

QTL mapping for yield related trait in a biparental cross of sugarcane

Anoni, CA¹; Mancini, MC²; Costa, E A²; Gazaffi, R³; Pastina, MM⁴; Pinto, LR⁵; Souza, AP²; Garcia, AAF¹

¹Departamento de Genética, Escola Superior de Agricultura Luiz de Queiroz (ESALQ), Universidade de São Paulo (USP), Piracicaba, SP, Brasil; ²Centro de Biologia Molecular e Engenharia Genética (CBMEG), Departamento de Genética e Evolução, Universidade Estadual de Campinas (UNICAMP), Campinas, SP, Brasil; ³Centro de Ciências Agrárias, Universidade Federal de São Carlos, Araras, SP, Brasil; ⁴Núcleo de Biologia Aplicada, EMBRAPA Milho e Sorgo, Sete Lagoas, MG, Brasil; ⁵Centro Avançado da Pesquisa Tecnológica do Agronegócio de Cana, IAC/Apta, Ribeirão Preto, SP, Brasil

canoni@usp.br

Keywords: polyploids; QTL mapping; outcrossing species

Modern sugarcane (*Saccharum* spp.) varieties are derived from interespecific hybridization between *S. officinarum* and *S. spontaneum*, resulting in highly polyploid and aneuploid plants. Due to the sugarcane genetic complexity, breeding programs take at least 10 years to the development of new varieties. Since the most of agronomic important traits have a quantitative nature, quantitative trait loci (QTL) mapping is a tool for identification of loci along the genome that contributes to the trait phenotypic variance. This information may be useful for sugarcane breeders in marker assisted selection. In this study we performed a QTL mapping using composite interval mapping in a biparental cross between two Brazilian commercial sugarcane varieties (IACSP95-3018 and IACSP93-3046), evaluated at two locations and two harvest years. We use 634 molecular markers (AFLP and SSR) and traits related with cane yield and sugar yield, namely: soluble solid content (Brix), fiber percentage (Fiber), sucrose content (Pol), stalk weight (SW), and stalk diameter (SD). We also report the segregation pattern and additive and dominance effects for each mapped QTL. A total of 19 QTLs were detected for Brix (three QTLs), Fiber (five QTLs), Pol (four QTLs), SW (three QTLs), and SD (four QTLs). QTLs were identified along of 14 linkage groups and seven distinct homology groups. For all traits at least one additive or dominance effects were significant, nevertheless the majority of QTLs had significant additive effects. The proportion of phenotypic variation explained by each QTL was low, as expected in sugarcane studies due to its polyploid nature, ranged from 0.10% to 6.67%. Additive effects and dominance effects estimated considering each mapped QTL were used to obtain the segregation pattern of QTLs that vary between 1:1:1:1, 1:2:1, 3:1 and 1:1 segregation ratio. Segregation pattern information guides the behavior of QTL alleles in the progeny. Some QTLs were mapped at nearby or common regions within the same linkage group and are important for future investigation involving linkage and pleiotropy. QTLs identified in this study are substantial to a better understand and dissection of complex traits of sugarcane.

Financial support: CNPq, CAPES, FAPESP.