

Identification of QTLs controlling yield traits in sweet sorghum using genotyping by sequencing

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Sweet sorghum, a C_4 tropical grass, is becoming an important bioenergy crop. Characterizing quantitative trait loci (QTLs) underlying bioenergy-related traits can lead to the identification of target regions for molecular breeding programs. These QTLs may be conserved in related species such as sugarcane, expanding their potential usefulness for bioenergy production. In this study, 223 recombinant inbred lines (RILs) derived from the sweet sorghum parents, Brandes and Wray, were genotyped by sequencing (GBS). A lattice experiment with three replicates was established in two years for evaluating four important yield traits: plant height (in m), plot weight (in kg), sucrose content (or Pol, in %), and volume of hydrated alcohol (in L). Phenotypic analysis and QTL scanning were conducted using mixed and general linear models approaches, in the respective softwares GenStat and TASSEL. GBS provided wide genome coverage, with ~1100 single-nucleotide polymorphisms (SNPs) per chromosome. Variance-covariance matrices for genetic and residual effects were appropriately fitted, allowing heterogeneous variances for harvest years. Major QTLs were co-located for plant height and plot weight on chromosome 10, and for Pol and hydrated alcohol on chromosome 3, explaining 20.7%, 14.0%, 23.1% and 23.8% of the phenotypic variance, respectively. Suggestive QTLs were additionally detected on others chromosomes for all traits. The QTLs identified here will be further investigated for possible use in marker-assisted selection targeting biofuel production in sweet sorghum. Financial Support: FAPESP, CNPq, Embrapa, and Seventh Framework Programme (FP7)