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Genetic divergence in muskmelon (*Cucumis melo* L.)

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ABSTRACT

Fifty diverse types of Muskmelon (*Cucumis melo* L.) were evaluated for genetic divergence for yield and its contributing characters. The genotypes were grouped in seven clusters on the basis of relative magnitude of D^2 values. The maximum genetic distance was observed between cluster clusters II and V followed by cluster IV and V cluster V and VI and cluster I and II. However, cluster III and VII displayed lowest degree of divergence. The mean value of five characters was highest in cluster III, while cluster II and VI showed highest values for two characters. Cluster II showed lowest mean values for maximum characters. Total soluble sugar followed by total soluble solids and fruit yield per plant contributed maximum towards divergence.

Key words : Muskmelon, Genetic divergence, D^2.

In India, vegetables are grown in 5.8 million hectares area with production of 87.5 million tonnes, of which melons are grown on an area of 1,66,000 ha (More, 2001). The main areas of muskmelon cultivation are the riverbeds of Jamuna, Ganges, Narmada in the north and the Pennar, Kaveri, Krishna and Godavari in the south (Singh, 1998). Muskmelon (*Cucumis melo* L., 2n = 24) is most common dessert vegetable crop grown all over the world. The fruits are sweet and musky in flavour and relished by millions. The fruits contain 0.6 per cent protein, 0.2 per cent fat, 3.5 per cent carbohydrates, 32 mg calcium, 14 mg phosphorous, 1.4 mg iron, 16 mg carotene and 26 mg vitamins (per 100 g fresh weight of fruit). The TSS content varies from 8 to 17 per cent. It is good source of dietary fiber, vitamins and minerals. Inspite of wide range of genetic variability available in muskmelon, very little attention has been paid towards this crop with respect to yield and other useful traits. Since, the success of crop improvement programme is based solely on diversity available in the breeding material. In the present study diversity was assessed to select elite and divergent parents for use in further crop improvement programmes.

MATERIALS AND METHODS

The experimental material comprised of 50 genotypes of muskmelon collected from various sources in India. The experiment was carried out at the Main Vegetable Research Station, Anand Agricultural University, Anand during 2004-05. All the genotypes were grown in randomized block design with three replications at spacing of 150 cm (row to row) and 90 cm (plant to plant) in a plot size of 6 x 4.5 m. All the recommended cultural practices were followed during experimentation. The observations were taken on the randomly selected 10 plants from each plot. All the recommended cultural practices were followed during experimentation. Observations were recorded on number of node on which first female flower appears, days to first picking, fruit weight (kg),fruit length (cm), fruit girth (cm), flesh thickness (cm), fruits per plant, fruit yield per plant (kg), moisture content (%), total soluble solids (TSS in %), total soluble sugars (mg g^{-1}) and acidity (%). Mean values of all the traits were subjected to statistical analysis. Genetic divergence was estimated by calculating Mahalanobis D^2 statistics (Mahalanobis, 1936) between different pairs of genotypes. Then different clusters were generated through Tocher's method given by Rao (1952).

RESULTS AND DISCUSSION

On the basis of Mahalanobis's D^2 values seven clusters were formed from fifty accession of different geographical area. These seven clusters formed from 50 genotypes are grouped depending upon the genetic constitution of strains (Table 1). The clustering pattern showed that genotypes from different sources were clubbed into one group and also genotypes of same sources forming different clusters indicated the absence of relationship between geographical diversity and genetic diversity. The genetic diversity among the genotypes may due to factors like history of selection, heterogeneity, selection under diverse environments and genetic drift. The results further indicated that a maximum number of similar genotypes (24) appeared in cluster I. Clusters II and V were composed of 12 and 8 genotypes, respectively whereas, cluster III, IV and VI, VII were composed of two and single genotype, respectively. Kalloo *et al.*