

Genomic Selection in Plants: Empirical Results and Implications for Breeding Programs

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Advancements in genotyping technologies are rapidly reducing marker costs and increasing genome coverage allowing the widespread use of molecular markers and methods in plant breeding. Genotyping by sequencing using reduced representation DNA libraries is a particularly useful whole-genome genotyping technology for species with few genomics tools. Marker assisted selection (MAS) and recurrent selection (MARS) are based on the selection of statistically significant, marker-trait associations. However, MAS strategies are not well suited for agronomically important complex traits controlled by many genes. Genomic selection (GS) incorporates genome-wide marker information in a breeding value prediction model, thereby avoiding biased marker effect estimates and capturing more of the variation due to small effect QTL. In GS, a training population representative of the breeding germplasm is genotyped with genome-wide markers and phenotyped in a target set of environments. That data is used to train a prediction model that is used to estimate the breeding values of candidate lines in a population using only the marker scores. Prediction models can incorporate performance over multiple environments, G x E effects, and identify a highly predictive subset of environments. Because of reduced generation time, annual genetic gain for GS is predicted to be two to three fold greater than for a conventional phenotypic selection program, even with only modest prediction accuracy greater than 0.50. We have developed a new strategy for using genome-wide marker effects to group environments and identify outliers. Our empirical results indicate that GS can outperform conventional breeding on a per year basis even at low accuracies. This new approach to crop improvement will facilitate a better understanding of the dynamic genome processes that generate and maintain new genetic variation.