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Comparison of molecular and phenotypic breeding strategies for soybean yield, protein, and oil

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Evaluating different selection methods for relative utility is necessary in order to choose those which maximize breeding results. Soybean [*Glycine max* (L.) Merrill] yield, protein, and oil are all commercially important traits that display quantitative inheritance. Thus, it is of interest to evaluate breeding methods for these traits that can account for the entire genome. In addition to phenotypic selection (PS), the molecular breeding methods chosen for this study were BayesB, G-BLUP, and Epistacy. These methods were evaluated in a soybean population consisting of 860 F5 derived recombinant inbred lines (RILs), which was genotyped with 11,633 polymorphic SNPs using the Illumina Infinium beadchip SoySNP50K. In order to simulate progeny rows, each RIL was grown in a single plot in 2010 in Knoxville, TN and phenotyped. The combined phenotypic and genotypic datasets were used to make predictions with the methods mentioned above. A subset of 276 RILs from this population was then grown in multi-location, replicated field trials in 2013 in order to evaluate the relative utility of each selection method. For each trait, G-BLUP, BayesB, and PS produced similar results, with few significant differences ($P < 0.05$) observed between selection methods. Epistacy produced similar predictions for yield and worse predictions for protein and oil in comparison with the other selections methods. However, since molecular selection methods can be made at reduced time intervals when compared with PS, these methods, particularly BayesB and G-BLUP offer great potential for improving these important soybean traits with increased efficiency. These findings are promising for soybean breeders seeking to maximize gain for yield, protein, and oil.