



## Genetic divergence analysis of yield and its contributing traits in tall field Pea (*Pisum sativum* L.)

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ARTICLE INFO	ABSTRACT
<p><b>Original Research article</b> Received on March 22, 2017 Accepted on May 13, 2017</p> <p><b>Article Authors</b> V. P. Rahul, Bharat Bhushan, Ravi Kumar, Ram Krishna <b>Corresponding Author Email</b> <a href="mailto:vprahul@iim.ac.in">vprahul@iim.ac.in</a></p>	<p>The experimental material consisting of forty advance genotypes including two checks (Rachna and Shikha) was evaluated in Randomized Block Design with three replications for eleven characters by using Mahalanobis's <math>D^2</math> statistic. The clustering pattern of genotypes showed no definite relationship between genetic divergence and geographical distribution of genotypes. The genotypes were grouped into seven clusters. The maximum ten lines were put cluster IV, it had maximum intra-cluster distance while inter-cluster distance was highest between I and II. Cluster means indicated that none of the clusters was superior for all the characters studies; however hybridization between genotypes belonging to different cluster (<i>viz.</i> I<sup>st</sup> and II<sup>nd</sup>) is suggested for development of superior genotypes in field pea.</p>
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Field pea (*Pisum sativum* L.) is an important cool season grain legume in the Indian sub-continent. Genetic variation is essential for effective selection. In order to genetic variability, hybridization between genotypes of diver origin is suggested to unlock new recombination. Genetic divergence has been used as indirect parameter of moderate effectiveness in selecting parental line to produce high yielding progenies. Success of the hybridization followed by selection depends largely in the selection of parents with high genetic diversity for traits of interest (Murthy and Arunachalam, 1966). Therefore, an effort was made to estimate the nature and magnitude of genetic diversity in a set of forty genotypes of field pea.

### MATERIALS AND METHODS

The experimental material comprising forty field pea germplasm lines including with two checks (Rachna and Shikha) were obtained from Legume Section of Department of Genetics & Plant Breeding CSAUA&T Campus Kanpur and showed at Oil Seed Research Farm, Kalyanpur, CSAUA&T Kanpur in randomized block design with three replications during rabi 2008-09. Each treatment was sown in 6 rows plot of 4 meter length with the

distance of 30 cm between row to row and 10 cm between the plants. All the recommended cultural practices were followed to raise a good crop. Ten competitive plants were randomly selected and observations were recorded on 11 quantitative/qualitative traits. Days to flower, Plant height (cm), Number of branches per plant, Biological yield per plant (g), Number of pods per plant, Pod length (cm). Number of seeds per plant, Harvest index (%), 100-seed weight (g), Protein Content (%) and Seed yield per plant (g). Protein Content was estimated by Kjeldahl method. The replicated data were subjected to genetic divergence analysis using Mahalanobis,  $D^2$  statistic (Mahalanobis, 1936) as suggested by (Rao, 1952). All the genotypes were grouped into respective clusters on the basis of  $D^2$  values following Tocher's method.

### RESULTS AND DISCUSSION

The analysis of variance revealed highly significant variation among the genotypes for all the character studied. These differences could be used in distinguishing genotypes on the basis of their morphology. Based on the  $D^2$  analysis, all genotypes were grouped into seven different clusters table 1. Cluster II was the biggest cluster having ten

**Table 1. Clustering pattern of genotypes on the basis of Mahalanobis D2 statistic in field pea (*Pisum sativum* L.)**

Cluster number	No. of genotypes	Genotypes
I	7	KPMR 747, KPMR 851, KPMR 886, KPMR 914, KPMR 916, KPMR 923, KPMR 927
II	6	KPMR 890, KPMR 892, KPMR 915, KPMR921, KPMR 926, KPMR 928
III	5	Rachna, Shikha, KPMR 853, KPMR 919, KPMR 920
IV	10	KPMR 888, KPMR 925, KPMR 930, KPMR 931, KPMR 932, KPMR 933, KPMR 934, KPMR 935, KPMR 936, KPMR 937
V	3	KPMR 839, KPMR 857, KPMR 860
VI	5	KPMR 745, KPMR 793, KPMR 834, KPMR 913, KPMR 917
VI	4	KPMR 918, KPMR 922, KPMR 924, KPMR 929

**Table 2. Intra and inter cluster distance (D2) among seven clusters in field pea (*Pisum sativum* L.)**

Cluster	I	II	III	IV	V	VI	VII
I	5.7696						
II	25.2909	3.9680					
III	8.0883	22.1558	4.9106				
IV	18.1305	7.6231	12.8737	5.1030			
V	12.2150	16.3863	21.6132	18.5158	2.6373		
VI	13.9801	9.6162	9.8031	6.9063	9.7032	2.4900	
VI	15.4920	23.9904	13.4102	19.0270	19.0270	15.5314	4.0441

**Table 3. Cluster mean and per cent contribution towards divergence for eleven characters in field pea (*Pisum sativum* L.)**

Characters/ Cluster	Days to flower	Plant height (cm)	Number of branches per plant	Biological yield per plant (g)	Number of pods per plant	Pod length (cm)	Number of seeds per plant	Harvest index (%)	100-seed weight (g)	Protein Content (%)	Seed yield per plant
I	60.09	131.38	2.50	27.56**	18.88**	4.78	3.29	31.88	17.79	19.93	8.90*
II	67.62*	131.70	2.37	20.82	11.73*	4.40	2.68*	25.06*	18.46**	19.50	5.29*
III	60.00	126.47	2.60**	23.51	17.09	4.47	3.11	32.39	15.93*	21.42**	7.58
IV	64.74	117.54*	2.36	18.75	12.69	4.22*	3.12	34.09	17.93	19.76	6.39
V	61.96	155.84**	2.07*	26.07	13.98	4.63	3.40**	27.30	18.43	19.16*	6.98
VI	59.06*	137.03	2.32	20.55	13.12	4.36	3.03	29.10	16.53	19.41	6.14
VII	62.03	134.10	2.28	17.97*	12.98	4.84*	3.34	42.05**	18.35	21.22	7.33
Contribution towards divergence(%)	18.72	37.44	00	8.34	17.44	00	00	12.18	0.76	1.41	3.71

\*,\*\* indicates lower and upper ranges, respectively

genotypes which followed by cluster I with seven genotypes, cluster II with six genotypes, cluster III & VI with five genotypes, cluster VII with four genotypes and cluster V with three genotypes. Similar results were also reported by Dobhal and Ram (1985), Saxena *et al.* (1985) and Singh *et al.* (2013). This indicated that there was a wide diversity among the tall field pea genotypes for the character studied. The average intra and inter cluster  $D^2$  values (table-2) indicated that cluster IV with ten genotypes, namely KPMR 888, KPMR 925, KPMR 930, KPMR 931, KPMR 932, KPMR 933, KPMR 934, KPMR 935, KPMR 936 and KPMR 937 exhibited maximum intra cluster distance ( $D^2=5.1030$ ).

This cluster was the most divergent group and genotypes falling in the cluster could be utilized as parents for hybridization. Cluster I ( $D^2=5.7696$ ) with seven genotypes, and cluster III ( $D^2=4.9106$ ) with five genotypes were next most divergent group. As far as inter-cluster divergence is concerned, cluster I and II were found to be highly divergent from each other as indicated by maximum  $D^2$  value (25.2909). This was followed by cluster II and VII showing average inter-cluster  $D^2$  value of 23.9904, cluster II and III ( $D^2=22.1558$ ), cluster III and V (21.6132), cluster IV and VII, and Cluster V and VII (19.0270) parents selected from these individual groups showing maximum inter cluster distance are likely to produce superior recombinants. Which indicate that genotype present in these clusters may give high heterotic response and better segregant. There are necessary attention is required to focus on these characters. Similar result was observed by Tiwari *et al.* (2004), Gupta and Singh (2006), Kumar *et al.* (2008) and Yadav *et al.* (2009). Singh and Mishra (2008), have also opined that diversity among the genotypes per measuring intra cluster distance was adequate for improvement of pea by hybridization and selection. Cluster means for different traits presented in table 3 showed that cluster means for days to flower varied from 59.60 days in cluster VI to 67.62 in cluster II with overall mean of 61.21 days. Similar was the case with days to maturity. Cluster means for seed yield per plant, pod length, number of pods per plant and biological yield per plant were recorded to be highest in cluster I while cluster with the lowest values for these traits were II, IV and VII. Cluster III exhibited highest mean values for number of branches per plant (2.60) and protein content (21.42). For number of seeds per pod

highest mean of 3.40% was recorded for cluster V and lowest for cluster II. This indicated that none of the clusters contained genotypes with all the desirable characters which could be directly selected and utilized. Also, most of the minimum and maximum mean values were distributed in relatively distant clusters. Therefore, hybridization between genotypes falling in different clusters is necessary for development of desirable varieties. Recombination breeding between genotypes of different clusters was also suggested by Sonawane and Patil (1991). The results of the present study suggest that hybridization between genotypes of distant clusters may provide a wide spectrum of variation in the segregating progeny.

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