

Genetic Divergence for Yield and its Component Traits in Pomegranate (*Punica granatum* L.)

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Twenty four genotypes of pomegranate, both exotic and indigenous were studied for genetic divergence for a set of eight traits by using Mahalanobis D^2 statistic. The genotypes were grouped into five clusters. The genotypes did not show any relation to the geographical diversity. Based on genetic divergence and superior cluster means, it is predicted that the crosses between genotypes from cluster IV and V may result in superior types.

Key Words: Pomegranate, Genotypes, Genetic divergence, Hybridization

Pomegranate (*Punica granatum* L.) is the most important minor fruit crop grown in the arid and semi-arid regions of the country. The foothills of Himachal Pradesh and Jammu and Kashmir have also accumulated wide range of variability in land races of pomegranate. Area of its cultivation is spreading to different climatic regions in the country due to its hardy nature, low maintenance cost and good yield. It is imperative to emphasize the need to develop location-specific superior cultivars. To cater these demands, large scale and long ranging breeding programmes are necessary. Choosing genetically diverse genotypes is a pre-requisite for any plant breeding programme because, it enables the expansion of genetic base to develop superior types. The use of Mahalanobis' D^2 statistic based on quantitative traits to estimate the genetic divergence has been emphasized by several workers (Bhattacharya *et al.*, 1979; Singh and Singh, 1980; Gaddekar *et al.*, 1992) to formulate the hybridization programme before effecting the actual crosses. Relatively little information is available in pomegranate. Therefore, present study was undertaken to measure the genetic diversity among pomegranate genotypes for yield and its related components to identify the suitable parent(s) for hybridization for yield improvement.

Materials and Methods

The experimental material consisted of 24 pomegranate genotypes collected from Mahatma Phule Krishi Vidyapeeth, Rahuri, District Ahmednagar (Maharashtra). However, they were different as per their centre of origin. The experiment was laid out in a randomized block design with three replications during 1999-2000 and 2000-01 at the experimental orchard of Fruits and Horticultural Technology Division, IARI, New Delhi. The recommended cultural practices were followed. Observations were recorded on three random plants per

genotype in each replication for 8 quantitative characters viz., plant height, E-W and N-S plant spread, duration of dormancy, flowering and maturity, number of fruits per plant and yield. The mean values were subjected to Mahalanobis' D^2 statistic to measure genetic divergence and the clusters were formed by Tocher's Method (Rao, 1952).

Results and Discussion

The analysis of variance showed highly significant differences among the genotypes for all the eight characters. On the basis of D^2 analysis, all the 24 genotypes were grouped into five clusters (Table 1). The maximum number of genotypes were in cluster II (10 genotypes), while cluster IV included the minimum number of genotypes (2 genotypes). The clustering of genotypes from different ecogeographical locations into one cluster could be attributed to the possible form of exchange of breeding materials or even varieties from one place to another (Sharma and Hooke, 1997). This may also be due to the fact that the unidirectional selection practiced for a particular trait in several places produced similar phenotypes, which were aggregated in one cluster irrespective of their geographic origin. On the other hand, many genotypes originating from one place were scattered over different clusters. Such genetic diversity among the genotypes of common geographic origin could be due to factors like; heterogeneity, genetic architecture of the populations, past history of selection, developmental traits and degree of general combining ability (Murty and Arunachalam, 1966).

The intra and inter-cluster divergence among the genotypes were of varying magnitude (Table 2). It may be seen that the intra-cluster distance was the highest for cluster II followed by cluster V while, cluster IV showed the minimum intra-cluster distance. The maximum

Table 1. Cluster classification of pomegranate genotypes for morphological and yield characters

Cluster	Genotypes included	No. of genotypes
I.	Jallore Seedless, Bassein Seedless, Jyoti, Muscat	4
II.	Siah Shirin, Achik Dana, Gul-e-Shah, Sur Sakkar, Speen Danedar, Speen Sakarin, Kali Shirin, Ak Anar, Khog, Shirin Anar	10
III.	P-23, Dholka, G-137, Bedana Sadana	4
IV.	Ganesh, Jodhpur Red	2
V.	Alandi, Kandhari, Kazak Anar, P-26	4

Table 2. Inter and intra-cluster distances (D2 values) for morphological and yield characters

Cluster	I	II	III	IV	V
I	1.590	3.586	3.034	4.894	3.493
II		1.997	3.681	4.394	2.757
III			1.140	2.937	3.630
IV				0.904	4.227
V					1.906

Bold letters denote the intra-cluster divergence (D^2) or average distance of cluster from cluster centroids

Table 3. Cluster means of pomegranate genotypes for different morphological and yield characters

Cluster	Plant height	Plant spread (m) (E-W)	(N-S)	Duration of dormancy (days)	Flowering duration (days)	Duration from fruits set to maturity (days)	Number of fruits per plant	Yield per plant (kg)
I	2.42	1.80	1.82	0.00	23.00	126.33	25.50	6.19
II	2.89	1.89	1.86	63.20	25.40	144.03	39.80	6.25
III	2.74	2.20	2.12	0.00	37.25	128.33	26.58	6.69
IV	3.15	2.62	2.50	0.00	28.50	133.33	29.00	7.26
V	2.70	2.00	1.97	32.00	23.50	134.58	45.00	10.01

Bold letters denotes the highest mean value within a column

inter-cluster distance was noted between cluster I and IV (4.894) followed by between II and IV (4.394). The distance between cluster II and V was the minimum (2.757) indicating close relationship between these clusters. Higher the genetic distance between the clusters, wider is the genetic diversity between genotypes. Similar findings were recorded by Dasgupta and Das (1984) and Jatasara and Paroda (1983) in wheat.

The cluster means for each character are presented in Table 3. The cluster V showed the highest mean values for the number of fruits per plant and yield. The highest mean for the plant height and E-W and N-S plant spread was observed in genotypes of cluster IV. The minimum values for all the eight traits were noted in cluster I genotypes. The comparisons of various methods for selecting the parents for hybridization in common bread wheat have been made by Bhatt (1973) which confirms the present findings.

On the basis of divergence, it is suggested that the maximum heterosis and good recombinants could be obtained in the crosses between genotypes of cluster IV and V. This information would be useful to the

breeders, who are engaged in the varietal improvement programmes of pomegranate.

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