

Selection of mango germplasm for cross breeding program based on multivariate analysis in the Brazilian Semi-arid

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In order to identify mango accessions for a cross breeding program, multivariate analysis was applied in a germplasm collection to estimate the genetic divergence among them. 48 accessions of the Embrapa Semi-Arid Mangoes Germplasm Bank, located at Juazeiro, BA, Brazil were evaluated for seven fruit quantitative traits. The multivariate technique was Tocher cluster, based on the averaged Euclidian distance of the standardized original data. It was observed a huge genetic divergence among accessions, suggesting a large genetic variability among them for many agronomic traits. The largest and the shortest genetic divergence were observed between the cultivar Parwin and Favo de Mel, and Bonita and Dama de Ouro, respectively. Taking in account the genetic distance and the agronomic performance, the crosses between Parwin x Espada Ouro, Parwin x Eldon, Parwin x Maia, Parwin x GI Proc. 006, Parwin x Favo de Mel, Palmer x Maçã, Palmer x Espada, Palmer x GI Proc 006, Palmer x Espada Ouro, Palmer x Pêssego, Manzanillo x Carabao, Smith x Foice and Momi-K x Kensington should result in a good genetic combinations, and therefore they are recommended for mango breeding program in the Brazilian Semi-Arid Region.