

Meeting Schedule

Wednesday, March 16

12:30-1:00 **REGISTRATION**

Opening Remarks

Nathan Springer, University of Minnesota

Larry Darrah Student Presentation Session Part I

- 1:05-1:25 **Luis Lopez-Zuniga, North Carolina State University**
Production of Chromosome Segment Substitution Lines for the identification of multiple disease resistance loci in Maize
- 1:25-1:45 **Camila Ribeiro, University of Florida**
Multiple roles of the Pentose Phosphate Pathway in maize seed development during heat stress
- 1:45-2:05 **Manfred Mayer, Technical University of Munich**
Characterization of population structure and linkage disequilibrium within and across 35 European maize landraces using high-density genomic data
- 2:05-2:25 **Mike White, University of Wisconsin**
Association of Expired Plant Variety Protection Inbred Lines from Private Sector Breeding Programs
- 2:25-2:40 **BREAK**

Larry Darrah Student Presentation Session Part II

- 2:40-3:00 **Joseph Gage, University of Wisconsin**
Genomic prediction within and between subpopulations of the USA national maize inbred collection
- 3:00-3:20 **Metthew Dziejewit, Iowa State University**
High-throughput phenotyping and genotyping to dissect canopy architecture in maize
- 3:20-3:40 **Matthew Murray, University of Wisconsin**
Signatures of selection in sweet maize suggest a single donor shapes modern elite se1 inbreds

3:40-4:00 **Ryan Huffman, Iowa State University**
Gametophytic cross-incompatibility: A genetic mechanism to maintain market class purity in maize

Community Funding Discussion

4:00-4:30 Multi Institutional Training Opportunities

4:30-5:00 Genomes2Fields

NCCC-167 Business meeting

5:00-5:30 NCCC-167 Business Meeting

Thursday, March 17

7:00-8:00 **BREAKFAST**

Early Career Session

- 8:00-8:30 **Anthony Studer, University of Illinois**
The use of stable isotopic ratio in leaf tissue to link photosynthesis and water use in maize
- 8:30-9:00 **Tim Beissinger, USDA-ARS**
Using Medical Subject Headings (MeSH terms) to make biological interpretations in maize
- 9:00-9:30 **Justin Walley, Iowa State University**
Transcriptome and proteome derived networks reveal distinct and complementary gene relationships
- 9:30-10:00 **Alexander Lipka, University of Illinois**
Exploration, embellishment, and implementation of statistical approaches for genome-wide association studies and genomic selection

10:00-10:20 **BREAK**

Phenomics Session

- 10:20-10:45 **Ivan Baxter, Donald Danforth Plant Sciences Center**
Elemental profiles are inherently the product of gene by environment interactions
- 10:45-11:10 **Nathan Miller, University of Wisconsin**
Image-Based Phenotyping: Seeds, seedlings and tensors
- 11:10-11:35 **James Schnable, University of Nebraska**
The greenhouse as another environment in field-based trials
- 11:35-12:00 **Jeff Gustin, University of Florida**
Expanding the Application of NIR toward Maize Seed Phenomics

12:00-1:30 **LUNCH AND POSTER VIEWING**

Genomes2Fields Research Session 1

- 1:30-1:50 **Natalia de Leon, University of Wisconsin**
The Effect of Artificial Selection on Phenotypic Plasticity: The

- 1:50-2:10 *Genotype by Environment Interaction Project in Maize*
Elizabeth Lee, University of Guelph
Genomes to Fields' Maize GxE Project: Expression of Productivity and Phenological Traits Across a Diverse set of Environments
- 2:10-2:30 **Jode Edwards, USDA-ARS**
Genotype by environment interaction in the 2014 G2F data set
- 2:30-2:50 **BREAK**

Genomes2Fields Research Session 2

- 2:50-3:10 **Aaron Kusmec, Iowa State University**
Distinct Genetic Architectures for Linear and Non-Linear Measures of Plasticity
- 3:10-3:30 **Diego Jarquin, University of Nebraska**
A multi-institutional multi-year collaboration to study the genotype-by-environment interaction in maize across a diverse set of hybrids, locations and years
- 3:30-3:50 **Shawn Kaeppler, University of Wisconsin**
An Overview of the 2016/2017 GxE Experimental Design
- 3:50-4:00 **ADJOURNMENT**