

Multi-trait multi-environment QTL mapping in a sugarcane commercial cross using mixed models

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Data collected from breeding trials usually comprise phenotypic observations for various traits evaluated at multiple test environments. Specifically for sugarcane, repeated measures are obtained for plant crop and one or more ratoons. Such scenario naturally lends itself to the use of mixed models for modeling heterogeneous genetic variances and correlations between traits, locations and harvests. This modeling approach also enables us to include molecular marker information, aiding in understanding the genetic architecture of quantitative traits through QTL mapping. Our work was aimed at detecting QTL and QTL by environment interaction by the Multiple Interval Mapping method, which also allows the inclusion of epistasis in the search process. Our mapping population was composed of 100 individuals derived from a biparental cross between the Brazilian pre-commercial cultivars SP80-180 and SP80-4966, evaluated at two locations and three harvest years for fiber content, sugar content (POL) and tonnes of cane per hectare (TCH). A genetic linkage map with 96 linkage groups covering 2468.14 cM was already available for this cross. We detected 13 QTL with main effects and 8 epistatic interactions, each exhibiting QTL by location, QTL by harvest or the three-way interaction. Thus, no QTL displayed stable effects across all environment combinations. Overall, 13 of the 21 effects presented some degree of pleiotropy, affecting at least two of the three traits. Furthermore, these QTL always affected fiber and TCH in the same direction, while POL was affected in the opposite way. There was no evidence in favor of the linked QTL over the pleiotropic QTL hypothesis for any of the detected genome positions. These results give some insights about the genetic basis of quantitative variation in sugarcane and about the genetic relation between traits.

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