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A breeding strategy based on the prediction of phenotypes in a progeny population: a demonstration experiment for improving seed protein content in soybean

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Important agronomic traits such as yield and nutrient content are controlled by polygenes. Marker-assisted-recurrent-selection (MARS) has been applied to improve these traits in cross-pollinated crops by accumulating a relatively large number of QTLs within a given population using a subset of markers associated with target traits. This method is based on the premise that several individuals are selected from an initial population and intermated to increase the probability of obtaining progenies with desirable allele combinations. However, when MARS is applied to self-pollinated crops, artificial crossing is laborious as the number of cross combinations is increased.

In this study, to efficiently perform MARS, trait segregation in the progeny population was predicted by computational simulation for all possible cross combinations using the information of marker genotypes and phenotypes of the initial population, then used for determining the cross combinations. We verified this strategy to increase seed protein content (SPC) in soybean using recombinant inbred lines (RILs). The SPC of 194 RILs was evaluated at four locations, and each RIL was genotyped using 513 SNPs. Twenty-nine markers significantly associated with SPC were used as variables for lasso regression model. The coefficient weight on each marker was calculated using the phenotypes and marker genotypes of the RILs, and the regression equation was used as a prediction model. Marker genotypes of F1 and F2 individuals were simulated for all possible crosses, and the SPC of each F2 individual was calculated using the genotype and prediction models. Among the simulated 18,721 cross combinations, one combination predicted to produce F2 individuals with higher SPC than that of the RIL with the highest SPC was selected and crossed. Some actual F2 individuals with desirable genotypes showed high SPC, which was confirmed in their progenies. These results suggest that the proposed strategy can efficiently improve a target quantitative trait.