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Short Communication

Genetic divergence in garden pea (*Pisum sativum* L.)

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Mahalanobis D^2 analysis was utilized in the present study to assess the genetic diversity among 83 genotypes of garden pea (*Pisum sativum* L.) and also the contribution of each character to the total diversity. Twenty-three lines of garden pea obtained from different sources and their 60 F_1's formed the materials for the study. The field experiment was laid out in Randomized Block Design with three replications during 2002-03. Each treatment consisted of single row of 3 m length and was kept 50 cm apart and plant to plant distance within row was maintained as 10 cm. All the recommended package of practices were followed to raise the normal crop. The observations were recorded on five randomly selected plants for each genotype replication wise on 18 quantitative characters *viz.*, days to first flowering (DFF), number of first flowering nodes (NFFN), days of first green pod picking (DFGPP), pod length (cm) (PL), 100 green pod weight (g) (HGPW), number of seeds/pod (NSPP), 100 green seeds weight (g) (HGSW), shelling percentage (SP), early yield/plant (g) (EYPP), total soluble solids (%) (TSS), number of green pods/plant (NGPPP), number of primary branches/plant (NPBPP), number of nodes/main stem (NNPMS), plant height (cm) (PH), green pod yield/plant (g) (GPYPP), days to seed maturity (DSM), dry matter weight/plant (g) (DMWPP) and dry seed yield/plant (g) (DSYPP). The genetic divergence was analysed using Mahalanobis D^2 statistics [1]. The genotypes were grouped in clusters according to Tocher's method as described by Rao [2].

The results revealed that the genotypes varied significantly for all the 18 characters studied. On the basis of D^2 values, 83 genotypes were grouped into 27 clusters (Table 1). Cluster I had the largest number of 17 genotypes. Six genotypes each in clusters II to V, four each in clusters VI to VIII, three each in clusters IX to XI, two each in clusters XII to XVI and one genotype fell in each cluster from XVII to XXVII. The clusters I, II, V, X, XI, XII, XVII, XVIII, XIX, XX and XXI included the F_1 crosses only, which showed that the genetic makeup of the crosses was altogether different from the parental lines. The perusal of clustering pattern (Table 1) indicated that the grouping was not influenced by the place of origin, rather genetic back ground influenced their clustering behavior. Saxena *et al.* [3], Singh and Ram [4], Pratap *et al.* [5] and Yadav *et al.* [6] also grouped different number of genotypes into various clusters. They pointed out that clustering of genotypes was random and geographic origin had negligible or no influence on them.

Intra and inter cluster D^2 values were computed for the 27 clusters. The intra-cluster D^2 value was least being zero in clusters XVII to XXVII and height (101.22) in cluster XII. The maximum inter-cluster distance of 2127.75 was found between clusters VI and XXIV followed by clusters II and XXIV (2076.79); and clusters XII and XXIV (1867.79) indicating that the genotypes falling in these clusters were highly divergent from each other. The line HUVP-3 (XXIV) had higher divergence from the parental lines PMR-43 (VI); PMR-31 and Punjab Agela-6 (XIV); Early Felthum First (XXVI); Azad P-I and Arkel (XV); VL-7(VII); PSM-3 (XXII); and NDVP-12 (XXIII). Similarly the line PMR-43 (VI) had high divergence from the parental lines FC-1, KS-245, Stop and Azad P-I (VIII); NDVP-250 (XXV); and PMR-34 and Bonneville (IV).

The mean of clusters for different characters indicated considerable difference between them for all the characters. The cluster XII had the highest mean (81.6g) for green pod yield/plant. The cluster XXIV had the highest mean for earliness [days to first flowering (89.6), number of first flowering nodes (20.4) and days to first green pod picking (103.0)] and shelling percentage (51.5); cluster XXII for pod length (9.2) and 100 green pod weight (776.9), cluster XIX for number of seeds (9), number of green pods (20.1) and days to seed maturity and cluster XVIII for plant height (121.7) and dry matter weight/plant. The clusters II, XI, XIII, XVII,

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Table 1. Grouping of 83 genotypes of garden pea in different clusters

Cluster no.	No. of genotype(s)	Genotype(s) included in the same cluster
1	17	PMR-34 × PA-6*, RP-3 × PA-6, NDVP-9 × PA-6, FC-1 × PA-6, FC-1 × Arkel, IP-3 × Arkel, IP-3 × PA-6, NDVP-12 × PSM-4, NDVP-9 × Arkel, Azad P-1 × PA-6, KS-168 PSM-4, Azad P-3 × PSM-4, PMR-34 × Arkel, Stop × PA-6, NDVP-9 × PSM-4, NDVP-250 × PA-6, Bonneville × PA-6
2	6	PSM-3 × PA-6, PSM-3 × Arkei, VL-7 × Arkel, NDVP-12 × PA-6, NDVP-12 × Arkel, PMR-31 × Arkel
3	6	PMS-3 × PMS-4, VL-7 × PSM-4, KS-168 × Arkel, PMR-31 × PSM-4, PMR-19 × Arkel, KS-168
4	6	PMR-34 × PSM-4, PMR-34, KS-245 × Arkel, KS-245 × PA-6, Bonneville, Stop × Arkel
5	6	Bonneville × PSM-4, NDVP-250 × PSM-4, KS-245 × PSM-4, HUVP-3 × PSM-4, RP-3 × PSM-4, Stop × PSM-4
6	4	PMR-31 × PA-6, PMR-43 × PA-6, PMR-43, VL-7 × PA-6
7	4	Azad P-3 × PA-6, VL-7, PMR-19 × PA-6, EFF × PA-6
8	4	FC-1, KS-245, Stop, Azad P-I
9	3	PMR-43 × PSM-4, Azad P-3 × Arkel, PMR-19
10	3	FC-1 × PSM-4, HUVP-3 × PA-6, Bonneville × Arkel
11	3	Azad P-1 × Arkel, IP-3 × PSM-4, Azad P-1 × PSM-4
12	2	PMR-43 × Arkel, KS-168 × PA-6
13	2	PMR-19 × PSM-4, NDVP-9
14	2	PMR-31, PA-6
15	2	Azad P-3, Arkel
16	2	IP-3, RP-3
17	1	HUVP-3 × Arkel
18	1	RP-3 × Arkel
19	1	NDVP-250 × Arkel
20	1	EFF × Arkel
21	1	EFF × PSM-4
22	1	PSM-3
23	1	NDVP-12
24	1	HUVP-3
25	1	NDVP-250
26	1	EFF**
27	1	PSM-4

*PA-6 = Punjab Ageta-6, **EFF = Early Felthum First

XXI and XXVI had maximum mean values for early yield/plant, dry seed yield/plant, TSS, number of nodes/main stem, number of primary branches/plant, and 100 green seeds weight, respectively. Based on the parental performance and inter-cluster distances, it is suggested that the line HUVP-3 may be crossed with the lines PMR-43, PMR-31, Punjab Agala-6, Early Felthum First, Azad P-3, Arkel, VL-7, PSM-3 and NDVP-12 for mid season; and the line FC-1, KS-245, Stop, Azad P-I, NDVP-250, PMR-34 and Bonneville for earliness are exploitation through recombination breeding following pedigree, bulk or single seed decent methods of generation advancement.

The relative contribution of different characters towards the expression of genetic divergence showed that early yield/plant had maximum contribution (42.37%) followed by days to first flowering (25.77%), dry seed yield/plant (14.96%), plant height (3.76%), dry matter weight/plant (3.47%) and green pod yield/plant (2.67%). These results are in agreement with those of Tikka and Asawa [7], and Singh and Ram [4] in peas. The contribution of pod length was however, zero showing minimum variability. The other characters contributed very less towards genetic diversity.

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