Validating Genomewide Predictions of Genetic Variance for Breeding

Improving crops for traits relies on selecting upon genetic variability within a population. Ideally, such populations would have both a favorable mean and a large genetic variance. Genomewide molecular markers could be used to predict which crosses will generate these more favorable populations, but such predictions have not been validated under realistic breeding conditions.

In the May–June 2019 issue of Crop Science, investigators report the validation of genetic variability predictions for potential crosses in a barley breeding program. Under conditions expected in a breeding program, the team generated predictions from a founder breeding population; they then validated the predictions by creating 2,661 genotypes in 27 large barley populations—all descendants of the founders—and evaluated them under field conditions for important traits.

The researchers found that the genetic variability in populations could be predicted accurately, but this depended on the trait. Predictions of agronomic traits such as flowering time were more accurate than those for disease resistance traits. Nevertheless, this validation work indicates that predictions of genetic variability can be a useful tool for plant breeders to prioritize crosses and accelerate crop improvement.


Comparing Wheat Stem Sawfly Resistance Genes in Wheat

Historically wheat stem sawfly (Cephus cinctus Norton, WSS) is a wheat pest of major economic importance in the Northern Great Plains of North America. Damage from WSS has recently expanded to other U.S. wheat-growing regions including Colorado, Idaho, Minnesota, Nebraska, and Wyoming. The most effective way to reduce WSS damage is with solid-stem cultivars. Solid-stem genes originally came from the variety Rescue; however, a new solid-stem gene was recently discovered in the variety Conan.

In a newly published Crop Science article, researchers evaluated near-isogenic line (NIL) pairs that varied for the solid-stem genes derived from Rescue and Conan to compare expression of solid stems, reaction to WSS infestation, and agronomic performance. The NILs with the Conan-derived gene expressed higher stem solidness early in plant development versus the Rescue-derived gene; however, genotypes with the Conan-derived gene lost stem solidness as plant development progressed. Genotypes with the Conan-derived gene had lower WSS infestation and reduced WSS stem cutting compared with genotypes with the Rescue-derived gene. Yield did not vary between NILs containing the Conan- or Rescue-derived genes. Cumulative data suggest that the Conan-derived gene provides a high level of resistance to WSS with a minimal impact on grain yield.