



High degree of genetic diversity among genotypes of the forage grass *Brachiaria ruziziensis* (Poaceae) detected with ISSR markers

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ABSTRACT. The grasses of the genus *Brachiaria* account for 80% of the cultivated pastures in Brazil. Despite its importance for livestock production, little information is available for breeding purposes. Embrapa has a population of *B. ruziziensis* from different regions of Brazil, representing most of existing variability. This population was used to initiate an improvement program based on recurrent selection. In order to assist the genetic improvement program, we estimated the molecular variability among 93 genotypes of Embrapa's collection using ISSR (inter-simple sequence repeat) markers. DNA was extracted from the leaves. Twelve ISSR primers generated 89 polymorphic bands in the 93 genotypes. The number of bands identified by each primer ranged from two to 13, with a mean of 7.41. Cluster analysis revealed a clearly distinct group, containing most of the *B. ruziziensis* genotypes apart from the outgroup genotypes. Genetic similarity coefficients ranged from 0.0 to 0.95, with a mean of 0.50 and analysis of molecular variance indicated higher variation within (73.43%) than among species (26.57%). We conclude that there is a high genetic diversity among these *B. ruziziensis* genotypes, which could be explored by breeding programs.

Key words: Genetic variability; Forage; Molecular markers