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Analysis of genetic diversity of Indian melon (*Cucumis melo L.*) land races and its comparison with global reference melon populations

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The present investigation entitled, “Analysis of genetic diversity of Indian melon (*Cucumis melo L.*) land races and its comparison with global reference melon populations” was conducted at Department of Vegetable Science and School of Agricultural Biotechnology, Punjab Agricultural University Ludhiana. Eighty-eight melon accessions collected from Utrakhand and Uttar Pradesh states of India representing four agro-ecological regions (six sub-regions) and eight reference accessions from USA were characterized and evaluated for nineteen morphological traits of plant and fruit, biochemical traits such as T S S, ascorbic acid content, titrable acidity and dry matter content, SSR genotyping and reaction to diseases. Significant differences were noted among all the accessions for all the characters observed. Phenotypic and genotypic coefficients of variation were found to be high for fruit weight and node at which first hermaphrodite flower appears. High heritability alongwith high genetic advance was recorded for fruit weight, node at which first hermaphrodite flower appears, fruit length, seed cavity length, number of primary branches per vine and total soluble solids content. D2 analysis grouped the accessions into ten clusters. The reference accessions obtained from USA and land races collected from different agro-ecological zones of India were found to be scattered in different clusters. No parallelism was found between genetic and geographic diversity. DNA polymorphism was utilized to cluster the genotypes into different clusters based on similarity as well as dissimilarity coefficients. On basis of SSR analysis, dendrogram clustered 96 accessions into three major groups. There was a significant correlation between botanical groups and the clustering pattern. Accessions belonging to cantalupensis cluster together in cluster I, accessions of reticulatus group cluster together in cluster II and momordica group cluster together in cluster III. However, some accessions of cantalupensis and reticulatus were intermixed in cluster I and II. Reference accessions cluster together forming a genetically unique assemblage in sub-group IIA and shared similarity coefficient of 0.65 with sub-group IIB. This suggested that reference accessions shared genetic affinities with Indian melon accessions that could not have been predicted based on their geographic origin. Four accessions were free from CMV and two accessions exhibited immune reaction to downy mildew. The results inferred that these melon accessions could be used to broaden the genetic base of melon.

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