



Genetic diversity of *Capsicum chinensis* (Solanaceae) accessions based on molecular markers and morphological and agronomic traits

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ABSTRACT. We estimated the genetic diversity of 49 accessions of the hot pepper species *Capsicum chinensis* through analyses of 12 physicochemical traits of the fruit, eight multi-categorical variables, and with 32 RAPD primers. Data from the physicochemical traits were submitted to analysis of variance to estimate the genetic parameters, and their means were clustered by the Scott-Knott test. The matrices from the individual and combined distance

were estimated by multivariate analyses before applying Tocher's optimization method. All physicochemical traits were examined for genetic variability by analysis of variance. The responses of these traits showed more contribution from genetic than from environmental factors, except the percentage of dry biomass, content of soluble solids and vitamin C level. Total capsaicin had the greatest genetic divergence. Nine clusters were formed from the quantitative data based on the generalized distance of Mahalanobis, using Tocher's method; four were formed from the multi-categorical data using the Cole-Rodgers coefficient, and eight were formed from the molecular data using the Nei and Li coefficient. The accessions were distributed into 14 groups using Tocher's method, and no significant correlation between pungency and origin was detected. Uni- and multivariate analyses permitted the identification of marked genetic diversity and fruit attributes capable of being improved through breeding programs.

Key words: Physicochemical traits; Multi-categorical variables; Multivariate analysis; *Capsicum chinensis*