Genomic Relations among 31 Species of *Mammillaria* Haworth (Cactaceae) Using Random Amplified Polymorphic DNA

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Thirty-one species of *Mammillaria* were selected to study the molecular phylogeny using random amplified polymorphic DNA (RAPD) markers. High amount of mucilage (gelling polysaccharides) present in *Mammillaria* was a major obstacle in isolating good quality genomic DNA. The CTAB (cetyl trimethyl ammonium bromide) method was modified to obtain good quality genomic DNA. Twenty-two random decamer primers resulted in 621 bands, all of which were polymorphic. The similarity matrix value varied from 0.109 to 0.622 indicating wide variability among the studied species. The dendrogram obtained from the unweighted pair group method using arithmetic averages (UPGMA) analysis revealed that some of the species did not follow the conventional classification. The present work shows the usefulness of RAPD markers for genetic characterization to establish phylogenetic relations among *Mammillaria* species.

Key words: Mammillaria spp., RAPD, Molecular Phylogeny