

43rd Annual Maize Genetics Conference

2001

THURSDAY, 15 MARCH

6:00-7:30 Dinner

7:15-7:30 PM **ANNOUNCEMENTS** **Torbert Rocheford**

7:30-9:00 PM **PLENARY TALKS** **Chair: Sue Wessler**

7:30 Kelly Dawe, University of Georgia
Abnormal chromosomal segregation: meiotic drive and neocentromeres

8:15 June Nasrallah, Cornell University
Evolution of breeding systems in crucifers, from outcrossing to autogamous in one step

9:00 PM Informal Poster Viewing, Hang Posters Thursday Night

BEER WILL BE AVAILABLE IN POSTER AREA UNTIL 1:00 AM

FRIDAY, 16 MARCH

7:00-8:30 AM BREAKFAST

8:30-10:10 AM **Session 1 THE PLANT** **Chair: John Doebley**

8:30 Erica Unger, Pioneer Hi-Bred Intl.
Ligand-dependent expression of MS45 results in the conditional regulation of male fertility in maize.

8:45-8:50 Discussion

8:50 Patricia Bedinger, Colorado State University
The male-sterile mutants of maize

9:05-9:10 Discussion

9:10 Mark Running, University of California - Berkeley
Regulation of meristem function by *thick tassel dwarf1* and interacting genes

9:25-9:30 Discussion

9:30 Erik Vollbrecht, Cold Spring Harbor Laboratory
The *ramosa1* gene regulates inflorescence architecture and encodes a small zinc finger protein

9:45-9:50 Discussion

9:50 Frank Baker, University of California - Berkeley

The glossy early flowering gene is required for proper embryogenesis and plant development

10:05-10:10 Discussion

10:10-10:40 BREAK WITH BEVERAGES

10:40-12:20 PM Session 2 THE GENOME Chair: Bob Meeley

10:40 Xiaoyu Zhang, University of Georgia

Isolation of a novel autonomous class 2 (DNA) element with strong target site preference and MITE family members

10:55-11:00 Discussion

11:00 Nathan Springer, University of Wisconsin

Identification of the genes involved in the establishment and interpretation of DNA methylation patterns in maize

11:15-11:20 Discussion

11:20 Maïke Stam, University of Arizona

Sequences between ~90 and 103 kb upstream of the *b1* transcription start site are required for paramutation and for high expression of the *b1* gene

11:35-11:40 Discussion

11:40 George Rudenko, Stanford University

Post-transcriptional regulation and epigenetic control of the *MuDR/Mu* transposon family in maize

11:55-12:00 Discussion

12:00 Surinder Chopra, Pennsylvania State University

Comparative analysis of regulation of phlobaphene biosynthesis in maize and sorghum

12:15-12:20 Discussion

12:30-1:30 PM LUNCH

POSTER SESSION

1:30-3:00 Contributors will be at ODD-NUMBERED posters

BEVERAGES WILL BE AVAILABLE FROM 3:00-3:30

3:30-5:00 Contributors will be at EVEN-NUMBERED posters

DINNER 5:30-6:30

7:00 – 10:00 PM RICE GENOMICS WORKSHOP Chair: Sue Wessler

Objective: To showcase rice as the anchor organism for grass genomics. To bring the maize community up to date on the rapid advances in rice sequencing and gene discovery. To make the community aware of the resources currently available/accessible (databases and comparative genomic web tools). To hear how the international genome sequencing project is progressing and integrating Monsanto's sequence/BACs/fingerprints and how Syngenta's recent announcement will impact all of the above. To foster a community wide panel discussion on opportunities/future strategies for maize geneticists to use rice and the roles of maize and rice in a collective grass model system.

Takuji Sasaki, National Institute of Agrobiological Resources – Rice genome sequencing efforts in IRGSP and RGP

Rod Wing, Clemson University – The CCW rice genome sequencing consortium: Sequencing the short arms of chromosomes 10 and 3

Gerard Barry, Monsanto - Where the Monsanto rice sequence fits in

Steven Briggs, Syngenta – Impact of Syngenta's recent announcement on rice

D. McElroy, Maxygen - Targeted deletions in rice

BREAK WITH REFRESHMENTS SERVED INCLUDING BEER

Sue Wessler, University of Georgia – The transposable elements of rice

Robin Buell, The Institute for Genomic Research – The TIGR rice genome project: Sequence and tools for plant biologists

Masahiro Yano, National Institute of Agrobiological Resources – Naturally occurring variations as a new resource for functional genomics in rice

Group Discussion - Moderator - **Jeff Bennetzen**

Panel Participants - All of above and **Ben Burr, Jo Messing, Mike Freeling**

POSTER SESSION

10:00-10:30 Contributors will be at ODD-NUMBERED posters

10:30-11:00 Contributors will be at EVEN-NUMBERED posters

BEER WILL BE AVAILABLE IN POSTER AREA UNTIL 1:00 AM

SATURDAY 17 MARCH

7:00-8:30 AM BREAKFAST

8:30-10:10 AM Session 3 THE SEED Chair: Al Kriz

8:30 Garg Preeti, Institut für Allgemeine Botanik

The Etched 1 gene product of *Zea mays* contains a zinc ribbon-like domain and is homologous to the eucaryotic transcription elongation factor TFIIIS

8:45-8:50 Discussion

8:50 Ed Buckler, USDA-ARS, North Carolina State University

Starch debranching enzyme sugary1 is key to maize kernel phenotypes and domestication

9:05-9:10 Discussion

9:10 Martha James, Iowa State University

Allelic variation at the *sugary1* locus provides insight into the molecular mechanisms of starch biosynthesis

9:25-9:30 Discussion

9:30 Paul Mathews, Lehman College - City University of New York

Maize phytoene desaturase (PDS) and zeta-carotene desaturase (ZDS) produce poly-Z-lycopene: Implications for genetic manipulation of carotogenesis in maize and rice

9:45-9:50 Discussion

9:50 Joanna Cross, University of Florida

ADP-Glucose Pyrophosphorylase activity from maize-potato mosaics

10:05-10:10 Discussion

10:10-10:40 BREAK WITH BEVERAGES

10:40-12:20 PM Session 4 ORGANELLES/PLANT DEFENSE

Chair: Becky Boston

10:40 David Stern, Cornell University

Mitochondrial RNA Polymerase: Reverse Genetics and Biochemistry

10:55-11:00 Discussion

11:00 Chris Chase, University of Florida

Programmed cell death in S male-sterile maize

11:15-11:20 Discussion

11:20 John Gray, University of Toledo

The cell death suppressing function of *lls1*, (*lethal leaf spot 1*) involves protecting chloroplast integrity

11:35-11:40 Discussion

11:40 Anke Lehmensiek, University of Stellenbosch

Genetic Mapping of gray leaf spot (GLS) resistance genes in maize

11:55-12:00 Discussion

12:00 Monika Frey, Technische Universitaet Muenchen

An herbivore elicitor activates the gene for indole emission in maize

12:15-12:20 Discussion

12:30-1:30 PM LUNCH

POSTER SESSION

1:30-2:20 PM Contributors will be at ODD-NUMBERED posters

BEVERAGES WILL BE AVAILABLE FROM 3:00-3:30

2:20-3:10 PM Contributors will be at EVEN-NUMBERED posters

3:30 – 6:00 PM MAIZE GENOMICS & FUTURE DIRECTIONS WORKSHOP

Chair: Torbert Rocheford

Donal O'Sullivan, University of Bristol – High resolution mapping of a 550 kb YAC contig spanning the *rp1* disease resistance locus

Michele Morgante, DuPont Agricultural Genomics – Construction of a physical map for positional cloning in corn: ESTs, SNPs and BACs

Pablo Rabinowicz, Cold Spring Harbor Laboratory – Using methylation filtered maize clones to identify new Mutator insertions in the Maize Targeted Mutagenesis

Paul Chomet, Monsanto – A Novel Method of Insertion Detection in Maize

Thomas Brutnell, Boyce Thompson Institute – Genome Mutagenesis Utilizing Ac in Maize

Kan Wang, Iowa State University – Agrobacterium-mediated transformation of maize Hi II immature zygotic embryos using a simple binary vector system

Antoni J Rafalski, DuPont Agricultural Genomics – Identification and uses of single nucleotide polymorphisms (SNPs) in maize

Donald McCarty, University of Florida – A functional genomics approach to endosperm development

BREAK WITH REFRESHMENTS INCLUDING BEER

Ken Feldman, CERES – Comparative genomics of *Zea* and *Arabidopsis* from a collection of full length cDNAs

Ed Coe, USDA-ARS, University of Missouri –Maize Genomics and MaizeDB

Evgueni Ananiev, Pioneer Hi-Bred Intl. – Long microsatellites in corn genome

Vicki Chandler, University of Arizona – Maize Gene Discovery Project: Microarray Production and Analysis

Maize Genetics Executive Committee Presentation/Discussion on Future Directions of the Community

Objective: A short description of the activities of the Maize Genetics Executive Committee over the last 12 months, followed by an open discussion of the community's ideas on what is needed to move maize forward as a genetic system. Featured issues will include the maize databases, maize genome sequencing, technology development, and possible implementation strategies.

6:00-7:00 Dinner

7:30-9:00 PM **PLENARY TALKS** **Chair: John Doebley**

7:30 **Laurie Smith, University of California - San Diego** – Cell biology of maize leaf development

8:15 **Alice Barkan, University of Oregon** – Genetic dissection of chloroplast gene expression: a tale of two gene families

9:00 PM **Informal Poster Viewing**

Informal Reception in Evergreen Room

BEER WILL BE PROVIDED UNTIL 1 AM

SUNDAY 18 MARCH

7:30-9:00 AM BREAKFAST

9:00-10:40 AM Session 5 THE GENE Chair: Dave Weber

9:00 Mike Scanlon, University of Georgia

Cloning of *narrow sheath2*, a duplicate factor gene required for recruitment of a lateral domain in the maize leaf

9:15-9:20 Discussion

9:20 Charles Dietrich, Iowa State University

Beta-keto acyl reductase activity is essential for maize development

9:35-9:40 Discussion

9:40 Shailesh Lal, Iowa State University

Discovery and Characterization of Maize Alternatively Spliced Genes by EST Analysis

9:55-10:00 Discussion

10:00 Sheila McCormick, University of California - Berkeley Isolation and characterization of sperm-expressed genes in *Zea mays*

10:15-10:20 Discussion

10:20 Jose Gutierrez-Marcos, Oxford University

Isolation of maize genes with an imprinted pattern of expression

10:35-10:40 Discussion

Break with Beverages

11:00 Meeting Adjourned (See you next year in Orlando!)