



## GENETIC DIVERGENCE IN PEA (*PISUM SATIVUM* L.)

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### Abstract

Genetic Divergence ( $D^2$ ) was studied in 26 genotypes of pea to quantify the nature and extent of diversity and to identify the most desirable genotypes by the Mahalanobis  $D^2$  technique. Analysis of variance revealed significant difference among the genotypes for all the 23 characters investigated. Twenty six genotypes were grouped into eight clusters. Among the eight clusters, it was observed that cluster I had the maximum of 10 genotypes followed by cluster VIII which had 4 genotypes. The maximum mean values for the twenty three characters were observed in cluster VII followed by cluster VIII and II. Genotypes Azad P-3, Arka Sampoorna, PSM-4, and Arka Karthik were found to be superior varieties for yield contributing traits.

**Key words :** Pea, genetic divergence, inter cluster.

### Introduction

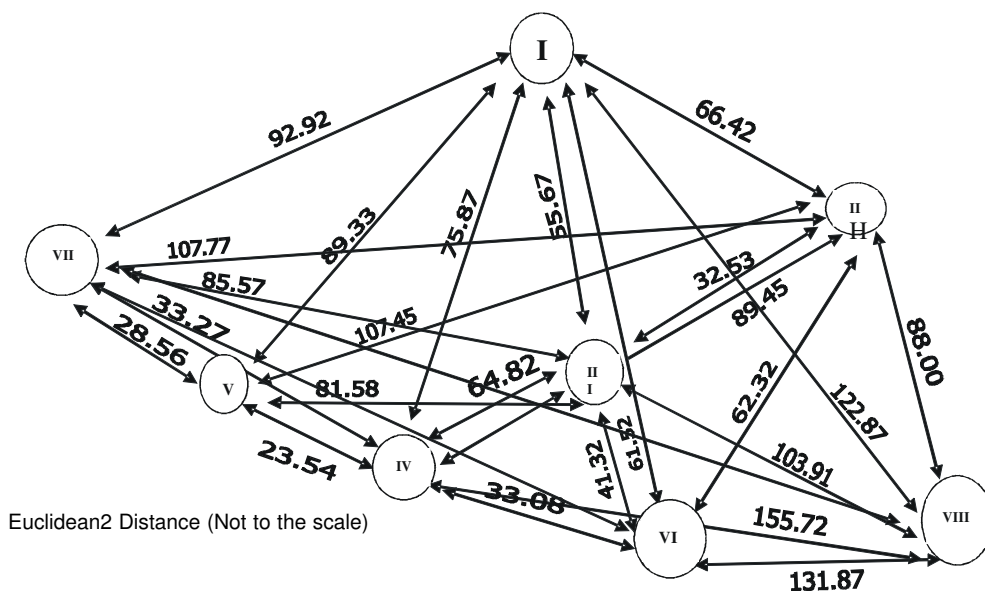
Pea (*Pisum sativum* L.) is an economically important pulse crop cultivated across the globe for its protein rich seed and soil improving characteristics of the plant. Pea is grown as a winter vegetable in the North Indian plains and South Indian hills for its protein rich seeds. India exports its cultivated pea in the form of dehydrated peas, frozen pea to the Middle East countries and also to the defense forces in domestic market. Commercial interest in peas and other pulses as a protein source (Santalla *et al.*, 2001) has been growing in recent years. In order to meet these demands, development of new high yielding varieties is greatly desired. However, limited parental materials and intensive breeding programs for desirable trait combinations have gradually decreased the genetic diversity in pea (Baranger *et al.*, 2004). Genetic diversity in crop ensures allelic variation that allows novel gene combinations, favourable phenotypes and facilitates development of future breeding lines (Hawkes, 1991.) Hence, knowledge of genetic diversity in the available cultivars of pea has an immense importance and in tune with immediate need in the selection of parents to be used in hybridization programme for obtaining desirable genetic combination. The genetically diverse plants are likely to produce high heterotic effects and larger frequency of better desirable segregants in subsequent generation as reported by Joshi (1979), Bartu *et al.* (1985), Kumar and Natarajan (1994). The  $D^2$  statistics is found to be an effective tool among the various techniques

available for genetic differentiation among the population (Rao, 1960). Therefore, an attempt was made to study the magnitude of genetic divergence in 26 genotypes and to identify suitable parents having wider genetic divergence for formulating a crossing programme.

### Materials and Methods

The experimental material for the present study comprised of 26 peas varieties. The experiment was conducted at Horticultural Research Station, Kodaikanal during *Rabi* 2012. Each accession was sown in four rows of 3 m length with a spacing of 45 cm between ridges and 10 cm between plants in two lines in a row. The experiment was laid out in Randomized Block Design with three replications. Observations on the quantitative characters *viz.*, plant height and number of leaves at vegetative stage (30 DAS), number of branches per node, first node bearing tendril, number of tendrils at the terminal end, internodal length, days to first flowering, plant height and number of leaves at flowering stage (60 DAS), number of branches at flowering stage, leaf area, first pod bearing node, pod length, pod girth, days to 50% flowering, number of seeds per pod, individual pod weight, individual seed weight, pod coat weight, number of pods per plant and qualitative characters *viz.*, yield per plant, 100 seed weight and shelling percentage were recorded on five randomly selected competitive plants.

Mahalanobis  $D^2$  statistics as suggested by Rao (1952) was used to measure the genetic divergence. The genotypes were grouped into different clusters based on



**Fig. 1 :** Cluster diagram representing diversity for 26 pea varieties.

**Table 1 :** Clustering pattern of 26 genotypes of peas

Cluster	No. of varieties	Name of the varieties
I	10	Arka Sampoorna, Arka Karthik, Arka Ajit, PSM-3, PM-2, PSM-4, Pant Uphar, U- Arkel, VL-7, Mithi Phali
II	2	Ooty-1, Peas Welcome 2010
III	2	Marina, Bonneville
IV	2	Khasi Mukti, P-Arkel
V	2	Khasi Utham, Khasi Shakti
VI	2	PB-89, PB-88
VII	2	Khasi Samrath, Local Samba
VIII	4	Azad-P3, Khasi Nandhini, MA-6, GS-10

Euclidean cluster analysis. The means over replications of the characters were used for this purpose.

### Results and Discussion

The analysis of variance indicated that differences among the genotypes were highly significant for all the 23 characters studied. This indicated the presence of appreciable amount of diversity among the genotypes studied. The computed  $D^2$  values for 26 genotypes had wide range showing high divergence among the genotypes. The  $D^2$  values were worked out for 325 pairs of combinations. By the application of clustering technique, all the 26 genotypes were grouped into eight different clusters. The composition of different clusters is presented in table 1. It was observed that cluster I had the maximum

of 10 genotypes followed by cluster VIII, which had 4 accessions. Clusters II, III, IV, V, VI & VIII exhibited two genotypes each in a cluster. These genotypes were superior for one or fewer characters, which made them divergent from the other clusters. It was interesting to note that 26 genotypes of differences in origin were grouped in the same cluster, indicating absence of relationship between genetic diversity and geographical diversity. Similar results have been reported by Rao *et al.* (2005), Srinivas *et al.* (2006) and Reddy *et al.* (2012). The use of Mahalanobis  $D^2$  statistics for estimating genetic divergence have been emphasized by many workers like Singh and Ram (1985), Singh and Mishra (2008), Pathak *et al.* (2009) in cluster bean, Borah and Khan (2001) in cowpea since, it permits precise comparison among all possible pairs of population in any given group effecting actual crosses.

The average intra and inter cluster distance among eight clusters (table 2) (fig. 1) revealed that the genetic diversity among the genotypes were generally superior for one or few characters, which made them divergent from other clusters. Maximum distance of 30608.90 was recorded between cluster VII and VIII, followed by clusters V & VIII, whereas the cluster II exhibited least divergent (163.13) followed by cluster III showing a distance of 200.50 between them. The lowest mean intra cluster distance of 12.77 was exhibited by cluster II, while the highest intra cluster distance was exhibited by cluster VIII.

The data on the means of all the 23 characters in respect of 8 clusters are summarized in table 3. Cluster I

**Table 2:** Mean intra-cluster (diagonal) and inter-cluster D<sup>2</sup> and D values

Cluster	I	II	III	IV	V	VI	VII	VIII
I	6271.56 (79.19)	4412.36 (66.42)	3099.57 (55.67)	5756.34 (75.87)	8016.54 (89.53)	3784.94 (61.52)	8635.02 (92.92)	15099.12 (122.87)
II		163.13 (12.77)	1058.21 (32.53)	8002.26 (89.45)	11546.45 (107.45)	3884.40 (62.32)	11616.16 (107.77)	7745.63 (88.00)
III			200.50 (14.16)	4202.57 (64.82)	6655.90 (81.58)	1707.59 (41.32)	7322.47 (85.57)	10797.51 (103.91)
IV				213.33 (14.60)	554.54 (23.54)	1094.76 (33.08)	1107.28 (33.27)	24249.41 (155.72)
V					229.56 (15.15)	2578.22 (50.77)	815.77 (28.56)	29759.96 (172.51)
VI						727.92 (26.98)	2935.26 (54.17)	17391.23 (131.87)
VII							1328.24 (36.44)	30608.90 (174.95)
VIII								11827.14 (108.75)

Intra cluster divergence- diagonal values, Inter cluster divergence- off diagonal values, D values- values in parenthesis.

**Table 3:** Cluster mean values for 23 characters in peas.

Clusters and characters	I	II	III	IV	V	VI	VII	VIII
Plant height at vegetative stage	24.26	24.09	<b>25.45</b>	20.36	24.53	<u>17.01</u>	25.36	24.61
Number of leaves at vegetative stage	26.38	29.44	29.83	25.00	29.33	<u>24.58</u>	<b>31.29</b>	26.91
Number of branches	7.06	6.91	7.25	5.83	6.67	<u>5.50</u>	<b>7.33</b>	7.20
First node bearing tendril	1.65	1.75	1.66	1.08	1.41	1.47	<b>2.00</b>	<u>1.37</u>
Number of tendrils	<b>5.43</b>	3.66	4.08	3.50	4.50	<u>3.33</u>	4.08	4.12
Internodal length	3.64	3.49	3.51	3.22	<b>3.92</b>	<u>2.80</u>	3.34	3.88
Days to first flowering	44.01	<b>47.41</b>	41.66	<u>32.91</u>	33.83	36.41	43.83	38.95
Plant height at flowering stage	54.77	58.61	68.53	46.69	45.45	<u>45.35</u>	<b>78.18</b>	48.82
Number of leaves at flowering stage	56.13	65.08	56.16	60.50	67.58	<u>45.08</u>	<b>86.50</b>	59.70
Number of branches at flowering stage	15.13	13.58	12.66	13.83	<u>11.66</u>	12.25	<b>16.41</b>	13.50
First node bearing pod	<b>9.18</b>	8.58	8.66	8.50	<u>8.25</u>	9.16	8.66	9.04
Days to 50 % flowering	47.36	<b>51.83</b>	46.33	38.75	<u>37.08</u>	39.50	48.16	43.12
Pod length	8.17	8.34	9.31	8.36	7.66	8.41	<u>7.57</u>	<b>10.76</b>
Pod girth	<u>4.53</u>	5.13	4.73	4.91	4.81	5.03	<b>5.26</b>	4.99
Number of seeds per pod	6.21	8.25	<b>7.67</b>	<u>4.58</u>	6.58	6.00	5.16	7.20
Individual pod weight	5.70	6.83	6.04	4.62	4.37	4.81	<u>3.71</u>	<b>8.51</b>
Individual seed weight	0.17	0.14	0.19	0.18	<b>0.20</b>	<u>0.13</u>	0.14	0.16
Pod coat weight	<b>3.78</b>	3.58	3.15	2.41	2.74	3.17	<u>2.40</u>	4.76
Leaf area	<u>8.05</u>	<b>17.29</b>	10.56	10.07	8.21	12.52	13.53	14.34
Number of pods per plant	21.79	18.77	21.49	18.54	<u>17.33</u>	<b>22.51</b>	20.42	21.09
Yield per plant	119.56	134.77	126.64	88.94	79.07	102.22	<u>70.33</u>	<b>174.91</b>
100 seed weight	20.18	19.19	<u>16.66</u>	24.49	21.71	<b>24.81</b>	20.89	20.78
Shelling percentage	<b>48.33</b>	42.50	<u>41.33</u>	48.00	45.66	46.50	43.83	44.58

Bold values- Highest mean, Underlined values- Lowest mean.

**Table 4 :** Contribution of each character to divergence.

Character	No. of first rank	% contribution
1	0	0.00
2	0	0.00
3	0	0.00
4	0	0.00
5	0	0.00
6	0	0.00
7	3	0.92
8	0	0.00
9	0	0.00
10	0	0.00
11	0	0.00
12	0	0.00
13	0	0.00
14	0	0.00
15	0	0.00
16	0	0.00
17	0	0.00
18	0	0.00
19	11	3.38
20	0	0.00
21	143	44.00
22	13	4.00
23	155	47.69
<b>Total</b>	<b>325</b>	<b>100</b>

exhibited the lowest mean values for pod girth (4.53) and leaf area (8.05). The same cluster possessed highest mean values for number of tendrils (5.43), first node bearing pod (9.18) and shelling percentage (48.33%). Cluster II possessed highest mean values for days to first flowering (47.41), days to 50% flowering (51.83), number of seeds per pod (8.25) and leaf area (17.29). Two lowest mean values was exhibited by cluster III *viz.*, 100 seed weight (16.66) and shelling percentage (41.33) and also it recorded a highest mean value of 25.45 for the trait plant height at vegetative stage. Cluster IV exhibited two lowest mean values for days to first flowering (32.91) and number of seeds per pod (4.58). Further cluster V recorded the lowest mean values for number of branches at flowering stage (11.66), first node bearing pod (8.25), days to 50% flowering (37.08), number of pods per plant (17.33) and highest mean values for internodal length (3.92), individual seed weight (0.20). Two highest values for number of pods per plant (22.51) and 100 seed weight (24.81) and eight lowest mean values for plant height at vegetative stage (17.01), number of leaves at vegetative stage (24.58), number of branches

(5.50), number of tendrils (3.33), internodal length (2.80), plant height at flowering stage (45.35), number of leaves at flowering stage (45.08) and individual seed weight (0.13) was observed in cluster VI. Cluster VII exhibited highest mean values for number of leaves at vegetative stage (31.29), number of branches (7.33), first node bearing tendril (2.00), plant height at flowering stage (78.18), number of branches at flowering stage (16.41) and pod girth (5.26). The same cluster possessed lowest mean values for pod length (7.57), individual pod weight (3.71), pod coat weight (2.40) and yield per plant (70.33). One lowest mean value of 1.37 for first node bearing tendril and four highest mean values for pod length (10.76), individual pod weight (8.51), pod coat weight (4.76) and yield per plant (174.91). In general cluster VII recorded highest mean for six characters namely number of leaves at vegetative stage, number of branches, first node bearing tendril, plant height at flowering stage, number of branches at flowering stage and pod girth. Selection of genotypes from divergent clusters, might prove more useful and when they are selected with due consideration of *per se* performance. However, looking at subjective and arbitrary nature of grouping with D<sup>2</sup> statistic (Singh and Ramanujam, 1981) and depending on breeder's interest more than one genotypes from a cluster could be selected for breeding programme.

The relative contribution of each character towards genetic divergence was estimated by the individual characters. The number of times each character appeared in first rank is presented in table 4. The character shelling percentage contributed the maximum percentage of 47.69 towards genetic divergence followed by yield per plant (44.00), 100 seed weight (4.00), leaf area (3.38). The character days to first flowering (0.92) showed negligible contribution to divergence.

Combined ranking resulted in the identification of superior genotypes for further exploitation as potential parents for hybridization programme. Combined ranking based on five characters *viz.*, days to first flowering, leaf area, yield per plant, 100 seed weight and shelling percentage, which had contributed maximum of genetic divergence resulted in the identification of genotypes followed by Arka Karthik, Arka Sampoorana, PSM-4, Peas Welcome 2010 and Bonneville. The above superior varieties were as desirable ones for further utilization as parents for hybridization programme.

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