

Impact of Racial Structure on Genomic Prediction for Grain Yield Components in Sorghum

ENVIRONMENTAL SCIENCES

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Introduction

Sorghum is an important cereal grain for food, feed, and fuel. Genetic variation in sorghum has been largely untapped, and breeding gene pools in United States are largely dependent on genetic diversity from historic lines primarily of kafir-caudatum types (citation). The ability to assess the breeding value of gene bank accessions will allow incorporation of novel genetic diversity in prebreeding and population development, and consequently enhance long term gain of breeding programs [?,?].

Genomic prediction/selection (GP/GS) uses a trained prediction model to estimate marker effects and subsequently estimate breeding values of non-phenotyped germplasm using just the genetic markers (Fig. 1-left, [?]).

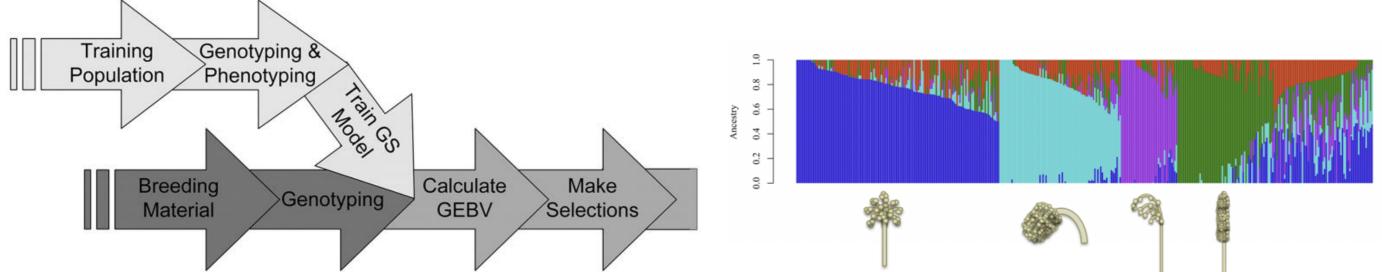
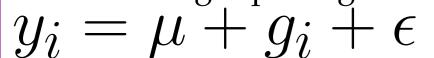


Figure 1: Left: Implementation of genomic selection model. Right: Population structure analysis of sorghum association panel (SAP). Each bar represents an individual and colors correspond to racial types caudatum, durra, guinea, kafir and mixed from left to right, respectively.

While several studies have been conducted on genomic prediction for major crops like maize, wheat, soybean, etc., there are very limited empirical genomic selection studies in sorghum. Few studies already conducted have shown that application of GS would help accelerate genetic gain in sorghum breeding programs. Among various factors population structure is known to affect accuracy of genomic prediction models [?]. We used the sorghum association panel (SAP) (Figure 1-right) representing sorghum racial types to study the impact of racial structure and divergence in prediction accuracy for grain yield components.

Data and Methods

- Plant Material: 389 diverse sorghum accessions.
- Field Design: RCBD with two replications, planted at PDREC, Florence, SC in 2013, 2014, and 2017 in two row plots.
- Traits: plant height (PH), days to anthesis (DTA), flag leaf height (FLH), grain number per primary panicle (GN), thousand grain weight (GW), grain yield per primary panicle (GY), panicle branch length(BL), panicle length
- **Genotyping**: Burrow-Wheeler aligner to Ref BTx623 v3.1, TASSEL 5.0 for SNP calling, imputation and filtering. The genotypic matrix with 224,007 SNPs used in prediction.
- Prediction Model: Genomic best linear unbiased prediction (GBLUP) implemented using R package rrBLUP:



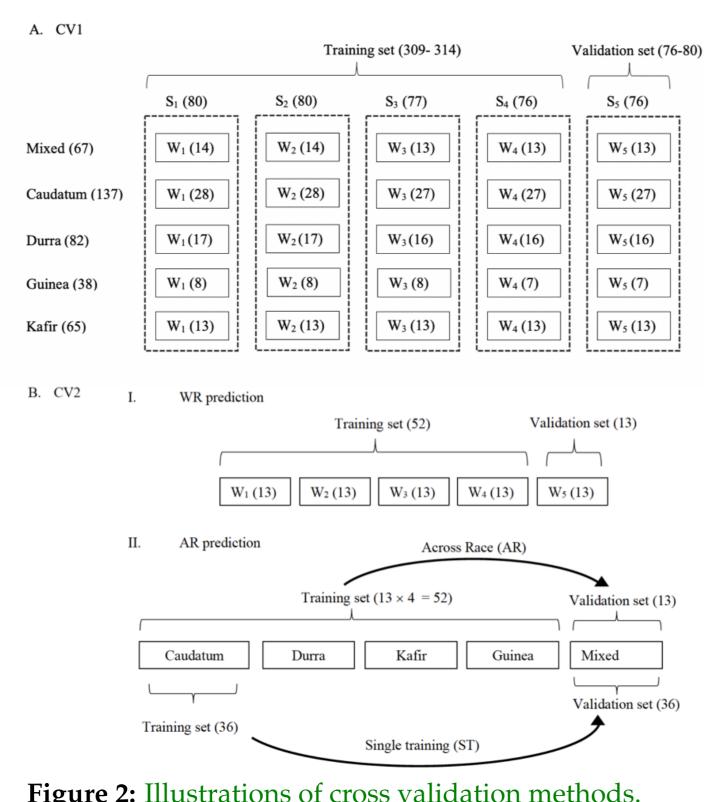


Figure 2: Illustrations of cross validation methods.

- Cross Validation (CV): Five-fold CV, CV1 = stratified sampling, CV2 = Across Race (AR), Within Race (WR), and Single Race Training (ST). For details see Figure 2.
- Prediction accuracy was calculated as correlation for predicted genetic values and observed phenotypic values.
- Covariance decomposition of CV1 accuracy:

 $Cov(x, y) = E_{race}[Cov(x, y|race)] + Cov_{race}[E(x|race), E(y|race)]$

Results

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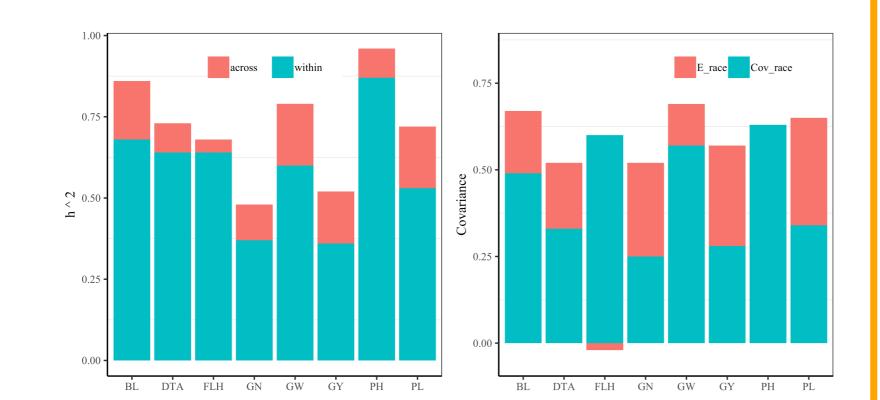


Figure 3: Left: Within and across race genomic heritability. Right: Covariance decomposition of CV1 accuracy.

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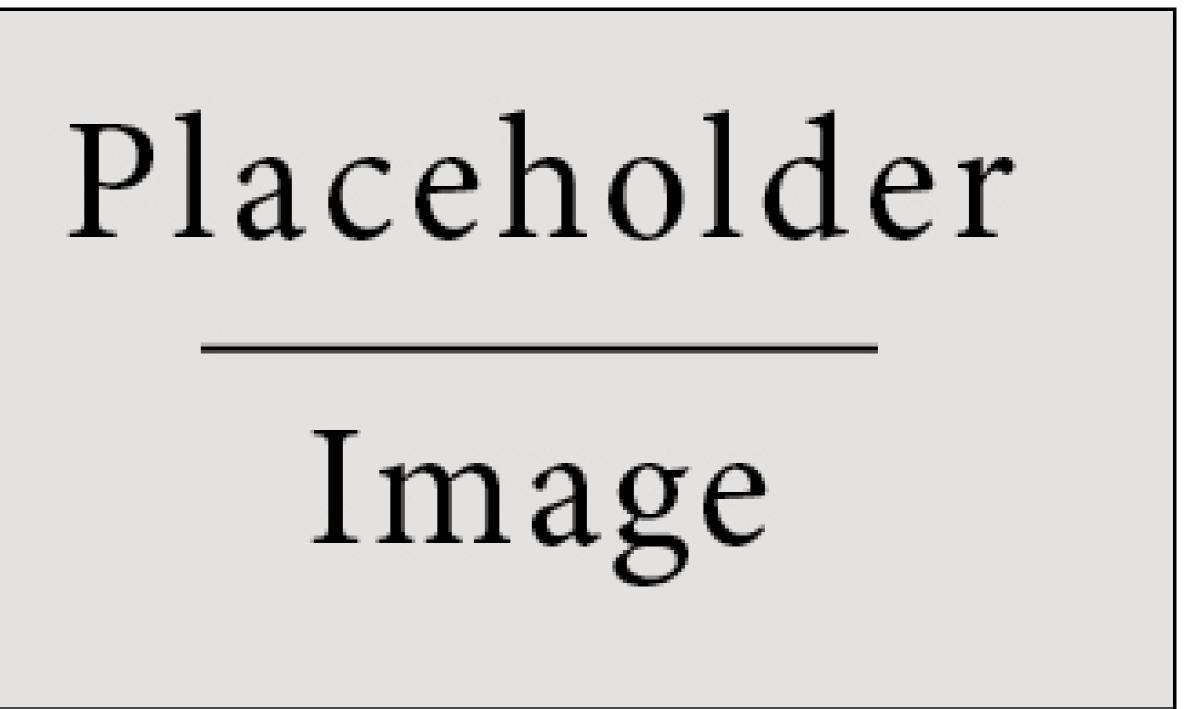


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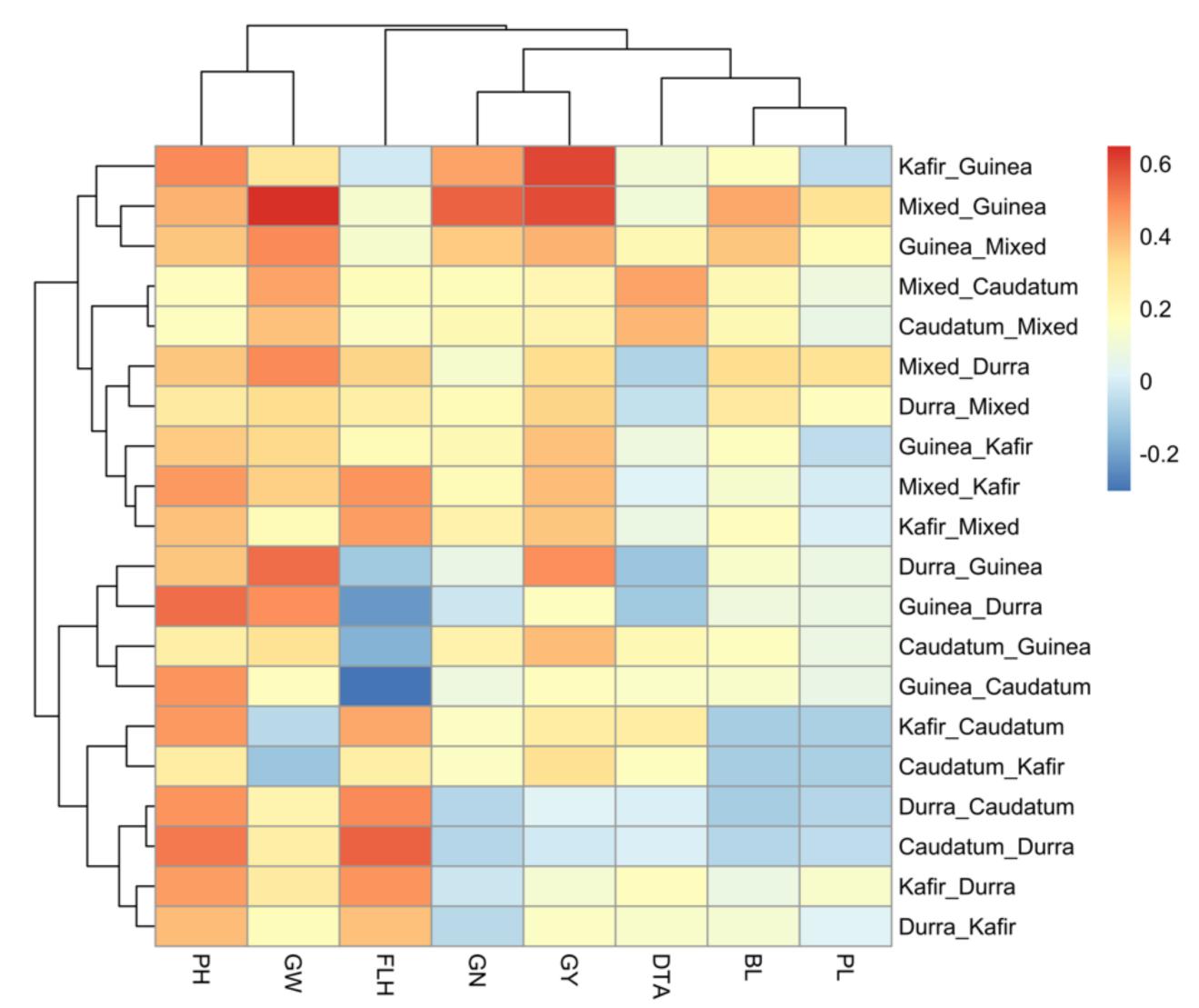


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Summary

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