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PROJECT 2 ABSTRACT
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Genomic selection is becoming a routine way to use markers to predict performance of breeding lines for quantitative traits. This approach has mostly been used to select lines to advance in a breeding program or to use as parents. Crossing parents with resistance alleles at different loci will lead to transgressive segregation and progeny with improved disease resistance. However, predicting which crosses will lead to such complementation is not effective when using only parent performance data. We have developed an R package, PopVar, that uses genome-wide marker effects of parents and simulation of progeny to predict genetic variance and superior progeny mean. In addition, PopVar will also predict correlations among traits for any parental combination. Using this predicted cross combination information should help inform breeders of the most fruitful crosses to make in their breeding programs. We propose to directly compare the performance, in our breeding program, of those breeding lines that trace back to crosses informed by this cross selection procedure to those breeding lines from cross combinations designed conventionally. We will simultaneously develop tools in the T3 database to automate these procedures for all wheat and barley breeders that store data in T3. If we empirically determine that this method of parent combination is successful, then the new tools will be available to accelerate implementation in breeding.