
Using genetic diversity to understand phenotypic variation in maize.

Michael McMullen¹ and the Maize Diversity Project².

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One of the goals of the Maize Diversity Project is the development of genetic resources for conducting joint linkage-association analysis in maize. We have designated our main genetic resource as nested association mapping (NAM). NAM is constructed from 26 inbred lines chosen to maximize genetic diversity. NAM has a reference design with B73 as the common parent and consists of 25 families of 200 RILs each from B73 crossed by 25 diverse lines (25DL). The broad sampling of allelic diversity and the 136,000 recombination events captured in NAM gives the population extensive power to describe the genetic architecture of agronomic traits for maize. For example, flowering time in maize is controlled by numerous, small-effect QTL that are shared among families, with multiple allelic effects segregating among the founder lines. The true power of NAM is based on ability to project polymorphism from the founder lines onto the RILs allowing genome wide association analysis for maize.

SESSION III: WHEAT TRANSFORMATION

Transgenic solutions to wheat biotic stresses.

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Although conventional breeding approaches will always play a major role in varietal development, transgenic technologies will become an increasingly valuable tool for our wheat breeders in the near future. The current climate for accepting biotech wheat is changing slowly to a more favorable position. Although it is unlikely that transgenic wheat will be released in the next few years, it is important to proceed with transgenic wheat research so that products can be readily deployed after the biotech wheat issue has been resolved. Providing resistance to biotic stresses is one area where transgenic wheat can make a significant impact. Highlighted in this presentation are collaborative efforts providing possible solutions for various biotic stresses including wheat streak mosaic virus, *Triticum* mosaic virus, Fusarium head blight, and Hessian fly resistance.

SESSION IV: BIOINFORMATICS

GrainGenes, the Triticeae Genome Database.

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The GrainGenes database has been serving genomic and genetic data for the Triticeae since 1993. It includes genetic and physical maps, probes used for mapping, nucleotide sequences, bibliographic references, and an address book of colleagues. The GrainGenes website includes additional information and publications, such as the Catalogue of Gene Symbols for Wheat, the *Barley Genetics Newsletter*, and the *Annual Wheat Newsletter*. Recent additions to the database are the physical/genetic map of wheat chromosome 3B, the OPA barley consensus map, and the OPA/DArT map of the Oregon Wolfe Barley population. A new GrainGenes service is TAWG, the Triticeae Annotation Working Group, a public repository for annotated genomic sequences of wheat and barley. Soon, GrainGenes will host The Hordeum Toolbox (THT), a database for genotyping and phenotyping data from the U.S. Barley CAP project.