

## Schedule of Events

**Talks will be held in Convention Hall 2 on the second floor.  
Posters will be displayed in the Exhibition Hall on the first floor.**

### Thursday, March 13

2:00 PM – 6:00 PM	<b>OPTIONAL PRE-CONFERENCE WORKSHOPS</b>
12:00 PM – 2:00 PM	<b>Positional Cloning in Maize Workshop</b> (Conference Room 303)
2:00 PM – 3:00 PM	<b>MaizeGDB Basics Workshop</b> (Conference Room 303)
3:00 PM – 4:00 PM	<b>MaizeGDB Advanced Workshop</b> (Conference Room 303)
4:00 PM – 6:00 PM	<b>Gramene Workshop</b> (Conference Room 303)
	<i>Pre-registration recommended for the above sessions.</i>
3:00 PM – 6:00 PM	<b>REGISTRATION</b> (Hotel Lobby)
3:00 PM – 6:00 PM	<b>POSTER HANGING</b> (Exhibition Hall)
6:00 PM – 7:00 PM	<b>DINNER</b> (Hotel Dining Rooms)
7:00 PM – 9:00 PM	<b>SESSION 1 – PLENARY TALKS</b> Chair: Wes Bruce <span style="float: right;">Pages 19 &amp; 20</span>
7:00 PM	<b>WELCOME AND ANNOUNCEMENTS</b> (Convention Hall #2) Ann Stapleton and Wes Bruce
7:15 PM	<b>Tom Brutnell, Donald Danforth Plant Science Center</b> [Plen 1] <i>A systems approach to understanding photosynthetic differentiation in the grasses</i>
8:05 PM	<b>Jiayang Li (李家洋), Chinese Academy of Sciences &amp; Chinese Academy of Agricultural Sciences</b> [Plen 2] <i>Molecular basis for designing high-yield and good-quality rice</i>
7:00 PM – 9:00 PM	<b>REGISTRATION</b> (Hotel Lobby)
9:00 PM – 11:59 PM	<b>INFORMAL POSTER VIEWING &amp; HOSPITALITY</b> (Exhibition Hall)
12:00 AM	<b>HOSPITALITY</b> (Café Restaurant)

## **Friday, March 14**

7:00 AM – 8:00 AM	<b>BREAKFAST</b> (Hotel Dining Rooms)
7:00 AM – 8:15 AM	<b>REGISTRATION</b> (Hotel Lobby)
8:15 AM – 9:55 AM	<b>SESSION 2 - DEVELOPMENTAL GENETICS, QUANTITATIVE GENETICS I</b> Chair: Peter Balint-Kurti Talks 1-5. Pages 24 - 28
8:00 AM	<b>ANNOUNCEMENTS</b> (Convention Hall #2) Ann Stapleton and Jinsheng Lai
8:15 AM	<b>George Chuck, USDA-ARS</b> [T1] <i>The SPB-box transcription factors unbranched2 and unbranched3 function redundantly with tasselsheath4 to regulate plastochron index</i>
8:35 AM	<b>Davide Sosso, Stanford University</b> [T2] <i>SWEET transporters and seed filling: tools for plants or opportunities for pathogens?</i>
8:55 AM	<b>Andrea Gallavotti, Rutgers University</b> [T3] <i>Auxin signaling in the early steps of maize inflorescence development</i>
9:15 AM	<b>Madelaine Bartlett, Brigham Young University</b> [T4] <i>The B-class mutant sterile tassel silky ear1 (sts1) provides a window into both conserved and divergent aspects of maize floral development</i>
9:35 AM	<b>Rachel Egger, Stanford University</b> [T5] <i>Transcriptomes and Proteomes Define Gene Expression Progression in Pre-meiotic Maize Anthers</i>
9:55 AM	<b>BREAK</b>
10:30 AM – 12:10 PM	<b>SESSION 3 – DEVELOPMENTAL GENETICS, QUANTITATIVE GENETICS II</b> Chair: Feng Tian Talks 6-10. Pages 29 - 33
10:30 AM	<b>Bao-Cai Tan, The Chinese University of Hong Kong</b> [T6] <i>Small kernell1 encodes a pentatricopeptide repeat protein required for mitochondrial nad7 transcript editing and seed development in maize and rice</i>
10:50 AM	<b>Andrea Eveland, Cold Spring Harbor Laboratory</b> [T7] <i>Regulatory networks controlling maize inflorescence architecture and the interface with early season drought responses</i>
11:10 AM	<b>Chung-Ju Rachel Wang, Academia Sinica</b> [T8] <i>DSY2 is required for meiotic recombination and synaptonemal complex formation</i>
11:30 AM	<b>Peter Bradbury, USDA-ARS</b> [T9] <i>The distribution of recombination breakpoints and their association with genomic features in two maize NAM populations</i>
11:50 AM	<b>Guohua Mi, China Agricultural University</b> [T10] <i>Enhancement of phosphorus efficiency through genetic improvement of root architecture in maize</i>

## **Friday, March 14 (continued)**

- 12:30 PM – 1:30 PM      **LUNCH** (Hotel Dining Rooms)
- 1:30 PM – 5:00 PM      **POSTER SESSION 1** (Exhibition Hall)
- 1:30 PM – 3:00 PM      *Presenters should be at **odd** numbered posters.*
- 3:00 PM – 4:30 PM      *Presenters should be at **even** numbered posters.*
- Beverages will be available from 3:30 PM to 5:00 PM.*

### **4:00 PM – 6:00 PM      OPTIONAL CONFERENCE WORKSHOP**

- 4:00 PM – 6:00 PM      **iPlant Collaborative Workshop** (Conference Room 303)
- Pre-registration recommended for the above workshop.*
- 6:00 PM – 7:00 PM      **DINNER** (Hotel Dining Rooms)

### **7:00 PM – 8:15 PM      SESSION 4 – MCCLINTOCK PRIZE WINNER**

Chair: Jeff Bennetzen      McClintock talk 1. Page 23

- 7:00 PM      **Introduction**  
Jeff Bennetzen
- 7:10 PM      **Prof. Sir David Baulcombe, University of Cambridge** [M1]  
*When genomes meet – RNA, epigenetics and phenotypes of hybrid plant*
- 8:15 PM – 11:59PM      **INFORMAL POSTER VIEWING & HOSPITALITY**  
(Exhibition Hall)
- 12:00 AM      **HOSPITALITY**  
(Café Restaurant)

## Saturday, March 15

7:00 AM – 8:00 AM	<b>BREAKFAST</b> (Hotel Dining Rooms)	
8:00 AM – 9:55 AM	<b>SESSION 5 – BIOCHEMICAL GENETICS, QUANTITATIVE GENETICS, RESOURCES I</b>	
	Chair: Gernot Presting	Talks 11-15. Pages 34 - 38
8:00 AM	<b>ANNOUNCEMENTS</b> Ann Stapleton and Jinsheng Lai	(Convention Hall #2)
8:15 AM	<b>Bailin Li, DuPont Pioneer</b> <i>Cloning and Characterization of a Major QTL for Northern Leaf Blight Resistance from Two Resistant Lines in Maize</i>	[T11]
8:35 AM	<b>Mingliang Xu, China Agricultural University</b> <i>A wall-associated kinase ZmWAK confers quantitative resistance to head smut in maize</i>	[T12]
8:55 AM	<b>Xiquan Gao, Nanjing Agricultural University</b> <i>Functional genomics analysis of maize 9-lipoxygenase gene family and 9-oxylipins in the basal resistance to ear rot and stalk rot caused by Fusarium spp. and the induced systemic resistance to anthracnose leaf blight by Colletotrichum graminicola</i>	[T13]
9:15 AM	<b>Alex Lipka, Cornell University</b> <i>Inference of metabolic pathway dynamics through quantitative genetics: a story of maize grain carotenoids in the nested association mapping panel</i>	[T14]
9:35 AM	<b>Jinliang Yang, Iowa State University</b> <i>GWAS for Trait-Associated SNPs that Exhibit Dominance Effects Provides Insight Into the Origin of Heterotic Groups</i>	[T15]
9:55 AM	<b>BREAK</b>	
10:30 AM – 12:10 PM	<b>SESSION 6 – BIOCHEMICAL GENETICS, QUANTITATIVE GENETICS, RESOURCES II</b>	
	Chair: Milena Ouzenva	Talks 16-20. Pages 39 - 43
10:30 AM	<b>Mei Guo, DuPont Pioneer</b> <i>Maize ARGOS1 (ZAR1) Transgenic Alleles Increase Hybrid Maize Yield</i>	[T16]
10:50 AM	<b>Xiaohuan Sun, VIB and Ghent University</b> <i>Mild drought specifically affects the transition between cell division and cell expansion in the growing maize leaf</i>	[T17]
11:10 AM	<b>Leandro G. Neves, RAPiD Genomics</b> <i>Maize Genotyping using RAPiD-Seq (Randomly-Amplified Polymorphic DNA Sequencing)</i>	[T18]
11:30 AM	<b>Doreen Ware, USDA-ARS; Cold Spring Harbor Laboratory</b> <i>Gramene: A Resource for Comparative Plant Genomics</i>	[T19]
11:50 AM	<b>Gerry Neuffer, University of Missouri</b> <i>Mutagenesis; characterization and evaluation</i>	[T20]

## **Saturday, March 15**

- 12:30 PM – 1:30 PM      **LUNCH** (Hotel Dining Rooms)
- 1:30 PM – 5:00 PM      **POSTER SESSION 2** (Exhibition Hall)
- 1:30 PM – 3:00 PM      *Presenters should be at **even** numbered posters.*
- 3:00 PM – 4:30 PM      *Presenters should be at **odd** numbered posters.*

*Beverages will be available from 3:30 PM to 5:00 PM.*

- 4:30 PM – 5:45 PM      **COMMUNITY SESSION - Maize Genetics Executive Committee**  
MGEC Chair: Jeff Bennetzen

- 6:00 PM – 7:00 PM      **DINNER** (Hotel Dining Rooms)

- 7:15 PM – 8:55 PM      **SESSION 7 – PLENARY TALKS**  
Chair: David Jackson Pages 21 & 22

- 7:15 PM      **Graeme Hammer, University of Queensland** [Plen 3]  
*Molecular breeding for complex adaptive traits – how integrating crop  
ecophysiology and modelling can enhance efficiency*

- 8:05 PM      **Toby Kellogg, Donald Danforth Plant Science Center** [Plen 4]  
*Polyploidy in maize and its relatives*

- 9:00 PM – 11:59 PM      **INFORMAL POSTER VIEWING** (Exhibition Hall)

- 12:00 AM      **HOSPITALITY**  
(Café Restaurant)

## Sunday, March 16

7:00 AM – 8:20 AM **BREAKFAST** (Hotel Dining Rooms)

**Posters should be taken down by 9 am!**

8:20 AM – 10:10 AM **SESSION 8 – DEVELOPMENTAL GENETICS, GENOME I**  
Chair: Phil Becraft Talks 21-25. Pages 44 - 48

8:20 AM **ANNOUNCEMENTS** (Convention Hall #2)  
Ann Stapleton and Jinsheng Lai

8:30 AM **Faqlang Li, University of Wisconsin** [T21]  
*Characterization of Maize Autophagy System Reveals a Central Role in Nitrogen Remobilization*

8:50 AM **Phil Taylor, Monsanto Company** [T22]  
*Expression of Arabidopsis thaliana HB17 gene in corn leads to improved sink potential*

9:10 AM **Cristian Forestan, University of Padova** [T23]  
*ZmHDA108 has an active role both in setting the histone code and controlling plant vegetative and reproductive development of maize.*

9:30 AM **Bob Meeley, DuPont Pioneer** [T24]  
*Impairment of a Chitinase-like1 is responsible for the phenotype of a brittle stalk mutant of maize*

9:50 AM **Felix Seifert, University of Hamburg** [T25]  
*Distinct small RNA populations act antagonistically in heterosis formation of maize*

10:10 AM **BREAK**

10:30 AM – 11:50 AM **SESSION 9 – DEVELOPMENTAL GENETICS, GENOME II**  
Chair: Mark Settles Talks 26-29. Pages 49 - 52

10:30 AM **Silong Sun, China Agricultural University** [T26]  
*De novo assembly of Maize Mo17 genome and its comparison with B73 genome*

10:50 AM **Haijun Liu, Huazhong Agricultural University** [T27]  
*Genomic, transcriptomic and phenomic variation reveals the complex adaptation of modern maize breeding*

11:10 AM **Jeff Gustin, University of Florida** [T28]  
*Machine vision phenotyping uncovers novel relationships between kernel and seedling characteristics*

11:30 AM **Jeff Bennetzen, University of Georgia** [T29]  
*Gene and genome changes in the grasses*

11:50 AM **ADJOURNMENT**