



Genome-Wide Association Studies for Lignin Content and Biomass Production in a Diverse Sorghum Panel Using Genotyping-by-Sequencing

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Sustainable production of future biofuels will require a consistent supply of lignocellulosic biomass for second-generation ethanol production. Sorghum has the potential to be an important crop for biomass production due to its high yield and lower water and fertilizer requirements. In this study, association mapping was performed to explore the genetic basis for traits related to biomass quality and yield in a diverse panel of 100 sorghum accessions from Embrapa and CIRAD germplasm collections. The panel was phenotyped for traits related to biomass yield (height, dry weight matter and flowering) and quality (lignin, ADF, NDF, cellulose and hemicellulose). Genotyping-by-Sequencing (GBS) was used for simultaneous Single Nucleotide Polymorphisms (SNP) discovery and genotyping. Missing genotypes were imputed, and then GBS data were filtered for a 5% MAF resulting in a total of 258,000 SNPs. Population structure was assessed by Principal Component Analysis and several association mapping models were compared (Naïve, Q, K and Q+K). Use of population structure as a co-factor in the generalized linear model (GLM + Q) gave the best fit and good correction for false positives. Two SNPs in chromosome 6 were significantly associated ($p < 0.0001$) with lignin content and the related genes are being investigated. A single SNP significantly associated ($p < 0.000002$) with dry weight matter and height was mapped to chromosome 6 in a region where QTLs for plant height have been reported, confirming the robustness of our data. SNP validation for lignin trait is being carried on in order to increase biomass yield and efficiency in sorghum breeding.

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