Phenotyping of *Passiflora edulis*, *P. setacea*, and their hybrids by a multivariate approach

E.A. Santos[1], A.P. Viana[1], J.C.O. Freitas[1], M.M. Souza[2], C.L. Paiva, D.L. Rodrigues[1] and R.F. Tavares[1]

[1]Laboratório de Melhoramento Genético Vegetal,
Centro de Ciências e Tecnologias Agropecuárias,
Universidade Estadual do Norte Fluminense Darcy Ribeiro,
Campos dos Goytacazes, RJ, Brasil
[2]Departamento de Ciências Biológicas,
Universidade Estadual de Santa Cruz, Ilhéus, BA, Brasil

Corresponding author: E.A. Santos
E-mail: eileenazevedo@yahoo.com.br

ABSTRACT. Morphological characterization is the most accessible and used method to quantify the genetic diversity of the available germplasm. The multivariate statistical method is highly important for this purpose. This study aimed to characterize parents and hybrids of *Passiflora* according to morphoagronomic descriptors and estimate the genetic divergence between them based on the joint analysis of qualitative and quantitative variables using the Ward-modified location model (MLM) procedure. One hundred and thirty-eight individuals were assessed (10 *P. edulis*, 10 *P. setacea*, and 118 interspecific hybrids) using 23 quantitative and 12 qualitative descriptors. The values for the quantitative descriptors were measured and subjected to multivariate statistics using the Ward-MLM strategy. Large genetic variability was detected by the morphoagronomic data in the 138 genotypes that were evaluated, and the hybrids presented higher variability than the parents. Pseudo-F and pseudo-t^2 criteria showed that the optimal number of groups was three.

Group I was composed of 118 hybrid genotypes; group II was composed of the 10 *P. setacea* genotypes, and group III was composed of the 10 *P. edulis* genotypes. The longest distance was found between groups II and III (474.96). The shortest distance was detected between groups I and II (198.78), which indicates that the segregating population is genetically closer to *P. setacea* than to *P. edulis*. The Ward-MLM procedure is a useful tool to detect genetic diversity and group accessions using both qualitative and quantitative variables.