



Genetic variability of watermelon accessions based on microsatellite markers

R.N.C. de S. Gama¹, C.A.F. Santos² and R. de C.S. Dias²

¹Programa de Pós-Graduação em Recursos Genéticos Vegetais,
Universidade Estadual de Feira de Santana, Feira de Santana, BA, Brasil

²Laboratório de Genética Vegetal, Embrapa Semiárido, Petrolina, PE, Brasil

Corresponding author: R.N.C. de S. Gama

E-mail: renata.natalia@hotmail.com

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ABSTRACT. We analyzed the genetic variability of 40 watermelon accessions collected from 8 regions of Northeastern Brazil using microsatellite markers, in order to suggest strategies of conservation and utilization of genetic variability in this species. These accessions are not commercial cultivars. They were sampled in areas of traditional farmers that usually keep their own seeds for future plantings year after year. An UPGMA dendrogram was generated from a distance matrix of the Jaccard coefficient, based on 41 alleles of 13 microsatellite loci. Analysis of molecular variance was made by partitioning between and within geographical regions. The similarity coefficient between accessions ranged from 37 to 96%; the dendrogram gave a co-phenetic value of 0.80. The among population genetic variability was high ($\hat{\phi}_{ST} = 0.319$). Specific clusters of accessions sampled in 3 regions of Maranhão were observed while the other 5 regions did not presented specific clusters by regions. We conclude that watermelon genetic variability is not uniformly dispersed in the regions analyzed, indicating that geographical barriers or edaphoclimatic conditions have limited open mating. We suggest sampling a greater number of

populations, so regional species diversity will be better represented and preserved in the germplasm bank.

Key words: *Citrullus lanatus*; Conservation; SSR; AMOVA; Dendrogram