Genetic diversity among air yam (*Dioscorea bulbifera*) varieties based on single sequence repeat markers

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**ABSTRACT.** *Dioscorea* is the largest genus in the Dioscoreaceae family, and includes a number of economically important species including the air yam, *D. bulbifera* L. This study aimed to develop new single sequence repeat primers and characterize the genetic diversity of local varieties that originated in several municipalities of Brazil. We developed an enriched genomic library for *D. bulbifera* resulting in seven primers, six of which were polymorphic, and added four polymorphic loci developed for other *Dioscorea* species. This resulted in 10 polymorphic primers to evaluate 42 air yam accessions. Thirty-three alleles (bands) were found, with an average of 3.3 alleles per locus. The discrimination power ranged from 0.113 to 0.834, with an
average of 0.595. Both principal coordinate and cluster analyses (using the Jaccard Index) failed to clearly separate the accessions according to their origins. However, the 13 accessions from Conceição dos Ouros, Minas Gerais State were clustered above zero on the principal coordinate 2 axis, and were also clustered into one subgroup in the cluster analysis. Accessions from Ubatuba, São Paulo State were clustered below zero on the same principal coordinate 2 axis, except for one accession, although they were scattered in several subgroups in the cluster analysis. Therefore, we found little spatial structure in the accessions, although those from Conceição dos Ouros and Ubatuba exhibited some spatial structure, and that there is a considerable level of genetic diversity in *D. bulbifera* maintained by traditional farmers in Brazil.

**Key words:** *Dioscorea bulbifera;* Genetic structure; Germplasm; Microsatellite; Microsatellite development; Traditional agriculture