

Preliminary assessment of the incidence of brown rust in bi-parental progeny sugarcane through EST-SSR markers

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The cultivation of sugarcane (*Saccharum spp.*) is one of the most important in Brazil, representing about 2.0% of national PIB. The increasing use of ethanol as a biofuel in Brazil and the world in recent years has generated a need by the sugar sector to increase the productivity of sugarcane cultivation and expand the cultivation area. The breeding programs of sugarcane have concentrated efforts to launch new varieties with agronomic traits that meet the demand of bioenergy sector. However, the genetic complexity of sugarcane due to its high level of ploidy and aneuploidy coupled with the multigenic nature and/or multiallelic most agronomic traits, has difficult the genetic breeding of this crop. The development of molecular markers and construction of genetic maps can help to develop strategies to be introduced into breeding programs in order to accelerate the development of new varieties. Considering the advances that will be achieved in the breeding of sugarcane with the construction of a functional genetic map, the purpose of this study was preliminary analysis for genetic mapping population of sugarcane from the bi-parental cross between SP80-3280 and RB835486, contrasting the components for production and for resistance to brown rust, using microsatellite markers. Also was evaluated the severity of brown rust incidence 6 months after planting the clones using a rating scale proposed by Tai *et al.* (1981). The statistical design was Federer's augmented blocks with three replicates and the experiment established in two locations, Araras-SP and Ipaussu-SP. Thirteen loci EST-SSR (SCA 07, SCA 17, SCA 44, SCA 48, SCA 61, 2006 SCB, SCB 37, SCB 82, 84 SCB, SCB 100, SCB 118, SCC 80 and SCC 91) were genotyped in 206 individuals the mapping population, thus allowing the analysis of segregation of the markers, with a mean of 9.53 alleles per locus. The segregation observed in the polymorphic alleles of each locus was tested using the chi-square test with significance level of 5% adjusted with Bonferroni correction for multiple tests. The calculation of the p-value for each test was performed using the software R. The segregation of the markers were analyzed in a single dose in two forms, usually considered to sugarcane sugar, 1:1 or 3:1. All had polymorphic products and significant for segregation 1:1 or 3:1. In the 13 loci analyzed in the mapping population was generated 124 marks, 102 were polymorphic (82.25%). Of the 102 polymorphic products, 38.83% (40 marks) showed 1:1 segregation and 28.15% (29 marks) showed 3:1 segregation. In the evaluation the severity of the disease in the clones was observed for two localities, segregation of the inheritance of resistance in the ratio 3:1, which indicates the presence of a gene of major effect, controlling the resistance. For construction of a linkage map that enables the study of the association of markers with resistance to brown rust and yield traits segregating would require a larger number of polymorphic loci and marks.

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