



Morphoagronomic and molecular profiling of *Capsicum* spp from southwest Mato Grosso, Brazil

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ABSTRACT. The genus *Capsicum* ranks as the second most exported vegetable in Brazil, which is also considered to be a center of diversity for this genus. The aim of this study was to rescue genetic variability in the genus *Capsicum* in the southwest region of Mato Grosso, and to characterize and estimate the genetic diversity of accessions based on morphoagronomic descriptors and inter-simple sequence repeat molecular markers. Data were obtained following the criteria of the International Plant Genetic Resources Institute, renamed Bioversity International for *Capsicum*. Data were analyzed using different multivariate statistical techniques. An array of binary data was used to

analyze molecular data, and the arithmetic complement of the Jaccard index was used to estimate the genetic dissimilarity among accessions. Six well-defined groups were formed based on the morphological characterization. The most divergent accessions were 142 and 126, with 125 and 126 being the most similar. The groups formed following agronomic characterization differed from those formed by morphological characterization, and there was a need to subdivide the groups for better distinction of accessions. Based on molecular analysis, accessions were divided into two groups, and there was also a need to subdivide the groups. Based on joint analysis (morphological + agronomic + molecular), six groups were formed with no duplicates. For all groups, the cophenetic correlation coefficient was higher than 0.8. These results provide useful information for the better management of the work collection. All correlations between the combined distance matrix were significant by the Mantel test.

Key words: Pepper; Molecular analysis, ISSR; Multivariate analysis; Genetic variability; Brazil