran

E-mail: goodarzn@yahoo.co.uk

<sup>2</sup>Agricultural Research Center, Blvd Keshavarz, Kermanshah, Iran

<sup>3</sup>Agricultural Research Station, Neishabour, Iran

In this trial 18 lines/varieties were evaluated along with two check cultivars, Shiraz and Pishtaz, over seven temperate zone stations during two crop seasons, 2003-2005. These materials had been forwarded through evaluation and screening in advanced regional wheat yield trials during the last temperate zone crop season. Experiments were planted in November of each crop season and were maintained over winter. Field observations of disease resistance, lodging, heading and maturity dates, plant height, kernel color, and shattering were recorded in the spring. Finally, after harvesting, kernel yield was recorded. A combined ANOVA was carried out for the seven stations over two years. AMMI (additive main effects and multiplicative interaction) analysis was carried out and the biplot of the interaction of principle components was evaluated for stability and adaptation relationships among genotypes and stations. Superior genotypes were selected on the basis of mean analysis, AMMI results and non-parametric ranking analysis, all recorded traits and also information from disease nurseries. According to two crop seasons' results, M-82-9 was the best performer for grain yield with 8.257 t/ha. Following that, entry numbers 1, 14, 2, 18, 6, 11, 4, 5 and 8 were also high yielders. The poorest genotype was M-82-7 with 7.183 t/ha. In AMMI analysis IPC1 was significant, defining 41.5% of interaction variation. The biplot of IPC1 and grain yield was used for interpreting G×E interaction. Overall two genotypes, M-82-9 and M-82-6, were selected for further testing in on-farm trials.

135. An adapted hexaploid wheat line for late season moisture stress in the temperate zone of Iran

Najafian, G.<sup>1</sup>, Nikooseresht, R.<sup>2</sup>, Ghandi, A.<sup>3</sup> and Jafar-Nejad, A.<sup>4</sup>

<sup>1</sup>Cereals Research Dept., Blvd. Shahid Fahmideh, SPII, Karaj, Iran

E-mail: goodarzn@yahoo.co.uk;

<sup>2</sup>Agricultural Research Center of Kermanshah, Iran

<sup>3</sup>Agricultural Research Center of Isfahan, Iran

<sup>4</sup>Agricultural Research Station of Neishabour, Iran

291 advanced lines/varieties of hexaploid wheat were evaluated in two trials (well-irrigated, and water stressed from the heading stage onward), without replication, in the 2001-02 crop season. Fifty-one lines/varieties were forwarded to a 2002-03 crop season experiment, under water deficit only (heading stage onward). Sixteen genotypes from the 2<sup>nd</sup> stage, plus 4 check cultivars, identified as WS-82-1 to WS-82-20, were studied in an adaptation trial, exposed to water stress from the heading stage onward, in four locations over two seasons (2003-2005). Stability was tested using the AMMI (Additive Main Effect and Multiplicative Interaction) method. Comparison of means showed that WS-82-12, with 6.285 t/ha, was the superior genotype and WS-82-4, with 4.239 t/ha, was the poorest. Pishtaz, an irrigated check cultivar, produced 5.703 t/ha. Cross Alborz, suggested for supplementary irrigation, showed a grain yield of 5.165 t/ha. Azar-2, a drought tolerant cultivar, yielded 4.553 t/ha. Many genotypes showed higher grain yields than the checks. Entries 12, 13, 7, 16, 14, 8, 6, 9, 10 and 18 had grain yields exceeding 6 t/ha. Thousand-kernel weight equaled or exceeded 35g for entries 3, 4, 7, 8, 9, 10 and 18. Interaction principal components 1 (IPC1) and IPC2 dimensions in the AMMI analysis were significant, defining 88% of interaction variation. Biplots of the first two IPCs were used for interpreting G×E relationships. Considering yield stability, disease resistance, resistance to grain shattering, water use efficiency and bread making quality, WS-82-9 was the superior entry for introduction for late season drought conditions in the temperate zone.



## 136. Wheat productivity improvement in Afghanistan

Osmanzai, M.

Country Coordinator, International Maize and Wheat Improvement Center (CIMMYT), PO Box 5291, Kabul, Afghanistan. E-mail: [m.osmanzai@cgiar.org](mailto:m.osmanzai@cgiar.org)

Afghanistan is a land-locked country with arid and semi-arid climates. Before 1978, the irrigated area covered roughly 85% of food and industrial crops. The current area under annual crops is approximately 3.7 million ha, with over 2 million ha under wheat. The national average wheat yield is 1.5 t/ha, while the potential is much higher. The main constraints to wheat production are: lack of improved adapted varieties; inefficient and ineffective production technologies; lack of quality inputs, farm machinery and equipment; damaged irrigation systems and poor market infrastructure. Important aspects in improving crop productivity in Afghanistan are improving the genetic basis of productivity and stability; agronomic, and plant protection measures. Developing and adapting appropriate technologies in wheat-based production systems has shown a significant increase in productivity. The approaches undertaken to improve wheat productivity are through applied research, training, and technical support in collaboration with National Agricultural Research Systems, and partners. Improved germplasms were obtained and evaluated from 2002 – 2006. A few improved high yielding varieties have been released, and many candidate cultivars are in the pipeline for release. It is expected that sustainable wheat improvement in production and productivity can assure food security, and contribute to a reduction in poverty and an overall improvement in livelihoods.

## 137. Nitrogen efficiency use in wheat breeding

Parodi, P.C.

Departamento de Ciencias Vegetales, Pontificia Universidad Católica de Chile, Casilla 306, Santiago 22, Chile. E-mail: pcpardi@uc.cl

Nitrogen (N) efficiency use (NUE) in wheat has been estimated at 33-36%. Therefore, approximately two thirds of the N fertilizer applied to the crop is lost through different pathways. In order to obtain high commercial yields, farmers N applications tend to be above the desired sustainable rates, thus making the crop less competitive because of high production costs, and additionally contaminating the soil, water and atmospheric components of the environment. Many wheat breeding programs conduct their selection procedures under high N levels, a practice that frequently precludes the identification of genotypes differentiated by higher NUE. Over 3 years, we have analyzed durum wheat (*Triticum turgidum* var. *durum*) advanced lines at four N rates, in order to identify genotypes that use N more efficiently, as expressed in grain yield, protein content and commercial quality. To maximize yields under restricted N inputs, productivity restricting management factors, such as weed infestation, disease and pest incidence and irrigation have been maintained at optimal practical levels. Results demonstrated that over 25% of the analyzed genotypes have some degree of enhanced NUE, which has allowed the selection of material that expresses competitive yields and quality parameters under limited N fertilizer rates.

## 138. Perennial wheat development for sustainable agriculture in the US Pacific Northwest

Piaskowski, J.\*, Murphy, K., Arterburn, M., Dawson, J., Gollnick, M. and Jones, S.  
Winter Wheat Breeding, Cytology & Genetics, Crop and Soil Sciences Department, Washington State University, 201 Johnson Hall, Washington State University, 99164-6420 Pullman, WA, USA.

\*Corresponding author e-mail: [julialouise@mail.wsu.edu](mailto:julialouise@mail.wsu.edu)

Soil erosion is a widespread scourge of agricultural systems that has adversely and extensively impacted the cultivated portions of the Palouse prairie of Eastern Washington and the Washington State steppe. The winter wheat breeding program at Washington State University initiated a perennial wheat breeding program in 1997 to stem this growing problem. The development of perennial wheat could greatly benefit dryland farming in Washington by preventing soil erosion, accessing soil nutrients and soil water more effectively, and increasing the genetic diversity of grain crops. The goal of the program is to develop a high quality perennial wheat which has vigorous regrowth for a minimum of five years in agricultural fields, and contributes to a sustainable form of agriculture. To achieve this, hundreds of hybrids between the wheatgrass species *Thinopyrum* and bread wheat (*Triticum aestivum* L.) have been developed. Many lines are currently being tested in nurseries throughout the wheat-growing regions of Washington State in collaboration with farmers. There are also three graduate research projects in progress addressing perennial wheat: (1) identification of chromosomes associated with the perennial growth habit; (2) identification of the gene or genes responsible for perennial and annual lifecycle choice; and (3) identification of perennial wheat lines which have increased nitrogen use efficiency. The cultivation of perennial wheat offers great promise for enhancing the ecological sustainability of dryland farming in Washington.

### 139. Winter wheat seed-growing problems imposed by varietal diversity

Romanenko, A.A. and Bespalova, L.A.\*

Wheat Breeding Department, Krasnodar Lukyanenko Research Institute of Agriculture, 350012  
KNIISH, Krasnodar, Russia

Corresponding author e-mail: [bespalova\\_1\\_a@rambler.ru](mailto:bespalova_1_a@rambler.ru)

A wide range of genetically diverse varieties helps increase and stabilize grain yields, resist attack by constantly changing pathogens, and provide an assortment of end products. A seed-growing system is needed which enables maintenance and regular change of varieties. The system of primary seed growing, developed in the mid-twentieth century, was based on individual family selection followed by two-year control of the developed seeds. Recently the approach has changed for several reasons: 1) most new varieties are more inclined to facultative self-pollination; 2) over-saturation of new varieties with recessive genes has increased the frequency of spontaneous mutation, especially under widespread viral diseases; 3) frequent abiotic stresses (late spring frost, very high temperature at flowering, etc.) and negative effects of pesticides also lead to biological infestation. Quality breeder seeds of homogeneous varieties, which have been passed to the State Variety Trial, are usually grown for two years. We select 1200-1300 typical ears. Their progenies are grown within the same crop variety to avoid cross-pollination, and evaluated. Off-type, segregating and weak families are removed. Within the remaining families, we do a second-year selection of individual ears. Those families that were not selected are harvested and sown in the next season to provide adequate isolation. Progenies of the 1000-1200 selected ears are sown in rows within this isolating crop stand. After the second cycle of selection, all families are harvested together and the seeds are stored for as long as there is reasonable demand. Foundation seeds are multiplied from this breeder seed stock.

## 140. New CIMMYT-derived bread wheat germplasm with high yield potential and wide adaptation

Sharma, R.C.<sup>1,2\*</sup>, Singh, R.P.<sup>1</sup>, Joshi, A.K.<sup>1,3</sup> and Huerta-Espino, J.<sup>1,4</sup>

<sup>1</sup>International Maize and Wheat Improvement Center (CIMMYT), Apdo. Postal 6-641, 06600, Mexico DF, Mexico

<sup>2</sup>Institute of Agriculture and Animal Science, Rampur, Nepal

<sup>3</sup>Department of Genetics and Plant Breeding, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi 221005, India

<sup>4</sup>Campo Experimental Valle de Mexico-INIFAP, Apdo. Postal 10, 56230, Chapingo, Edo. de Mexico, Mexico

\*Corresponding author e-mail: sharmar@cimmyt.exch.cgiar.org

Attaining increased yield potentials, wide adaptation, and improved end use quality characteristics constitute core activities of the CIMMYT bread wheat improvement program. International yield data from the 22<sup>nd</sup>, 23<sup>rd</sup>, 24<sup>th</sup> and 25<sup>th</sup> Elite Spring Wheat Yield Trials (ESWYT) and the 10<sup>th</sup>, 11<sup>th</sup> and 12<sup>th</sup> Semi-Arid Wheat Yield Trials (SAWYT) were analyzed to identify genotypes with high and stable yield across testing sites in many developing and a few developed countries. GGE-biplot analyses showed that in most cases the highest yielding genotypes were also among the most stable genotypes globally and produced significantly higher grain yield than the mean of the local checks. It is worth noting that certain genotypes such as Weebill1 and Prl/2\*Pastor were the highest yielders both in the irrigated (ESWYT) and rainfed (SAWYT) trials. Fret2 was an outstanding performer in the 22<sup>nd</sup> as well as 23<sup>rd</sup> ESWYT. We also analyzed data separately for high and low productivity environments. Some genotypes were outstanding under both environments in some years. Most exceptional lines could be traced to a few outstanding parents. A number of these genotypes represent a change in plant architecture that is particularly suited to the raised bed planting system, as well as being well adapted to the traditional flat bed. The results underscore the merits of new improved wheat genotypes that could be used in a crossing program to further increase yield potential and also suggest that such genotypes are protected from important diseases and pests through the incorporation of diverse and durable genetic resistance.

## 141. Virulence spectrum of wheat leaf and yellow rust in the South Caucasus

Sikharulidze, Z. and Natsarishvili, K.

Plant Immunity Research Institute, #90 Tavisupleba Street, Kobuleti 6200, Adjara, Georgia

E-mail: zoia\_sikharulidze@yahoo.com

Leaf rust and yellow rust are major wheat diseases in most wheat growing areas. Both diseases are observed in nearly all regions of Georgia with their severity varying from low to medium. In Azerbaijan, yellow rust is distributed more widely than leaf rust. To assess the virulence of leaf and yellow rust in the region, their spores were collected in the major wheat growing regions of Georgia and Azerbaijan in 2005. To identify virulence, a total of 192 monopustule isolates of *Puccinia triticina* were evaluated using 39 differentials. Virulence to Lr3, Lr12, Lr13, Lr14a, Lr14b, Lr16, Lr22a, Lr22b, Lr30, Lr32, Lr33, Lr34, Lr37 and LrB was found in all isolates. Virulence frequencies to genes Lr1, Lr3ka.Lr3bg, Lr17, Lr21, Lr26, Lr25, Lr35 and Lr36 were very high. A few isolates were virulent to lines with the gene Lr2a. Eighty-one pathotypes were described in the population. The frequency of most isolates was very low (i.e. one isolate). No significant differences were found in the virulence structures of the leaf rust population of Georgia compared to that of Azerbaijan. Sixty-three isolates (51 from Georgia, 12 from Azerbaijan) were tested using a differential set consisting of Yr1, Yr5, Yr6, Yr7, Yr8, Yr9, Yr10, Yr11, Yr12, Yr15, Yr17, Yr18, Yr24, Yr26, YrSP, YrSK, YrIR, YrIS, YrAS, YrAR, YrSD and YrCV. Analysis of the virulence of both populations showed that the effective resistance genes were: Yr1, Yr5, Yr10, Yr12, Yr15, Yr24, Yr26, YrSD and YrCV. The frequency of virulence observed for Yr6, Yr7, Yr8, Yr9, Yr11, Yr17, Yr18, YrSK, YrIR, YrIS and YrAS was very high. Virulence to gene Yr10 was found only in the Azerbaijani population. Eight and six pathotypes were described in Georgian and Azerbaijani populations, respectively. The prevalent pathotype was: 1,5,10,12,15,24,26,SP, AR, SD,CV/6,7,8,9,11,17,18,SK,IR,IS,AS.

## 142. Wheat breeding in cold regions of Iran

Yazdan Sepas, A. and Najafi Mirak, T.

Seed and Plant Improvement Institute, Mahdasht St, Karadj, Jahanshahr, Iran

E-mail: ayazdansepas@yahoo.com

Of the 2.3 million hectares of irrigated wheat in Iran, between 850 and 900 thousand hectares are located in cold regions of the country. These regions are characterized by low temperatures (less than  $-14^{\circ}\text{C}$  average absolute minimum temperature), altitudes of more than 1000 meters above sea level, and around 90 days of frost per year. Winter and/or facultative irrigated wheat cultivars are grown in these regions. Experimental trials are executed annually in 12 research stations in these areas. Jolgerokh (in the northeast), Karadj (in the center north), Ardebil (in the northwest) and Miandoab (in the northwest) are the main research stations from the point of view of yield potential and/or biotic stresses (e.g. stripe rust). In order to prepare national genetic materials for cold regions, around 250 crosses are made at Karadj research station annually. In addition, international germplasm is also received, predominantly from CIMMYT Turkey. Data from the last 17 years' breeding programs in cold areas (from 1988 to 2005), show that average grain yield of promising genotypes in elite experiments has increased from  $4148\text{ kg ha}^{-1}$  in 1988 to  $6815\text{ kg ha}^{-1}$  in 2005, an increment of  $157\text{ kg ha}^{-1}\text{ year}^{-1}$ . Despite this, the average grain yield in farmers' fields in cold areas is still only  $2900\text{ kg ha}^{-1}$ .

143. Heterosis and combining ability in diallel F<sub>1</sub> offspring of six selected bread wheat (*Triticum aestivum* L.) cultivars

Yildirim, M.

Wheat Program, Anatolian Agriculture Research Institute, P.K.17, Eskisehir, Ankara, Turkey

E-mail: myildirim02@yahoo.com

This study was made in the 2002-03 crop season, using Sultan-95, Bezostaya-1, Süzen-97, Altay-2000, Harmankaya-99 and Gerek-79 winter bread wheat cultivars, which are not closely related to one another. Using these cultivars, 6x6 half-diallel crosses were performed. We aimed to select the best parents and hybrid combinations by studying the genetic structure of the F<sub>1</sub> populations for some physiological and plant yield characteristics. Effects of general and specific combining abilities and heterosis effects were studied through analysis of genetic parameters. The experiment was carried out, including the parents, in a randomized complete block design with 4 replications. The calculations were made according to the Griffing method-II (1956). According to the findings related to general and specific combining abilities and heterosis, it was seen that selection for characters like canopy temperature, translocation ratio, chlorophyll ratio and plant grain yield can be successful. Combining abilities of the parents gave different values for all characteristics studied. Altay-2000, Bezostaya-1 and Harmankaya-99 were found to be good parents for physiological properties. All genotypes except for Gerek-79 were found to be suitable parents for the property of plant grain yield. Since Gerek-79 contains the *Ne<sub>1</sub>* gene and Süzen-97 and Harmankaya-99 contain the *Ne<sub>2</sub>* gene, their combinations resulted in hybrid necrosis due to the additive dominant gene effect, and these combinations gave extreme values for all parameters. Findings of this study confirmed the great significance of the selection of parents in bread wheat breeding programs.



---

## **Cultivar development methodologies – other crops**

---

### 144. Cereal breeding for the drylands of north-eastern Kazakhstan

Abdullayev, K.

Director, Pavlodar Research Institute of Agriculture, 82/1 Kamzina St. Apt. 8, 140000 Pavlodar, Kazakhstan. E-mail: k.abdullayev@mail.ru

The north-eastern region of Kazakhstan is characterized by a continental climate with a short growing season (mid-May to late August) and low precipitation (250-300 mm.) The soils are sandy and their fertility is poor. However, the region grows 0.5 million hectares of spring wheat as well as spring barley, millet and buckwheat. The cultivation technology is based on a fallow-crop rotation which aims to preserve moisture. Drought tolerance is a major objective for all crops. Most of the precipitation falls in winter as snow. The summer precipitation is unpredictable and adapted varieties need to have drought tolerance throughout the season. The biotic stresses include diseases and pests, which affect yield substantially during the rare years with sufficient precipitation. The breeding strategy for cereals is based on crosses within the local germplasm itself, as well as incorporation of traits from diverse germplasm from drought prone areas. Multilocational testing of spring wheat varieties developed under the dry conditions of the region has shown that they perform well across locations, including those with higher precipitation. This suggests that breeding in Pavlodar under dry conditions generates broad adaptation.

## 145. Genetic progress over 20 years of sunflower hybrid release in central Argentina

de la Vega, A.J.<sup>1</sup>, DeLacy, I.H.<sup>2</sup> and Chapman, S.C.<sup>3</sup>

<sup>1</sup>Advanta Semillas S.A.I.C., Ruta Nac. 33 Km 636, C.C. 559, 2600 Venado Tuerto, Argentina.

E-mail: avega@waycom.com.ar

<sup>2</sup>School of Land and Food Sciences and A.C.P.F.G., The University of Queensland, Brisbane, Qld 4072, Australia. E-mail: i.delacy@uq.edu.au

<sup>3</sup>CSIRO Plant Industry, Queensland Bioscience Precinct, 306 Carmody Rd., St. Lucia, Qld 4067, Australia. E-mail: scott.chapman@csiro.au

Linear mixed model analyses were conducted on 122 on-farm trials of commercial and near-commercial sunflower (*Helianthus annuus* L.) hybrids grown over 15 years in 32 locations of central Argentina to quantify increases in oil yield and to determine the contributions of change in characteristics of germplasm pools to such yield increases. The best linear unbiased predictors (BLUPs) from this analysis can be regarded as measures of 'Relative Peak Performance' of hybrids in environments for which they were selected. The BLUPs of 49 commercial hybrids released between 1983 and 2005 showed a genetic gain of 11.9 kg ha<sup>-1</sup> yr<sup>-1</sup>, 0.19 % yr<sup>-1</sup> and 16.1 kg ha<sup>-1</sup> yr<sup>-1</sup> for oil yield, grain-oil concentration and grain yield, respectively. Special purpose hybrids that were converted for single traits or that were developed for low-technology markets lagged by 5 to 15 years in terms of genetic gain. Based on the data and the estimated time lag between commercial release and peak of use, the improvement in oil and grain yield of conventional hybrids in central Argentina will be sustained until at least 2010, with evidence that the new germplasm pools still have substantial genetic variance to be exploited. A biplot of genotype-by-attribute BLUPs summarized 20 years of breeding to demonstrate how the merging of two germplasm pools of differing maturity, achene type and grain-oil concentration resulted in step-wise improvements in grain yield and grain-oil concentration and a move toward an intermediate maturity.

## 146. Development of breeding material using somatic hybridization and polyploidization within the *Solanum* genus

Greplová M.<sup>1\*</sup>, Polzerová H.<sup>1</sup>, Vlastníková H.<sup>1,2</sup>, Kopecký D.<sup>3</sup>, Švecová R.<sup>1</sup>, Domkářová J.<sup>1</sup>

<sup>1</sup>Potato Research Institute, Ltd., Dobrovského 2366, CZ-580 01 Havlíčkův Brod, Czech Republic. \*Corresponding author e-mail: greplova@vubhb.cz

<sup>2</sup>Czech University of Agriculture, Kamýcká 129, CZ-165 21 Praha 6, Czech Republic.

E-mail: vlastnikova@af.czu.cz

<sup>3</sup>Institute of Experimental Botany, Olomouc Research Center, Sokolovská 6, CZ-772 00 Olomouc, Czech Republic. E-mail: kopecky@ueb.cas.cz

Supported by projects NAZV QF 4108, NAZV 4133.

The goal of this study is to use wild species of the genus *Solanum* in somatic hybridization and *in vitro* polyploidization. The effort is especially focused on the introduction of resistance genes for late blight from wild potato to cultivated *Solanum tuberosum*. Breeding using somatic hybridization was done by an electrofusion of mesophyll protoplasts. Mesophyll protoplasts of *Solanum tuberosum*, *S. berthaultii*, *S. bulbocastanum*, *S. pinnatisectum* and *S. verrucosum* were used. Regenerated plants were obtained after 140 days in some combinations. These plants were evaluated by flow-cytometry and a RAPD (Random amplified polymorphic DNA) method. We obtained somatic hybrids, for which morphological evaluation was performed and selected individuals will be included into the breeding program. Obtaining breeding material by using polyploidization was performed with colchicine and oryzaline application to nodal segments of the wild potatoes *S. berthaultii*, *S. bulbocastanum*, *S. pinnatisectum*, *S. verrucosum* and dihaploid hybrids of *S. tuberosum*. Regenerants were evaluated by flow-cytometry and derived tetraploids are used in crosses with *Solanum tuberosum*. They are further evaluated under field conditions.

147. Evaluation of heterosis in soybean [*Glycine max* (L.) Merr.]

Perez, P.T.<sup>1\*</sup>, Ortiz-Perez, E.<sup>1</sup>, Cianzio, S.R.<sup>1</sup>, Wiley, H.<sup>2</sup>, Davis, W.H.<sup>3</sup>, Horner, H.T.<sup>4</sup>, and Palmer, R.G.<sup>5</sup>

<sup>1</sup>Department of Agronomy, Iowa State University, Ames, Iowa 50011-2010 USA

<sup>2</sup>Dairyland Seed Co., Inc. Otterbein, Indiana 47970 USA

<sup>3</sup>Verde Seeds, Inc., Plainview, Texas 79072 USA

<sup>4</sup>Department of Genetics, Development and Cell Biology and Bessey Microscopy Facility, Iowa State University, Ames, Iowa 50011-1010 USA

<sup>5</sup>USDA-ARS-CICGR, and Department of Agronomy, Iowa State University, Ames, Iowa 50011-1010 USA

\*Corresponding author e-mail: ptperez@iastate.edu

In soybean [*Glycine max* (L.) Merr.], manual cross-pollination is difficult and time consuming, and not conducive to an economical way of producing large quantities of hybrid seed. Male sterility systems identified in soybean, combined with insect-mediated cross-pollination have been shown to produce large quantities of hybrid seed that can be useful for the identification of heterotic patterns in soybean. This procedure was used in this study to produce hybrid seed for the conduct of replicated yield trials. The objective of the study was to evaluate yield in hybrid soybean lines developed by single-crosses, three-way crosses, four-way crosses, and backcrosses (BC<sub>1</sub>F<sub>1</sub> and BC<sub>2</sub>F<sub>1</sub>). Parental genotypes were male-sterile lines and a group of male parents selected by their agronomic performance. In 2003, eight F<sub>1</sub> single-cross families were evaluated in replicated experiments at three locations. Three-way and BC<sub>1</sub>F<sub>1</sub> crosses for each family were evaluated in 2004, and in 2005. Also in 2005, four-way crosses, and BC<sub>2</sub>F<sub>1</sub> crosses were evaluated at one location. Parental lines were evaluated each year. High-parent heterosis (HPH) for yield in single-crosses ranged from -41.11% to +11.19%; three-way crosses from -30.21% to -3.57%, four-way crosses from -44.2% to -26.04%, BC<sub>1</sub>F<sub>1</sub> crosses from -33.64% to +41.97%, and from -31.32% to -8.17% for BC<sub>2</sub>F<sub>1</sub>. The finding of positive HPH values suggests that hybrid soybean production may become possible for US farmers.

## 148. Effectiveness of early generation selection in winter barley

Pržulj, N. and Momčilović, V.

Institute of Field and Vegetable Crops, Maksima Gorkog 30, 2100 Novi Sad, Serbia

E-mail: przulj@ifvcns.ns.ac.yu

Selection in early generations is important for success in barley breeding. Although early generations are substantially heterozygous, early generation selection relies on the assumption that properties of lines in early generations will be inherited by late generations. Earliness is a major selection criterion in semiarid environments. The purpose of this study was to determine whether time to heading (PAP) of  $F_2$  plants could be used to predict the performance of  $F_{2:3}$  and  $F_{2:4}$  lines, i.e., whether early generation selection is worthwhile. Twelve parents of winter two-rowed barley, which differed in time to heading, were crossed and eight populations derived. 30 early and 30 late plants were selected from each cross and  $F_{2:3}$  and  $F_{2:4}$  lines produced. Correlations between PAP of  $F_2$  plants and PAP of their  $F_{2:3}$  lines were significant in all crosses. Heritability values for PAP exceeded 0.69. This study revealed that PAP is a highly heritable trait. There is no strong genetic consistency in the relationship between PAP and other development phases, yield and physiological characteristics. The usefulness of each cross would be determined in the environment where selection is taking place and where the selected variety will be grown. Various combinations of length of PAP and grain filling period can produce lines with favorable agronomic performances. Due to non-genetic effects, early generation selection has partial usefulness in breeding. Since time to heading is highly heritable, a possible strategy could be to select for time to heading in early generations and for yield and quality in later generations.

149. Deoxynivalenol content in grain of cereals after artificial inoculation with *Fusarium culmorum*

Šliková, S., Vančo, B. and Šudyová, V.

Slovak Agricultural Research Centre, Research Institute of Plant Production, Bratislavská cesta 122, 92168 Piešťany, Slovak Republic. Corresponding author e-mail: slikova@vurv.sk

Supported by the Ministry of Agriculture of the Slovak Republic, Project No. 2006 UO 27 091 05 01 091 05 11.

The mycotoxin deoxynivalenol (DON) is frequently found in agricultural crops affected by *Fusarium* head blight (FHB). DON is toxic and causes reduced feed intake, a considerable loss of body weight and vomiting in exposed animals; it also inhibits the synthesis of DNA and RNA. The aim of this work was to evaluate 39 winter wheat, 8 barley and 5 oat cultivars for DON accumulation in the grain and for the percentage of *Fusarium* damaged kernels (FDK) in 2004 and 2005, after artificial inoculation with *F. culmorum*, and to identify possible sources for resistance breeding. Differences were found in FDK and the DON content between wheat, barley and oat and between cultivars. The highest content of DON was found in cultivars of wheat (165,3 mg.kg.<sup>-1</sup>) followed by barley (95,1 mg.kg.<sup>-1</sup>), while oat had the lowest content (23,5 mg.kg.<sup>-1</sup>). The mean DON content was highest in the wheat cultivars Alana, Axis, Elpa and Estica, and lowest in Alka, Malyska, Sana and Zerda. The correlation coefficients were statistically high between DON content and FHB rating (0.79\*\*), and between DON and FDK (0.73\*\*) in both years. The barley cultivars Saloon and Vladan accumulated high levels of DON; Ludan and Atribute showed the lowest levels of DON. High levels of DON were accumulated in the oat cultivars Avenuda and Izák; the cultivar Detvan had a low percentage of FDK but accumulated a high level of DON.

## 150. Breeding for melonworm resistance in tropical pumpkin

Wessel-Beaver, L., Pérez-Maisonave, R., Pérez-Arocho, J. and Segarra, A.

Department of Agronomy and Soils, University of Puerto Rico, 277 Cumbres Las Mesas, 00680 Mayaguez, Puerto Rico, USA.

Corresponding author e-mail: lwesselbeaver@yahoo.com or lbeaver@uprm.edu

Melonworm (*Diaphania hyalinata*) is one of the most damaging pests of squash and pumpkins (*Cucurbita* sp.) in the tropical regions of the Americas. Tropical pumpkin (*C. moschata*) is an important vegetable crop throughout the Caribbean. Growers often schedule regular applications of chemical insecticides to prevent foliar damage by the melonworm. An objective of the tropical pumpkin breeding program at the University of Puerto Rico is to develop locally adapted cultivars with improved melonworm resistance. Both qualitative (identifying and incorporating genes for resistance) and quantitative (recurrent selection) approaches might lead to this goal. Both approaches initially require the development of protocols for evaluating resistance and for manipulation of the insect population. In the case of tropical pumpkin, the crop itself also presents challenges to the breeder doing field evaluations since a single plant can easily occupy 25 m<sup>2</sup> or more of space. Furthermore, collections of tropical pumpkin typically consist of open-pollinated land races, not inbred lines. Thus, control of variation, be it due to micro-environment heterogeneity in inherently large field experiments, to within-accession genetic variability, or to insect population variability, is a challenge that the breeder aiming to improve melonworm resistance in tropical pumpkin must face. Here we report on field and laboratory evaluations of 360 accessions of *C. moschata* and a related species, *C. argyrosperma*. To date, we have been unsuccessful in identifying useful sources of resistance to the melonworm. It is not clear whether this is due to lack of genetic variation or our inability to detect this variation.

151. How many genes might be involved in aluminium stress tolerance in alfalfa (*Medicago sativa* L.)?

Zhang, X.G., Humphries, A. and Auricht, G.C.

South Australian Research and Development Institute, Waite Campus, GPO Box 397, Adelaide 5001, Australia

Corresponding author e-mail: zhang.xianguang@saugov.sa.gov.au

Aluminium (Al) toxicity is the predominant plant growth-limiting factor in acid soils. A better understanding of the genetic basis of Al stress tolerance is of fundamental importance in establishing an effective breeding strategy for crop plants. Alfalfa (or lucerne) is a particularly valuable perennial fodder plant in Australia but it is limited by acid soil intolerance. This study was made to quantify the genetic variability and then to estimate the number of genes that might be involved in Al tolerance, to facilitate the planning of breeding programs aimed at improved Al stress tolerance and hence enhanced plant productivity. Root regrowth was measured for relative Al tolerance using a hydroponic system in controlled glasshouse conditions. A full diallel analysis was made with 4 genotypes in winter active lucerne (winter vigor ranging from 6 to 8). Considerable variation due to both general combining ability (GCA) effects and specific combining ability (SCA) effects indicated the importance of both additive effects and non-additive effects in Al tolerance. The number of effective factors for Al tolerance was estimated at 1.9, suggesting that the genetic control of variation for Al tolerance is a complex polygenic system involving at least 2 pairs of genes in those genotypes used.



---

## Cultivar development methodologies – modeling

---

### 152. Parental selection in self-pollinating crops using breeding values

Bauer, A.M. and Léon, J.\*

Institute of Crop Science and Resource Conservation, University of Bonn, Katzenburgweg 5, D-53115 Bonn, Germany

\*Corresponding author e-mail: [j.leon@uni-bonn.de](mailto:j.leon@uni-bonn.de)

Selection of favorable parental lines is an essential requirement for breeding success. For this purpose all available information should be used. However, as breeders get only phenotypic information about lines and especially if all line testing trials are considered, the selection decision will be biased. Often the genetic relationship among potential lines (pedigree or marker information) is not part of the estimation process. Predicting breeding values using best linear unbiased prediction (BLUP), which is commonly applied in animal breeding, is able to integrate relationship information and to manage even extremely unbalanced data. In our study we generated a virtual parental population of 500 inbred lines by computer simulation. Each line was influenced by 150 loci each with 2 to 7 alleles, the respective additive and additive x additive epistatic effects which form the genotypic value, and environmental and genotype x environmental effects. Coefficient of coancestry is possibly a biased estimator of relationship information among inbred lines, especially when the selection pressure is high. We compared BLUP(E+GS) (considering genetic similarities as an alternative to coefficient of coancestry) and BLUP(E+A) (using coefficient of coancestry) in self-pollinating crops. Regarding traits with a medium to low heritability, both BLUP(E+GS) and BLUP(E+A) increased the selection response. Assuming unbiased conditions, BLUP(E+GS) leads to a marginally higher selection response than BLUP(E+A). Hence, we discuss the replacement of coefficient of coancestry by genetic similarities in BLUP of self-pollinating crops. Further studies are needed to determine the limitations of genetic similarities (number of markers, distribution, etc.) in this application.

### 153. Bayesian modeling of heterogeneous error and genotype by environment interaction variances: model assessment

Orellana, M.\*, Edwards, J., Carriquiry, A. and Jannink, J.L.

Department of Agronomy, Iowa State University, 50011, Ames, IA, USA

\*Corresponding author e-mail: [massiel@iastate.edu](mailto:massiel@iastate.edu)

Identifying plant varieties that provide superior performance for growers across a wide range of growing conditions is a very important and expensive task. Varieties must be evaluated in many environments and performance data summarized in order to identify not only the best varieties, but also those with the most stable performance. Edwards and Jannink, in a previous work, used a Bayesian approach to estimating heterogeneous error and genotype by environment interaction variances applied to yield data from the Iowa State University Oat Variety Trial for the years 1997 to 2003. The objectives were i) to take advantage of technological advances in statistics and computing in order to provide more precise rankings of experimental varieties, and ii) to provide a more precise method for identifying varieties that provide stable performance across varying environmental conditions. In this work we perform a model assessment, i.e., we test whether or not the heterogeneous variance model really provides better predictors of cultivar performance. We used two approaches: Cross-Validation and Posterior Predictive Checking. The first one is a widely used method for estimating prediction error. We set aside a validation set and use it to assess the performance of our prediction model. The second method is a Bayesian approach, where simulated values are drawn from the posterior predictive distribution of replicated data and then compared to the observed data. The dataset has a total of 34 environments and 80 total genotypes, with 40 tested in each year; only some genotypes were tested in all years.

#### 154. On the meaning of Busbice's prediction formula

Sahagún-Castellanos, J., Rodríguez-Pérez, J.E., Villanueva Verduzco, C. and Peña-Lomelí, A.  
Depto. de Fitotecnia, Universidad Autónoma Chapingo, Km 38.5 Carretera México-Texcoco, CP  
56230, Chapingo, México  
E-mail: jsahagun@correo.chapingo.mx

Synthetic varieties (SV) of maize (*Zea mays* L.) are grown worldwide possessing advantages particularly attractive for low-income farmers. In a plant breeding program, however, to identify the best of the numerous SVs that can be derived, plant breeders must resort to prediction. A formula that describes the genotypic mean of a SV ( $Y_2$ ) is Busbice's (1970):

$Y_2 = A + (1 - F_2)B$ , where  $F_2$  is the inbreeding coefficient of the SV; but estimators for  $A$  and  $B$  were not provided. The objective of this work was to determine the existence of the derivation of estimators for them to predict the genotypic mean of a SV derived from  $m$  individuals of each of  $n$  parents. On the basis of the expected genotypic array and mean of the SV,  $A$  is the expected mean of the genotypes formed with two identical-by-descent genes, and if the expected mean of the values of the remaining genotypes of the SV is  $H_e$ ,  $B = H_e - A$ . Only when parents are fully inbred and unrelated can  $A$  and  $B$  be properly estimated. Despite this limitation, based on the definition of  $A$  and  $B$ , it was possible to express  $Y_2$  as linear combinations of the expected means of subpopulations of the SV that can be experimentally evaluated and thus the expected mean ( $Y_2$ ) of the SV can be predicted.

## Index of Authors

Abdullayev, K. Cereal breeding for the drylands of north-eastern Kazakhstan	174
Abertondo, V. and Lee, M. Phenotypic analysis of intermated B73xMo17 (IBM) populations	79
Acosta Roca, R., Ríos Labrada, H., Martínez Cruz, M., Miranda Lorigados, S., Ortiz, R., Ponce Brito, M. Participatory plant breeding: a maize case study from Cuba	107
Ado, S.G., Abdullahi, U.S., Usman, I.S. and Falaki, A.M. Progress in quality protein maize breeding at Samaru, Nigeria	53
Aguirre, A., C. and Crisóstomo P., F. Early testing for inbreeding tolerance in four local maize populations from the Peruvian Andes	108
Ahmed, K.Z., Allam, H.Z., Moussa, A.M. and Ali, M.S.A. Doubled-haploid studies in elite Egyptian bread wheat ( <i>Triticum aestivum</i> L.) cultivars	153
Alarcón-Zúñiga, B., Cervantes-Martinez, T. and Sachiko, I. Morphological and molecular characterization of alfalfa populations adapted to Central Valley of Mexico	32
Alarcón-Zúñiga, B., Cervantes-Martinez, T. and Warburton, M. Heterosis and combining ability of tropical maize in the Central Valley of Mexico: morphological and molecular characterization for silage	109
Arcos, A.L., Medina, S., Narro, L.A. and Salazar, F. Inheritance of callose formation in tropical maize inbreds	110
Asea, G., Bigirwa, G., Vivek, B., Lipps, P.E. and Pratt, R.C. Validation and characterization of candidate resistance quantitative trait loci for host-resistance to multiple foliar pathogens of maize	80
Bauer, A.M. and León, J. Parental selection in self-pollinating crops using breeding values	182
Bayuelo-Jiménez, J.S., López-Gomez, R. and Bahena-Betancourt, L. The role of carbohydrate accumulation in osmotic adjustment of salt-stressed <i>Phaseolus</i> species	33
Bayuelo-Jiménez, J.S., Rivera Alcantar, N., Ochoa, I. Quality attributes of mamey fruit ( <i>Pouteria sapota</i> ) and their potential use in crop improvement	54
Bergvinson, D.J. and García-Lara, S. Consensus mapping for field and storage pest resistance in tropical maize	81
Bespalova, L.A. Results and prospects of breeding wheat in the South of Russia	154
Bhatta, M.R., Ortiz Ferrara, G., Sharma, R.C. Alleviating rural poverty through participatory wheat varietal selection	155

Bradová, J. and Šásek, A. Utilisation of genetic protein markers for the prediction of wheat baking quality	83
Bucheyeki, T.L. and Simon, S.M. Participatory breeding for maize varieties tolerant to maize streak virus in the western zone of Tanzania	111
Burt, A.J., Smid, M.P., Shelp, B.J. and Lee, E.A. High carotenoid maize project: increased accumulation and modified chemical profiles	55
Butruille, D., Diniz Silva, H., Bockelman, D. and Tianxing Zhang Linkage disequilibrium in haploids extracted from old open-pollinated maize varieties and synthetics	84
Cakmak, I. Using wild wheats to improve zinc nutrition of cultivated wheats	56
Castañeda, L. and Graef, G. A national program for quality traits in soybean: Effects of environment	57
Cervantes-Martínez, J.E. Combining ability of tropical and temperate maize inbreds	112
Cervantes-Martínez, J.E., Betanzos-Mendoza, E., Gomez-Montiel, N. and Coutiño-Estrada, B. Heterotic responses of white tropical maize inbred lines	113
Choe, E. and Rocheford, T. Detection of quality trait loci (QTL) for pericarp thickness and ear inflorescence traits in waxy corn	85
Choukan, R. Establishment of heterotic groups within Iranian maize inbred lines	114
Claire Iriarte, T. Compilation, characterization and purification of two native varieties of maize	34
Córdova, H. and Krivanek, A. Yield potential and combining ability of tropical quality protein maize inbred lines	58
Coutiño-Estrada, B. and Marquez-Sanchez, F. Advances in cyclic hybridization based on three prolific corn varieties	115
Cruz Núñez, O. Evaluation of fourteen varieties of high quality protein maize in Honduras	59
Cukadar, B. and Gupta, A. Quantitative trait loci associated with husk traits in maize ( <i>Zea mays</i> , L.)	86
de la Vega, A.J., DeLacy, I.H. and Chapman, S.C. Genetic progress over 20 years of sunflower hybrid release in central Argentina	175
Denic, M., Mariote, D., Chauque, P., Fato, P., Senete, C. and Haag, W. Breeding approaches in simultaneous selection for multiple stress tolerance of quality protein maize	116

Diallo, A.O., Kanampiu, F., Mugo, S., and Mbogo, P. Combining ability of imidazolinone resistant maize inbred lines and performance of their hybrids under <i>Striga</i> infestation	117
Djunusova, M. History of wheat breeding in Kyrgyzstan and current challenges	156
Dotlačil, L., Hermuth, J. and Stehno, Z. European winter wheat landraces and obsolete cultivars and their value for breeding	35
Dreisigacker, S., Warburton, M., van Ginkel, M., Balfourier, F., Xueyong, Z., Miloudi, N., Thachunk, C. and Crossa, J. Genetic characterization of global wheat genetic resources and their wild species	36
El Felah M. and Bettaieb-Ben Kaab L. Barley <i>in situ</i> -conservation: a significant risk	37
Espinosa-Calderón, A., Tadeo-Robledo, M., Gómez-Montiel, N., Sierra-Macías, M., Sandoval, A., Coutiño E.,B., Caballero H.,F., López-Pereira, M., Piña D.V., Martínez M., R. Criss cross and interchange of line order for maize hybrids and seed production in normal and quality protein maize (QPM)	119
Espinosa-Calderón, A., Tadeo-Robledo, M., Gómez-Montiel, N., Sierra-Macías, M., F. Caballero H., A. Palafox C., F. Rodríguez-M., R. Valdivia B., R. Martínez M. Plant breeding, seed production and andro-sterility in normal and quality protein maize (QPM) in Mexico	118
Ewool, M.B., Sallah, P.Y.K., Nelson-Quartey, F. and Menkir, A. Potentials for improving maize for iron, zinc and beta-carotene content in Ghana	60
Fernández, L., Castiñeiras, L., Fundora, Z., Shagarodsky, T., Cristóbal, R., García, M., Giraudy, C., Harper, V., Acuña, G., Puldón, G., Pérez, M.F. and Figueroa, M.B. Variability of maize landraces on farm in two rural areas in Cuba	38
Fuentes López, M.R. Advances in maize biofortification in Guatemala: achievements and perspectives	61
García-Lara, S. and Bergvinson, D.J. Seed deterioration of tropical maize varieties stored under accelerated aging conditions	120
Gelalcha, S., Debelo, D., Yaie, B., Girma, B., and Mamo, B. Grain yield stability of bread wheat genotypes in favorable and stressed environments in Ethiopia	153
Gethi, J.G. Can we reduce maize postharvest losses through host plant resistance?	121
Gevers, H.O. Quality protein maize: a review	62
Gharbi, M.S. Durum wheat breeding in Tunisia: new varieties for the post-green revolution.	158
Gregová, E., Šliková, S. and Mihálik, D. Breeding for breadmaking quality in common wheat ( <i>Triticum aestivum</i> L.) in Slovakia	63

Greplová M., Polzerová H., Vlastníková H. , Kopecký D., Švecová R. , Domkářová J. Development of breeding material using somatic hybridization and polyploidization within the <i>Solanum</i> genus	176
Grudloyma, P. and Prasitwatanaseree, S. Performance of promising tropical late yellow maize hybrids ( <i>Zea mays</i> L.) under water stress conditions in Thailand	122
Gutierrez, L., Jannink, J.-L. and Nason, J. Genetic diversity in cultivated barley and wild barley	39
Hafsi, M., Hadji, A., Pfeiffer, W.H. and Monneveux, P. Leaf senescence and carbon isotope discrimination in durum wheat ( <i>Triticum durum</i> Desf.)	159
Hassan, L. Development of salt tolerant rice varieties using marker assisted selection	87
Hauck, A. and Bohn, M. Stem borer resistance in maize – a joint analysis	88
Hyrkas, L. and Lamkey, K.R. Alternative maize cultivar types for sustainable farming systems	123
Ininda, J., Danson, J., Langat, M., Gichuru, L. and Njuguna, J.G.M. Application of simple sequence repeats to study within and between family variations for resistance to maize streak virus disease	89
Iriany M., R.N., Takdir M., A., Yasin HG, M. and Mejaya, M.J. Tolerance of sixteen maize genotypes to drought stress	124
Islam, A. Maize Research in the Bangladesh Rural Advancement Committee (BRAC)	125
Jlibene, M. Breeding drought tolerant wheat in Morocco: an integrated approach for a complex problem	160
Jones, H., Leigh, F., Mackay, I., Smith, L. and Powell, W. The diversity of European <i>Hordeum vulgare</i> ssp. <i>vulgare</i> landraces for the adaptive trait photoperiod response <i>PPD-H1</i>	40
Khonje, P., Ngwira, P. and Vivek, B. Managing maize diseases through breeding for resistance in Malawi	126
Kinyua M.G., Njau P.N., Wanyera R and Muchui J. The diversity of reaction of bread wheat ( <i>Triticum aestivum</i> ) germplasm to yellow rust ( <i>Puccinia striiformis</i> ) infection over environments and years in Kenya	161
Kirkpatrick, K.M., Lamkey, K.R., Scott, M.P., Moore, K.J., Haney, L.J., Coors, J.G., Lorenz, A.J. Identification and characterization of maize varieties with beneficial traits for biobased industries	127
Kitenge, K.M., Kirubi, D. and Mduruma, Z.O. The status of quality protein maize in Tanzania	64

Kobiljski, B. Use of the TRAP (Trace Relevant Allele Polymorphism) approach in breeding for complex traits – a wheat example	90
Kocourková Z., Bradová J., Kohutová Z., Křenek P., Slámová L., Vlastníková H., Vejl P. Characterization of high molecular weight glutenin of the gene locus Glu-B1 in common wheat ( <i>Triticum aestivum</i> L.)	65
Kohutová, Z., Kocourková, Z., Slámová, L., Vlastníková, H., Křenek, P., Vejl, P. and Zoufalá, J. Molecular markers for leaf rust resistance genes and genes controlling vernalization in wheat	91
Křenek, P., Vlastníková, H., Mazáková, J., Kocourková, Z., Kohutová, Z., Slámová, L., Zouhar, M., Domkařová, J., Škodáček, Z. Development of specific PCR markers for <i>Solanum</i> ssp. late blight resistance genes and detection of their homologues	92
Krivanek, A.F., Córdova, H. and Ramirez, A. Stability and reliability analysis of lowland tropical quality protein maize ( <i>Zea mays</i> ) three-way and single-cross hybrids	66
Leigh, F. and Powell, W. Wheat cytoplasmic diversity	41
Lorea, R.D.; Delucchi, C.; Eyhéabide, G.H.; López, C.G. Identifying Argentine maize populations as a source of favorable alleles for grain yield	42
MacKay, I. and Powell, W. Prospects for association mapping in UK winter wheat	43
Magorokosho, C, Bänziger, M, and Betrán J Genetic diversity for abiotic stress tolerance of maize landraces selected for 100 years in southern Africa	44
Magulama, E.E., Sillote, C.C. and Madriaga, W.Q. Morphology-based grouping and heterotic pattern analysis in ten white Mindanao maize varieties	128
Makumbi, D., Bigirwa, G. and Diallo, A.O. Combining ability and identification of maize three-way cross hybrids adapted to the mid-altitude ecology of Uganda	129
Mamo, B., Gelalcha, S. and Girma, B. Evaluation of bread wheat genotypes in diverse environments of Ethiopia	162
Manirakiza, A., Mbagaye, G. and Barisize, T. Introduction and evaluation of early, stress tolerant and quality protein maize varieties in Burundi	67
Mariote, D., Denic, M., Haag, W., Chauque, P. and Fato, P. Breeding for resistance to Downy Mildew in quality protein maize in Mozambique	130



Mashingaidze, K. Farmer-participatory maize ( <i>Zea mays</i> L.) cultivar evaluation and selection in Eastern Cape province of South Africa	131
Mayor, M.L. and Lee, M. Quantitative trait loci mapping for ear shoot development in maize	93
McIntyre, L. Using mating designs to uncover quantitative trait loci and the genetic architecture of complex traits	94
Mduruma, Z., Twumasi-Afriyie, S., Napir, G., Demmisew, A. and Ombakho, G. Collaboration in Eastern and Central Africa bears fruit: increasing the availability of enhanced maize germplasm.	132
Menkir, A., White, W., Maziya-Dixon, B. and Rocheford, T. Genetic potential for increasing pro-vitamin A content in tropical maize	68
Mongi-Henday, R. and Elanga, A.M. Grain yield potential stability and agronomic performance of some wheat genotypes in the Southern Highlands of Tanzania	163
Moreira, P.M., Santos, J.P., Antunes, M., P., Moura, R., Santos, J.P., Vaz Patto, M.C. and Pêgo, S. Pre-breeding on Portuguese maize landraces: biometric and pest evaluation	45
Moreira, P.M.; Pego, S.; Vaz Patto, C. and Hallauer, A.R. Twenty years of mass selection within the some degree fasciated Portuguese synthetic maize variety 'Fandango'	133
Morgounov, A., Gómez-Becerra, H.F., Abugalieva, A., Massalimov, A., Yessimbekova, M., Muminjanov, H., Zelenskiy, Y., Ozturk, L. and Cakmak, I. Iron and zinc grain density in bread wheat grown in Central Asia	69
Muasya, W.N.P., and Diallo, A.O. Strategies for developing high yielding maize varieties for the dry mid-altitude ecology of Kenya	134
Mugo, S., Gichuki, S.T., Murenga, M., Taracha, C., Songa, J., Bergvinson, D., Hoisington, D. and Pellegrineschi, A. Control of stem borers by Bt maize in confined field trials in Kenya	135
Muongani, D., Mhike, X., Kwazira, K., Madamba, R. Evaluation of maize ( <i>Zea mays</i> L.) hybrids and open pollinated varieties for yield stability in Zimbabwe	136
Najafian, G., Kafashi, A.K. and Jafar-Nejad, A. AMMI analysis of grain yield stability in hexaploid wheat genotypes grown in temperate regions of Iran	164
Najafian, G., Nikooseresht, R., Ghandi, A. and Jafar-Nejad, A. An adapted hexaploid wheat line for late season moisture stress in the temperate zone of Iran	165

Nakamura, H. Genetic variation of common wheat <i>Glu-1</i> alleles in the noodle-culture zone compared with the bread-culture zone	70
Narro, T.P, Hidalgo E., and Jara W. Adaptation of yellow quality protein maize hybrids in Perú	71
Nass, L.L., Fávero, A.P., Bianchetti, L.B. , Ferreira, F.R. and Mendes, R.A. Utilization of autochthonous germplasm in Brazilian pre-breeding programs: <i>Ananas</i> , <i>Arachis</i> , <i>Capsicum</i> and <i>Manihot</i>	46
Negrão S., Jayamani P., Rocheta M., Maçãs B., Mackill D. and Oliveira M.M. Gene pyramiding to improve rice by marker assisted backcrossing	95
Ngaboyisonga, C., Njoroge, K., Kirubi, D. and Githiri, S.M. Effects of low nitrogen and drought on grain yield and endosperm hardness of quality protein maize single cross hybrids	137
Nginamau, D., Mwala, M.S. and Bänziger, M. Implications of genotype-by-environment interactions in maize ( <i>Zea mays L.</i> ) variety selection using mother and baby trials	138
Nigussie, M., Diallo, A.O., Mduruma, Z., Gezahegne B. and Lealem T. Status of quality protein maize research in the drought stressed areas of Ethiopia	72
Novaris, J., Fonseca, R., Grift, T., and Bohn, M. Genetic evaluation of maize root complexity	82
Orellana, M., Edwards, J., Carriquiry, A. and Jannink, J.L. Bayesian modeling of heterogeneous error and genotype by environment interaction variances: model assessment	183
Orquera, E. and Paz, P. 'Valluno', an open pollinated maize variety for the Cruceño valleys of Bolivia	139
Osmanzai, M. Wheat productivity improvement in Afghanistan	166
Palacios-Rojas, N., Beck, D., Bänziger, M., Rocheford, T. and Pixley, K. Genetic variation for improving micronutrient content in maize	73
Parodi, P.C. Nitrogen efficiency use in wheat breeding	167
Pascual, C.B., Guzman, P.S. and Salazar, A.M. Reaction of maize germplasm to <i>Stenocarpella macrospora</i> (Earle) infection and effect of resistance to disease development	140
Pascual, C.B., Salazar, A.M. and Guzman, P.S. Development of multiple disease resistant maize populations and inbreds	141
Pérez Lara, E., Rodríguez, L., García, H. and Valdez, M. Is it possible to complement the Shiltz scale with biochemical and molecular analysis to evaluate tobacco varieties' ( <i>Nicotiana tabacum L.</i> ) resistance to blue mold?	96

Perez, P.T., Ortiz-Perez, E., Cianzio, S.R., Wiley, H., Davis, W.H., Horner, H.T., and Palmer, R.G. Evaluation of heterosis in soybean [ <i>Glycine max</i> (L.) Merr.]	177
Piaskowski, J., Murphy, K., Arterburn, M., Dawson, J., Gollnick, M. and Jones, S. Perennial wheat development for sustainable agriculture in the US Pacific Northwest	168
Poland, J.A., Wisser, R.J., and Nelson, R.J. Recurrent selection mapping in two diverse maize populations selected for northern leaf blight resistance	97
Preciado-Ortiz, R., Guerrero, R., Ortega, A., Terrón, A., Crossa, F., Córdova, H., Reyes, C., Aguilar, G., Tut, C., Gómez, N. and Cervantes, E. Superior quality protein maize (QPM) hybrids for different mega-environments in Mexico using the Biplot methodology	142
Pržulj, N. and Momčilović, V. Effectiveness of early generation selection in winter barley	178
Reddy, B.V.S., Ramesh, S., Longvah, T., Elangovan, M. and Upadhyaya, H.D. Prospects of breeding micronutrient-dense sorghum	74
Romanenko, A.A. and Bespalova, L.A. Winter wheat seed-growing problems imposed by varietal diversity	169
Sahagún-Castellanos, J., Rodríguez-Pérez, J.E., Villanueva Verduzco, C. and Peña-Lomelí, A. On the meaning of Busbice's prediction formula	184
Salazar, F., Narro, L. and Alirio Vallejo, F. General and specific combining ability for phosphorus deficiency in acid soil maize inbreds	143
San Vicente, F. and Garcia, P. Inbreeding depression before and after full-sib recurrent selection in tropical maize	144
Sedlák, P. and Vejl, P. Plant breeding – an important part of study programs at the Czech University of Agriculture in Prague	31
Setimela, P., Vivek, B., Bänziger, M. and Crossa, J. Biplot analysis of early to medium maturing open pollinated maize varieties in southern Africa	145
Sharma, D. and Adhikari, K. Diallel analysis of intermediate to late Nepalese maize inbred lines for grain yield	146
Sharma, R.C., Singh, R.P., Joshi, A.K. and Huerta-Espino, J. New CIMMYT-derived bread wheat germplasm with high yield potential and wide adaptation	170
Shimelis, H., Mashela, P. and Hugo, A. Characterization of vernonia ( <i>Vernonia galamensis</i> var. <i>ethiopica</i> ) as an alternative industrial oil crop in Limpopo Province	75
Sikharulidze, Z. and Natsarishvili, K. Virulence spectrum of wheat leaf and yellow rust in the South Caucasus	170

Silva, H.S. and Rocheford, T.R. Detection of donor alleles for enhanced starch concentration in maize	99
Singh, D., Park, R.F., Bariana, H.S. and Wellings, C.R. Characterization of leaf, stem and stripe rust resistance genes in CIMMYT wheat germplasm	99
Singh, D., Park, R.F., Snape, J., Simmonds, J. and Bariana, H.S. Genetic analysis of resistance to leaf rust in European winter wheat cultivars	100
Singh, R.K., Gregorio, G.B., Adorada, D., Mendoza, R. and Sajise, A.G. Molecular breeding strategy to combine multiple abiotic stress tolerance in rice	101
Slámová, L., Vejl, P., Veškrna, O., Kohutová, Z., Kocourková, Z., Křenek, P. and Vlastníková, H. Detection of the <i>Bdv2</i> gene in some wheat varieties by means of molecular-genetic markers	102
Šliková, S., Vančo, B. and Šudyová, V. Deoxynivalenol content in grain of cereals after artificial inoculation with <i>Fusarium culmorum</i>	179
Son, B.Y., Hyeon-Gui Moon, Tae-Wook Jung, Ja-Hwan Ku, Sun-Lim Kim and Si-Ju Kim Identification of quality protein maize lines by marker assisted selection, differential chemical composition and lysine content analysis	78
Stamati K, Mackay I., Russell J., Booth A., Baum M., Morgante M., Radovic S. and Powell W. <i>Cis</i> -acting regulatory variation in cereals	103
Stehno Z., Dotlačil L., Faberová I., Evaluation of wheat genetic resources in the Czech Republic for their use in breeding	47
Taba, S., Chavez-Tovar, V.H., Rivas, M., Rodriguez, M. and Ramirez, M. Maize genetic resources and prebreeding at CIMMYT International	48
Taboada-Gaytan, O.R., Pollak, L., Johnson, L., Fox, S. and Duvick, S. Wet milling efficiency of hybrids from exotic by adapted inbred lines of corn	76
Takdir M., A., Iriany M., R.N., Isnaeni, M., Mejaya, M.M. and Dahlan, M. Combining ability of CIMMYT maize lines with two Indonesian tester parents	147
Takdir M., A., Iriany M., R.N., Mejaya, M.J. and Dahlan, M.M. Hybrid maize adaptations at several locations in Indonesia	148
The, C., Mafouasson, A., Calba, H., Menkir, A. and Horst, J.W. Establishment of heterotic patterns of maize ( <i>Zea mays</i> L.) inbred lines with tolerance to acid soils	149
Twumasi-Afriyie, S., Nepir, G. and Mduruma, Z. Use of heterotic classification of inbred maize lines to develop hybrids for the highlands of Eastern and Central Africa	150
Upadyayula, N., Bohn, M., Johnson, R. and Rocheford, T. Enhanced detection of inflorescence architecture QTL in Intermated B73 x Mo17 (IBM) RIL population	104

Vanegas Angarita, H., De León, C. and Narro León, L. Inheritance of resistance to <i>Cercospora</i> spp. complex in tropical maize ( <i>Zea mays</i> ) inbred lines	151
Vázquez-Carrillo, G., Ortega Corona, A., Vidal Martínez, V.A., Salinas Moreno, Y., Guerrero Herrera, M., Cota Agramont, O. and Palacios Velarde, O. The protein quality of native maize from northwest Mexico	49
Vejl, P., Melounová, M., Zoufalá, J., Sedlák, P., Blažek, J. and Dandová, M. Application of PCR markers of the <i>Vm</i> and <i>Vf</i> genes controlling apple resistance to <i>Venturia inaequalis</i> in Czech apple breeding	105
Velu, G., Rai, K.N., Muralidharan, V., Kulkarni, V.N., Longvah, T. and Raveendran, T.S. Iron and zinc content in pearl millet grain: genetic variability and breeding implications	77
Vlastníková H. , Křenek P. , Domkářová J. , Kohutová Z. , Kocourková Z. , Slámová Z. and Vejl. P. Estimation of molecular genetic markers used for detection of <i>Phytophthora infestans</i> (Mont.) de Bary in infected plant tissue of some <i>Solanum</i> species	106
Wessel-Beaver, L., Pérez-Maisonave, R., Pérez-Arocho, J. and Segarra, A. Breeding for melonworm resistance in tropical pumpkin	180
White, J., Smith, S., Law, J., Powell, W. and Wolters, P. The genetic diversity of UK and US wheat varieties, 1930 – 2005	50
Worku, M., Abera, W., Tadesse, B., Wolde, L. and Wegary, D. Performance of variety cross hybrids of maize ( <i>Zea mays</i> L.) in the mid-altitude and highland transition areas of Ethiopia	152
Yáñez, C, Franco, J, and Taba, S The core collection of highland Ecuadorian maize genetic resources	51
Yazdan Sepas, A. and Najafi Mirak, T. Wheat breeding in cold regions of Iran	172
Yildirim, M. Heterosis and combining ability in diallel F <sub>1</sub> offspring of six selected bread wheat ( <i>Triticum aestivum</i> L.) cultivars	173
Zencirci, N. and Karagoz, A. Effect of developmental stage length on yield and some quality traits of Turkish durum wheat ( <i>T. turgidum</i> L. Conv. <i>durum</i> (Desf.) M. K.) landraces	52
Zhang, X.G., Humphries, A. and Auricht, G.C. How many genes might be involved in aluminium stress tolerance in alfalfa ( <i>Medicago</i> <i>sativa</i> L.)?	181

## Mexico City Center – local information

Map of the area

The Hotel Sheraton is located at:

Avenida Juarez 70, Colonia Centro, Mexico City, Distrito Federal 06010, Mexico.

Telephone number: (52) (55) 51 30 53 00



Restaurants in the area

Restaurants in the vicinity of The Sheraton Hotel include:

- **Danubio** (Fish and seafood): República de Uruguay, No. 3. Col. Centro Histórico. Tel.: 55 21 09 76.
- **El Cardenal** (within the Sheraton Hotel):
- **Los Girasoles** (Mexican): Tacuba, No. 8. Col. Centro Histórico. Tel.: 55 10 06 30
- **Mercaderes** (International and Mexican): Av. 5 de Mayo, No. 57. Col. Centro Histórico. Tel.: 55 10 22 13.
- **Café Tacuba** (Mexican): Tacuba, No. 28. Col. Centro Histórico. Tel.: 55 12 84 82.
- **El Encino** (International and Argentine): Insurgentes Sur, No. 3846. Col. Centro Histórico. Tel.: 56 65 50 00.
- **Centro Castellano** (European and Spanish): Mariano Escobedo, No. 700. Col. Anzures. Tel.: 52 27 72 00.

## Points of interest

- Centro Histórico (Historic Center): The area around the *Zócalo* (central square) and cathedral, with numerous colonial palaces, churches, squares and museums.
- Palacio de Bellas Artes (Fine Arts Palace): Includes murals by the four most famous Mexican painters (Rivera, Siqueiros, Orozco and Tamayo).
- The Alameda Central: Mexico City's first park, with many fountains and trees, a popular family meeting point.
- Paseo de la Reforma: The principal avenue of Mexico City, stretching between the Alameda and Chapultepec Park, lined with sculptures and modern architecture.
- Museums: Diego Rivera, Museo Nacional de Arte (National Art Museum), Franz Mayer, Museo Nacional de Antropología (National Anthropology Museum)

