

## QTL mapping for yield components in a sugarcane commercial cross

Anoni, CO<sup>1</sup>; Gazaffi, R<sup>1</sup>; Pastina, MM<sup>1</sup>; Mancini, MC<sup>2</sup>; Costa, EA<sup>2</sup>; Mollinari, M<sup>1</sup>; Marconi, TG<sup>2</sup>; Pinto, LR<sup>3</sup>; Souza, AP<sup>2</sup>; Garcia, AAF<sup>1</sup>

<sup>1</sup>Escola Superior de Agricultura “Luiz de Queiroz”, Departamento de Genética, Universidade de São Paulo, Piracicaba, SP; <sup>2</sup>CBMEG – Universidade Estadual de Campinas, Campinas, SP; <sup>3</sup>Instituto Agrônômico de Campinas, Centro de Cana, Ribeirão Preto, SP

carina.anoni@gmail.com

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The majority traits in sugarcane are quantitative and highly influenced by the environment. Thus, quantitative trait loci (QTL) mapping is an important tool to identify and locate QTLs along the genome, in order to understand the genetic architecture of these traits. This should be useful for sugarcane breeding programs. In this study, we performed QTL mapping for yield components in a sugarcane commercial cross via composite interval mapping. The segregating population was developed from a biparental cross between IAC95-3018 and IACSP93-3046 and consisted of 189 individuals planted in two locations and evaluated in the first and second harvest years. The yield components evaluated were Brix, Sucrose Content (POL), Fiber percent, Weight of Culms (WC), Diameters of Culms (DC) and Stalk Height (SH). A mixed model approach was performed to phenotypic data in order to obtain an appropriated genetic co(variance) structure between location and harvest. An integrated genetic linkage map was constructed using the OneMap software, considering 634 molecular markers (AFLP and SSR) displaying an 1:1 and 3:1 segregation ratio. The presence of single QTL was tested for a discrete grid of 1 cM along the genome. Phenotypic analysis provided the assumption of a specific genetic correlation for each combination of harvest and location. The genetic linkage map had 113 linkage groups, with a total length of 4370 cM and established 15 putative homology groups. In the QTL mapping procedure 45 QTLs were detected within 113 linkage groups: 7 were detected for Brix, 9 for POL, 7 for Fiber Content, 5 for WC, 11 for DC and 6 for SH. The LOD Threshold considered was 4.7. The proportion of phenotypic variation ( $R^2$ ) explained by each QTL individually ranged from 0.02% to 6.53%. For each QTL, at least an additive effect for each parental or dominance effect for both parental was significant. In this sense, the present study mapped QTLs successfully, and contributes to a better understanding of the inheritance of quantitative traits in sugarcane. Financial Support: CNPq and FAPESP