

Meta-Analysis Identifies Pleiotropic Loci Controlling Phenotypic Trade-offs in Sorghum

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Project Goals:

Here we sought to assemble publicly accessible and internally generated trait datasets from a common association population of sorghum to identify genes associated with phenotypic variation in one or more phenotypes to serve as a training dataset for machine learning models which will predict which additional sorghum genes most likely to exhibit loss of function phenotypes.

Abstract text.

Most of the agronomic traits are complex in nature and are influenced by many genetic loci and environmental conditions as well as their interactions. However, there are some instances where some traits show correlated variations as they are influenced/controlled by same genetic loci/gene which is pleiotropic in nature. Not only the investigation and understanding of the genetic association of complex traits but also pleiotropy and genotype by environment interactions are of paramount importance in strategizing the breeding program for crop improvement. The current approaches to link phenotypic variation to natural genetic variation using quantitative genetic tools are primarily conducted one trait at a time, because scoring multiple traits across large population is labor intensive and economically challenging. Also, most of the individual research groups focus on few of the specific traits of interests. Thus to bring together all the traits scored on a community population we conducted a meta-analysis of Genome Wide Association Studies (GWAS), employing a set of 234 separate trait datasets, including both published and unpublished trait datasets for the Sorghum Association Panel (SAP) with 406 sorghum genotypes, and multiple genetic marker datasets to empirically evaluate both the degree of saturation achieved by current genetic marker sets and the degree to which detectable loci controlling phenotypic variation in the SAP tend to be pleiotropic or non-pleiotropic using a multi-trait approach based on meta-analysis and adaptive shrinkage. Our results based on comparison of GWAS conducted with two independently generated marker sets to screen this population, suggest that the existing genetic marker sets are not enough to saturate the genome and capture only 35 to 45% of potentially detectable loci controlling variation for traits scored in this population. Cross-GWAS comparisons showed a limited evidence of pleiotropy, thus a multivariate adaptive shrinkage approach was adopted. The multivariate approach aided in recovering both known pleiotropic effects of existing loci and various new

pleiotropic effects, which might go unaccounted in direct comparison of GWAS results. The known pleiotropic effects detected in this study included the significant impacts of known dwarfing genes on root architecture, and the new pleiotropic loci detected were consistent with known trade-offs in sorghum development. These results demonstrate the potential of detecting new associations as new, denser genetic marker datasets are generated for the Sorghum Association Population.

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