Genetic diversity in sugarcane varieties in Brazil based on the Ward-Modified Location Model clustering strategy

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ABSTRACT. We evaluated the genetic diversity of 77 clones of sugarcane used in crosses made by the Brazilian interuniversity network for the development of the sugar/energy sector (RIDESA) breeding program. Characterization of the genotypes was carried out at the ratoon stage, based on eight morphological traits and seven agronomic traits. Diversity analysis was carried out beginning with the Ward-Modified Location Model. The ideal number of groups was three. Groups 1, 2, and 3 were composed of 37, 21, and 19 accessions, respectively. Group 1 was formed entirely of commercial varieties (hybrids of advanced generations) and elite clones, with the exception of the old varieties 'Caiana Fita' and 'Cana Blanca' (hybrids of *Saccharum officinarum*). In general, group 2 had more divergent accessions regarding origin, including L60-14, NG57-6, TUC77-42, IN84-105 (hybrid of *S. officinarum*), and 28NG289 (species of *S. robustum*). Group 3 was formed entirely of commercial varieties and elite clones from the RIDESA program, with the exception of genotypes Co285 (India), Q124 (Australia) and VAT90-212 (unknown origin). The analysis based on the Ward-Modified Location Model

procedure resulted in an adequate and clearly discriminating grouping of sugarcane accessions, allowing the use of all the available information about the genotypes, in a mix of continuous and categorical variables.

Key words: *Saccharum* spp; Germplasm characterization; Genetic diversity; Multivariate analysis