

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

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Genet. Mol. Res. 8 (1): 364-374 (2009)

Received October 22, 2008

Accepted February 12, 2009

Published March 31, 2009

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