Heirloom tomato gene bank: assessing genetic divergence based on morphological, agronomic and molecular data using a Ward-modified location model

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ABSTRACT. Accessions in gene banks need to be characterized and evaluated to determine their genetic diversity. We made a joint diversity analysis of the tomato gene bank of the Universidade Estadual do Norte Fluminense Darcy Ribeiro in Rio de Janeiro State, using the Ward-modified location model. Forty Solanum lycopersicum accessions were characterized and evaluated for 22 morphoagronomic descriptors and 131 random amplified polymorphic DNA markers. Based on the pseudo-F and pseudo-t² criteria, the optimal number of groups was established as five. Variability within groups was high for
both continuous and discrete nominal data. The first two canonical variables explained about 90% of the inter-group variability. Care should be taken in using the Ward-modified location model technique to avoid incorporating excessive and unnecessary markers, which could favor molecular markers when compared with morphoagronomic variables. However, the minimum number of markers is germplasm-dependent and must be recalculated for each new divergence analysis.

**Key words:** *Solanum lycopersicum*; Joint analysis; Ward-MLM; Random amplified polymorphic DNA markers