

45th Annual Maize Genetics Conference.
March 13th-16th 2003.

Thursday, March 13

5:30-7:00 PM DINNER

7:00-7:15 PM **Announcements**

Dave Jackson

Session 1 EVENING SESSION

7:15-9:15 pm

Chair: Sarah Hake

7:15-8:00 PM **Neelima Sinha, University of California, Davis, CA**

The Development and Evolution of Leaves

8:15-9:00 PM **Vicki Vance, University of South Carolina, Columbia, SC**

Suppression of RNA Silencing in Plants: The Role of Small Regulatory RNAs

9:15 PM **Informal Poster Viewing (hang Posters Thursday Night)**

BEER & SNACKS AVAILABLE IN POSTER AREA UNTIL 1:00 AM

Friday, March 14

7:00-8:30 AM BREAKFAST

Session 2 GENE REGULATION AND GENOMICS 8:30-10:20 am Chair: Bob Meeley

- 8:30-8:45 **Lyudmila Sidorenko, University of Arizona, Tucson, AZ**
Identification of cis-acting regulatory sequences and trans-acting regulatory factors are the stepping stones to the elucidation of the mechanism of p1 paramutation
8:45-8:50 Discussion
- 8:50-9:05 **Julia Marcela Hernandez, Ohio State University, Columbus**
Transcriptional regulation of the flavonoid biosynthetic pathway: the dual role of the HLH coactivator R/B
9:05-9:10 Discussion
- 9:10-9:25 **David W. Galbraith, University of Arizona, Tucson, AZ**
The future of maize expression arrays: what can we learn from working with Zea and Arabidopsis?
9:25-9:30 Discussion
- 9:30-9:45 **Trent Seigfreid, Iowa State University, Ames, IA**
Maize GDB: A Next Generation Maize Database
9:45-9:50 Discussion
- 9:50-10:00 **Brad Barbazuk, Donald Danforth Plant Science Center, St. Louis, MO**
The Maize genome Sequencing Project at the Donald Danforth Plant Science Center
- 10:00-10:10 **Cathy Whitelaw, The Institute for Genomic Research, MD**
Consortium for Maize Genomics - Approach Evaluation for Targeted Sequencing of Maize Genes
10:10-10:20 Discussion

10:20-10:50 am - BREAK WITH BEVERAGES

Session 3 DEVELOPMENTAL GENETICS 10:50-12:30 pm Chair: Gunter Feix

- 10:50-11:05 **George Chuck, Plant Gene Expression Center, Albany, CA**
The Control of Spikelet Meristem Development by the branched silkless1 Gene
11:05-11:10 Discussion
- 11:10-11:25 **John Fowler, Oregon State University, Corvallis, OR**
A Role for Maize ROP2 GTPase in the Male Gemetophyte
11:25-11:30 Discussion
- 11:30-11:45 **Peter Rogowsky, RDP, ENS-Lyon France**
ZmPRPL35-1 encodes a plastid ribosomal protein required for suspensor morphogenesis in maize embryos
11:45-11:50 Discussion
- 11:50-12:05 **Peter Bommert, University of Koln, Koln, Germany**
Thick tassel dwarf1 encodes a LRR-receptor kinase with high homology to CLAVATA1
12:05-12:10 Discussion
- 12:10-12:25 **Erik Vollbrecht, Cold Spring Harbor Laboratory, New York**
Molecular and evolutionary analysis of ramosa1 in inflorescence architecture
12:25-12:30 Discussion

12:30-1:30 PM - LUNCH

Friday, March 14 Cont'd

1:30-3:30 pm - POSTER SESSION - Contributors will be at EVEN-NUMBERED Posters

3:00-3:30 pm - BEVERAGES SERVED

Session 4	MAIZE GENOMICS WORKSHOP	3:30-5:30 pm	Chair: Pat Schnable
3:30-3:35	Introductory Remarks		
3:35-3:50	John Bon, Affymetrix <i>Expression analysis in plants: a look at some approaches to array design using GeneChip technology</i>		
3:50-4:05	Sean Coughlan, Agilent Technologies Inc. <i>Global analysis of gene expression using high density in situ 60mer oligonucleotide arrays: Applications to Maize</i>		
4:15-5:30	Genomic Posters <i>Here many of the recipients of NSF funded genome grants for maize research will present the goals of their projects and highlight the deliverables to be provided to the maize community.</i>		

6:00-7:30 pm - DINNER

Session 5	EVENING SESSION	7:30-9:00 pm	Chair: Mike Scanlon
7:30-8:15	Susan McCouch, Cornell University, Ithaca, New York <i>Identifying genes and functional nucleotide polymorphisms underlying QTLs in rice</i>		
8:30-9:15	Steven Henikoff, HHMI-FHCRC, University of Washington, Seattle, WA <i>Traditional Genetics Meets Functional Genomics</i>		
9:30	Informal Poster Viewing		

BEER & SNACKS AVAILABLE IN POSTER AREA UNTIL 1:00 am

Saturday, March 15

7:00-8:30 AM BREAKFAST

Session 6 GENOME ORGANIZATION AND EVOLUTION 8:30-10:10 am Chair: Lynn Senior

- 8:30-8:45 **Yves Vigouroux, University of Wisconsin, Madison, WI**
Population structure and gene diversity of american maize landraces
8:45-8:50 Discussion
- 8:50-9:05 **Volker Brendel, Iowa State University, Ames, IA**
The genomic origin of maize revisited
9:05-9:10 Discussion
- 9:10-9:25 **William Sheridan, University of North Dakota, Grand Forks, ND**
Global Analysis of the Maize Genome: Relating Genes and DNA Sequences to Chromosome Regions
9:25-9:30 Discussion
- 9:30-9:45 **Shavannor Smith, Kansas State University, Manhattan, KS**
Identification and Characterization of Rp1 Genes with Novel Phenotypes in Maize
9:45-9:50 Discussion
- 9:50-10:05 **Ning Jiang, University of Georgia, Athens, GA**
Identifying active DNA transposons in the genomic era
10:05-10:10 Discussion

10:10-10:40 am - BREAK WITH BEVERAGES

Session 7 TRANSPOSONS AND CYTOGENETICS 10:40-12:20 pm Chair: Dave Weber

- 10:40-10:55 **Robert Meeley, Pioneer Hi-Bred Intl. Inc., Johnston, IA**
Diagnosis of hot spots for Mu integration in the maize genome and their association with binding sites for host-encoded nuclear protein(s)
10:55-11:00 Discussion
- 11:00-11:15 **Jianbo Zhang, University of Iowa, Ames, IA**
Transposition of Reversed Ac Element Ends Shuffles Exons and Rearranges Chromosomes in Maize
11:15-11:20 Discussion
- 11:20-11:35 **Rebecca Mroczek, University of Georgia, Athens, GA**
Distribution of retroelements in centromeres and neocentromeres of maize
11:35-11:40 Discussion
- 11:40-11:55 **Stephen Stack, Colorado State University, Fort Collins, CO**
Cytological crossover maps for all maize bivalents using recombination nodules
11:55-12:00 Discussion
- 12:00-12:15 **Zac Cande, University of California, Berkeley, CA**
The pathway of early meiotic prophase events in maize
12:15-12:20 Discussion

12:20-1:30 pm - LUNCH

Saturday, March 15 Cont'd

1:30-3:30 pm - POSTER SESSION - Contributors will be at ODD-NUMBERED Posters

3:00-3:30 pm - BEVERAGES SERVED

Session 8	QTL: Practical Aspects and New Approaches.	3:30-5:30 pm	Chair: Torbert Rocheford
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Oral workshop presentations of 10 min. approx. will be followed by an open discussion

Torbert Rocheford, University of Illinois, Champaign-Urbana, IL

Overview of Maize QTL Studies

Mike Lee, Iowa State University, Ames, IA

Map Construction and Use for Mutant Clone & QTL Mapping

Martin Bohn, University of Illinois, Champaign-Urbana, IL

Methodologies of QTL Analysis and Statistical Considerations

Mike McMullen, University of Missouri, Columbia, MO

QTL Approaches to study of a Pathway

Nick Lauter, University of Illinois, Champaign-Urbana, IL

High Resolution Mapping and functional Dissection of QTL Affecting Leaf Epidermal Traits

Ed Buckler, USDA-ARS, North Carolina State University, NC

Principles of Associative Genetic Analysis

6:00-7:30 pm - DINNER

Session 9	EVENING SESSION	7:30-8:30 pm	Chair: Daniel Grimanelli
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7:30-8:15 **Hugo K. Dooner, Waksman Institute, Rutgers University, Piscataway, NJ**

Convergence of genetics and genomics at a bronze point in the map

BEER & SNACKS AVAILABLE IN EVERGREEN THEATER

Sunday, March 16

Session 10	BIOCHEMICAL AND SEED GENETICS	9:00-10:40 am	Chair: Martha James
9:00-9:15	Tim Porch, University of Florida, Gainesville, FL <i>Initial cloning and characterization of vp13 in maize</i>		
	9:15-9:20 Discussion		
9:20-9:35	Christopher Goodman, Stanford University, Stanford, CA <i>A multidrug-resistance associated protein involved in anthocyanin transport in Zea mays</i>		
	9:35-9:40 Discussion		
9:40-9:55	Cynthia Gallagher, City University of New York, Bronx, NY <i>Characterization of gene families that influence maize endosperm carotenoid content</i>		
	9:55-10:00 Discussion		
10:00-10:15	Joao Leiva-Neto, University of Arizona, Tucson, AZ <i>Expression of a dominant negative mutant of cyclin-dependent kinase A (ZmCDKA) reduces DNA endoreduplication during maize endosperm development</i>		
	10:15-10:20 Discussion		
10:20-10:35	Bo Shen, Pioneer Hi-Bred International, Inc., Johnston, IA <i>The supernumerary maize aleurone layer gene <i>superal1</i> encodes an orthologue of the human CHMP family member of class E vacuolar sorting proteins</i>		
10:40	FINAL ANNOUNCEMENTS		
10:45	ADJOURN, Beverages available.		