

Genomic Prediction in Maize: From Diverse Collections to Single-Cross Hybrids

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Genomic prediction is increasingly embraced as a major tool in maize breeding. Here, we evaluated genomic prediction of both (i) GCA of lines within one heterotic pool and (ii) hybrids of lines from two heterotic pools. Using experimental data from two testcross series of 285 diverse dent lines with large genetic variance for biomass-related traits, our results show that GCA is predictable with high accuracy ($\sim 0.7 - 0.8$) using 56k SNP data. In this setting, we found leaf metabolic profiles to be able to predict GCA with similar accuracy, thus representing promising intermediate phenotypes. In comparison to highly polygenic agronomic traits, predicting metabolites with single major QTL (GWAS: $P = 3.8 \times 10^{-18}$) revealed that genomic prediction models differ only slightly among traits with contrasting genetic architecture. The chromosomal distribution of the genetic variance was found useful for guiding model selection if trait architecture is unclear. In the presence of consistent linkage phases across heterotic pools, we found a combined training population to yield significantly better prediction accuracies for both pools. For evaluating genomic prediction of hybrids, we simulated 10,000 line \times line combinations using real genotypic data of the parental lines. Results suggest that prediction accuracies are mainly determined by whether both (T2), one (T1), or no parental gamete (T0) are represented in the training population. Incorporating dominance in the prediction model was only superior in case of a high SCA-to-GCA ratio. In summary, our conclusions show great promise for establishing genomic prediction in hybrid maize breeding.