



—Scientific Note—

Genomic Prediction of Sweet Sorghum Agronomic Performance under Drought and Irrigated Environments in Haiti

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The discovery and application of molecular markers such as single nucleotides polymorphism (SNP) and simple sequence repeats has revolutionized modern plant breeding. Through advancement in high-throughput sequencing platforms, previously expensive marker-genotyping platforms have become affordable for many plant-breeding programs. However, high-throughput phenotyping remains costly and inaccessible to most plant breeding programs. Over the last decade, genomic selection has gained momentum as a tool for predicting genetic gain in plant breeding populations, while lowering costs associated with phenotyping. Different statistical models and approaches have been developed to implement genomic selection (GS) in plant breeding, and strategies that promote accurate and resource-efficient prediction are of increasing interest. Since its establishment in 2010, the sweet sorghum breeding program at CHIBAS, Haiti, has led efforts to develop and release cultivars resilient to abiotic and biotic stress. Among abiotic constraints, drought stress is the most limiting since growers depend on erratic rainfall for sorghum production in Haiti. The goal of the present study was to predict the genomic estimated breeding values (GEBVs) of a sweet sorghum breeding population ($n = 250$) under contrasting environments in Haiti using four statistical models [Bayes A, B, C, and Bayesian ridge regression (BRR)]. We evaluated twelve sorghum traits across three environments (irrigated, preflowering water stress and vegetative water stress) and performed within and across environments prediction scenarios.

Results

The vegetative water stress was severe and led to substantial reductions in almost all the traits. The genomic heritability estimates varied substantially for all the traits across the three environments. The highest values were obtained for heading (0.82), days to maturity (0.82), soluble solids concentration (0.61), grain yield (0.61), and juice weight (0.60) in the preflowering water stress condition. Phenotypic correlations varied in terms of magnitude across the environments. Grain yield was positively and significantly correlated with all eleven traits in the irrigated environment. For the water stress environments (vegetative and preflowering water stress), no significant correlations were observed between grain yield, heading and maturity. Overall, the values varied from 0.16 to 0.65 for vegetative water stress, 0.29 to 0.82 for the irrigated condition and 0.35 to 0.82 for preflowering water stress. Overall, the four methods showed similar results, however Bayes B and BRR were superior in prediction accuracy and computation time, respectively. Generally, prediction accuracy was higher for within-environment (0.31–0.7) than across-environment (0.06–0.7) involving vegetative water stress scenarios. Prediction accuracy varied substantially for all traits, with total green leaf showing the highest mean value (0.70), and grain yield showing the least (0.49). Accuracies of genomic prediction obtained here are encouraging for implementation of GS in small breeding programs for drought tolerance.

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