3rd International Conference on

FOOD CHEMISTRY & NUTRITION

May 16-18, 2018 | Montreal, Canada

Identification of novel QTLs linked with sugarcane yield traits and smut resistance

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Yield potential of sugarcane crop depends upon various yield parameters viz., number of tillers, cane length, cane weight, girth, sugar recovery and disease resistance. In this study, the performance of 103 sugarcane lines/varieties was checked over a period of two successive cropping years under high inoculum conditions for whip smut. Phenotypic data of both years was integrated with genotypic data (molecular identification profiles) of all the sugarcane lines/varieties using bioinformatic tools which helped in the identification of various quantitative traits loci (QTLs) associated with these traits. Using Structure and TASSEL software, out of the total 314 alleles, eighty-seven alleles were found associated with various yield parameters (p≤0.05): 34 with smut resistance followed by 27 with sugar recovery, 13 alleles with cane weight and 20 alleles with each of cane length and girth. Few alleles were found even linked with more than one trait. The alleles linked with cane weight explained phenotypic variance of 2.9-14.34%, those with cane length (2.81-23.46%), cane girth (1.75-12.8%), sugar recovery (2.67-22.5%) and smut resistance (3.1-24.6%). The identification of multiple alleles explaining varying proportions of phenotypic variance for each trait shows that these traits may be controlled by many genes with little to moderate effects and no single gene with widespread effect is involved in controlling these traits. The allele 52-121 showed maximum association with cane length, 82-184 with cane girth, 51-131 with sugar recovery, 51-145 and 51-146 with cane weight and smut resistance. These alleles could help in marker assisted selection of these sugarcane lines/varieties for these traits.

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