



# Genetic divergence and admixture of ancestral genome groups in the sugarcane variety ‘RB867515’ (*Saccharum* spp)

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**ABSTRACT.** We analyzed 80 plants of the sugarcane (*Saccharum* spp) variety ‘RB867515’ in order to investigate its diversity and genetic structure at the molecular level. Four simple sequence repeat (SSR) loci (UGSM51, SMC1237, SEGMS1069, and UGSM38) and five expressed sequence tag (EST)-SSR loci (ESTA68, ESTB92, ESTB145, ESTC66, and ESTC84) were used as molecular markers. The polymorphic loci rate was 66.6%. A total of 17 alleles and an average of 1.88 alleles/locus were detected. The number of alleles in the EST-SSR loci was lower

than the number of alleles in the SSRs of non-expressed loci. The mean observed heterozygosity among the nine SSR loci was 0.3291. Genetic structure analysis showed that 'RB867515' contains alleles from three ancestral groups ( $K = 3$ ), but there is little admixing of alleles in the same plant (from 0.8 to 17.3%); only 1.88% of the plants shared alleles from two or three groups. ESTB92, ESTC84, and UGSM38 were monomorphic, but there was evidence of polymorphism in ESTA68, ESTB145, ESTC66, UGSM51, SMC1237, and SEGMS1069, indicating that 'RB867515' has variability at the molecular level and the potential to be used as a parent in breeding programs. The molecular variability observed in 'RB867515' indicates that the clone terminology that is used to identify this cultivar is inconsistent with the original meaning of "clone", which is defined as a sample of genetically identical plants.

**Key words:** Genetic variability; Molecular polymorphism; 'RB867515' sugarcane variety; EST-SSR loci