

The Effects of Artificial Selection and Planting Density on G x E and Plant Morphology in Maize

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The expression of plant phenotypes is a function of their genotype, the environment in which they grow and the differential response of specific genotypes to different environments, known as the genotype-by-environment (G x E) interaction. While G x E affects plant performance, little is known about how artificial selection for high productivity has altered this adaptation response of genotypes to environmental variations. The aims of this research are to: assess how G x E responses for various traits have been altered through selection, determine the types of genetic controls of stability and measure the effect of differing plant densities on the expression of various plant phenotypes.

In 2016 and 2017, inbreds ranging from highly selected (recently expired plant variety protection) to founder lines from the Iowa Stiff Stalk Synthetic (BSSS) maize population were crossed to an inbred tester and evaluated in replicated trials across 32 locations as part of the Genomes to Fields (G2F) Initiative. The effect of selection on G x E will be assessed based on the performance of the set of unselected and selected lines relative to each other across environments. A Finlay-Wilkinson regression will be then be used to dissect the performance of individual lines in a hybrid context for various agronomic traits to determine the types of genetic control of stability. In 2018 and 2019, ~300 diverse hybrids derived from the Wisconsin Diversity Set and ~400 hybrids resulting from the cross of bi-parental derived double haploids from G2F will be planted in replicated trials. Each plot within these trials will accommodate six planting density treatments. Several agronomic traits including leaf senescence, plant height and ear components will be phenotyped and a subset of plots will be used for destructive harvest. The overall effect of variable planting densities on the phenotypic expression of these diverse hybrids will be evaluated through a genome-wide association study (GWAS). This research will enhance our understanding of G x E and its role in phenotypic expression in the context of plant breeding.