GENETIC MOLECULAR SIMILARITY AMONG 20 Paspalum notatum ACCESSIONS

Oliveira FA¹, Souza AP^{1,2}, Fávero AP³, Matta FP³, Souza FHD³, Vigna BBZ³.

¹Center for Molecular Biology and Genetic Engineering-University of Campinas, Campinas-SP, Brazil. ²Plant Biology Institute-University of Campinas, Campinas-SP, Brazil. ³Embrapa Southeast Livestock, São Carlos-SP, Brazil.

The genus Paspalum is native to the American continent and comprises great morphological variability. P. notatum present turf and forage usage. The Germplasm Bank of Paspalum at Embrapa comprises about 350 accessions from 50 species, from which 20 accessions of bahiagrass were visually selected for low height. These accessions were originally collected from Argentina to Amapá State in Brazil. The objective of this study was to estimate the genetic similarity among these accessions using microsatellite markers and aiming conservation and use of germplasm in breeding programs. Leaves were collected in the field at Embrapa Southeast Livestock and total DNA was extracted. PCR was performed and resolved in 6% denaturing polyacrilamide gels stained with silver nitrate. Genetic similarity among accessions were estimated using 16 microsatellite loci previously developed for the species. Jaccard's similarity coefficient (J) was calculated and a dendrogram was obtained through UPGMA clustering method. J among accessions ranged from 0 to 0.56, being the accession BRA025046 the most divergent from the others. Accessions BRA012254 and BRA019178 were the most similar between each other. The dendrogram separated the accessions into five main groups. These information will be useful for cultivar registration and for the breeding program of the species.

Corresponding author: Bianca B. Z. Vigna, bianca.vigna@embrapa.br