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Quantitative Trait Loci Mapping for Sugar-Related Traits in Sweet Sorghum based on High-Density SNP Markers

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Room: Grand Exhibit Hall
Guilherme S. Pereira , University of São Paulo, Piracicaba, SP, Brazil
Vander Fillipe Souza , Federal University of São João Del-Rei, Sete Lagoas, Brazil
Rafael Augusto C. Parrella , Embrapa Maize and Sorghum, Sete Lagoas, Brazil
Cynthia Maria B. Damasceno , Embrapa Maize and Sorghum, Sete Lagoas, Brazil
Maria Lucia F. Simeone , Embrapa Maize and Sorghum, Sete Lagoas, Brazil
Robert E. Schaffert , Embrapa Maize and Sorghum, Sete Lagoas, Brazil
Serge Braconnier , CIRAD, Montpellier, France
Antonio Augusto F. Garcia , University of São Paulo, Piracicaba, Brazil
Jurandir V. Magalhaes , Embrapa Maize and Sorghum, Sete Lagoas, Brazil
Sweet sorghum, a C_4 tropical grass, is becoming an important bioenergy crop. Characterizing quantitative trait loci (QTL) controlling sugar content in its stem 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 for evaluating three sugar related traits: soluble solids content (BRIX, in °Brix), sucrose content (POL, in %), and reducing sugars (RSU, in %). Phenotypic analysis and QTL scanning were conducted using mixed and general linear models approaches, using the softwares GenStat and TASSEL, respectively. GBS provided wide genome coverage, with ~1200 single-nucleotide polymorphisms (SNPs) per chromosome. Major QTLs were detected for BRIX and POL on chromosome 3, and for RSU on chromosome 4, explaining up to 20.8%, 18.9% and 15.5% of the phenotypic variance. False discovery rate correction suggested that QTLs were co-located on chromosome 1 for all traits as well. The QTLs identified here will be further investigated for possible use in marker-assisted selection targeting biofuel production in sweet sorghum.