

Morphological Characterization and Genetic Diversity Mapping of Local Mango Genotypes Using Microsatellite (SSR) Markers in Far-Western Hills of Nepal

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Abstract

The present study was conducted during 2018-19 A.D. to assess the morphological and genetic variation that exists in 39 mango genotypes of Doti district of Nepal. A total of 35 International Plant Genetic Resources Institute (IPGRI) descriptors were used to characterize 34 mango genotypes (33 local and 1 hybrid variety) morphologically. Genetic diversity among 39 genotypes was assessed using 20 simple sequence repeat (SSR) markers. The genomic DNA was extracted from young leaf samples using cetyl trimethyl ammonium bromide (CTAB) method. The results of the study showed considerable variation exist in terms of tree, leaf, fruit, stone and seed character. Data on 14 quantitative traits were subjected to principal component analysis (PCA) and cluster analysis. Three major principal components were formed with cumulative diversity of 82.6%. Results of cluster analysis grouped 34 mango genotypes into four groups with test genotype Amrapali, an improved variety, felt into separate cluster. Out of 20 primer pairs, 19 produced polymorphic bands and one monomorphic band. The average polymorphism information content (PIC) value of 0.53 was obtained across all genotypes. The 39 mango genotypes were separated into four main clusters using unweighted pair group method with arithmetic mean (UPGMA) based on Dice similarity coefficient. Similarity level of 59-100% was observed among 39 genotypes showing some level of genetic diversity. The study was able to show variation among mango genotypes using morphological characters and genetic analysis. These genotypes may be source of gene pool for utilization in breeding programmes and thus needs to be conserved.

Keywords: Genetic diversity, Mango, SSR marker, Principal Component Analysis, Cluster analysis