Applying Genotyping-by-Sequencing (GBS) and Population Sequencing (POPSEQ) to Predict Genetic Variance in Two-Row Barley Breeding

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ABSTRACT

The ability to accurately predict the genetic variance (*VG*) that may result from a cross would be invaluable to breeders. Several methods to predict *VG* have been proposed recently that incorporate genomic prediction and virtual bi-parental populations. Some of these methods require marker genetic map positions, information not readily available for newer genomics technologies such as genotyping-by-sequencing (GBS). Here we demonstrate the use of population sequencing (POPSEQ) in barley (*Hordeum vulgare* L.) to assign genetic positions of *de novo* GBS markers for predicting *VG*. A 183-line training set was established and evaluated in six environments for days to heading, plant height, and grain yield. Forty bi-parental populations were created from parents within this set, and using the R package PopVar, we simulated *post hoc* 34 of these populations. This package uses marker effects estimated by RR-BLUP to predict the mean (*μ*), *VG*, and superior progeny mean (*μsp*)of each virtual population. We used the same marker effects and observed GBS genotypes for 1,020 F3 progeny across the 34 populations to obtain genomic estimated breeding values (GEBVs), from which population predictions of *μ*, *VG*, and *μsp* were made. Correlations between the PopVar and GEBV predictions of *VG*were moderate (0.19 – 0.39), but mirrored the cross-validation accuracy of each trait (0.43 – 0.89). Correlations for *μsp* were high (0.85 – 0.93) and significant (α = 0.05). To determine the optimal resource allocation for validating predictions, we conducted simulations using varying trait architecture, marker density, and size of breeding populations. Simulation results will be included in the poster. This pilot experiment demonstrates the utility of POPSEQ information to order and position genomic data for use in breeding predictions. Additionally, we outline procedures to be used in validation experiments with intentionally selected crosses and larger population sizes.