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Research Proposal Seminar

February 16, 2018 at 3:30 PM

Moore Hall Room 351

Dissecting yield components in two multi-parent advanced generation intercross populations of maize

Midwestern agriculture is dominated by the production of hybrid maize (*Zea mays ssp. mays*), where the economic unit of yield is the number of bushels produced per acre. Yield is a highly heterotic and quantitative trait but may be dissected into yield components such as number of plants per acre, number of ears per plant, number of kernels per ear, and kernel size. In addition, during inbred parent development, female seed parents must meet minimum standards for agronomic and yield characteristics. An otherwise promising new female inbred may be discarded due to insufficient number of seeds or an anthesis to silking interval that is too long for practical parent seed production. This proposal will outline our approach for improving selection of parents for hybrid crosses with optimized yield components and creating a threshold for female parent seed production to improve efficiency in inbred development.

Our first objective is to characterize the phenotypic variation present in two Stiff Stalk multi-parent advanced generation intercross (MAGIC) populations through *per se* field observation and high-resolution ear phenotyping. Next, we will make associations between genotype and phenotype to dissect quantitative trait loci (QTL) linked with these anatomical and morphological characteristics. Then, we will use hybrid yield trials to make correlations between inbred traits and hybrid performance to improve our grain breeding and selection program. To accomplish these goals, approximately 800 doubled haploid lines across two populations were grown along with the parents as checks in two field replicates in 2016 and 2017 in Wisconsin. Several agronomic traits were evaluated and three ears per plot were collected at harvest for phenotyping. Lines were genotyped using exome capture sequencing and hybrids were generated using two testers: DK3IIIH6 and PHJ89. The results from this project will inform our grain breeding selection program and provide a list of QTL associated with yield components for future study.