



Comparison of multivariate statistical algorithms to cluster tomato heirloom accessions

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ABSTRACT. Use of multivariate statistical algorithms is considered an important strategy to quantify genetic similarity. Local varieties and traditional (heirloom) seeds of genotypes are key sources of genetic variation. The Universidade Estadual do Norte Fluminense (UENF), Rio de Janeiro, Brazil, has a tomato gene bank with accessions that have been maintained for more than 40 years. We compared various algorithms to estimate genetic distances and quantify the genetic divergence of 40 tomato accessions of this collection, based on separate and joint analyses of discrete and continuous variables. Differences in continuous variables and discrete and joint analyses were calculated based on the Mahalanobis, Cole Rodgers and Gower distances. Although opinions differ regarding the validity of joint analysis of discrete and continuous data, we found that analyzing a larger number of variables together is viable and can help in the discrimination of accessions; the information that is generated is relevant and promising for both, the accessions conservation and the use of genetic resources in breeding programs.

Key words: *Solanum lycopersicum*; Gower dissimilarity;
Morphoagronomic descriptors; Molecular markers