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STUDIES ON GENETIC DIVERSITY UNDER VARYING ENVIRONMENTS IN PEA (*PISUM SATIVUM* L.)

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ABSTRACT

Genetic diversity in pea with 30 genotypes using D^2 statistics revealed significant differences among the genotypes for yield and its component characters. The genotypes were grouped into 4 clusters in E_1, 4 clusters in E_2, 5 clusters in E_3, 5 clusters in E_4, 4 clusters in E_5, 5 clusters in E_6, 5 cluster in E_7 and 5 cluster in E_8. The intra cluster distance varied from 2.50(II) to 3.786 (III) in E1, 2.489 (II) to 3.409 in E2 (III), 2.546(V) to 3.065 (II) in E3, 2.494 (IV) to 3.282 (II) in E4, 2.684 (III) to 3.020 (II) in E5, 2.667 (II) to 3.008 (IV) in E6, 0.000 (V) to 2.948 (I) in E7 and 0.000 (V) to 2.903 (III) in E8. The results revealed that clustering pattern of genotypes was not consistence over environments. Number of clusters as well as number of genotypes in the cluster differed from environment to environment.

Key words : Pea, Genetic diversity, Environments.

INTRODUCTION

Field pea (*Pisum sativum* L.) is one of the most important pulse crops. It is a cool season crop grown in many parts of the world. Peas are important source of protein and good source of vitamins, A, B and C for human food. It is consumed in various forms. Dry peas are used as split pea (dal) and besan for various preparation and green pods are used as vegetables. The green plants are used as fodder for cattle and used as green manure to enrich soil fertility (McPhee, 2003). Success of the plant breeding programme targeted for development of high yielding, better quality and disease and pest resistance varieties depends on selection of suitable plants to be used in the breeding programme. The D^2 analysis technique for multivariate analysis has been successfully used to select divergent genotypes in order to exploit heterosis and for bringing together higher frequency of desirable genes in genotypes. To make the crossing programme effective, parents should belong to the different genetic clusters. It is usually observed that genetically diverse parents are likely to produce maximum heterotic expression in F1's and provide scope for the selection of desirable segregants in segregating populations. The diversity parameters were studied in grain legumes to measure the genetic distance but it is still very important to know the information pertaining the measurement of diversity under varying environments. Therefore, the present study was undertaken to know the genetic divergence among the pea genotypes by means of Mahalanobis Generalised Distance method, which would enable us to classify the available genotypes into distinct groups on the basis of their genetic diversity.

MATERIAL AND METHODS

Thirty genotypes procured from National Bureau of Plant Genetic Resources, New Delhi used in the experiment were grown during *rabi* seasons of the year 2004-05 and 2005-06 simultaneously at two locations research farms of Kisan Post Graduate College, Simbohali and Ch.Charan Singh University, Meerut. The experiment was laid out in randomized block design (RBD) with three replications under two moisture regimes. Four row of each genotype

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Table 1. Details of the environments used in the study

Location	Year	Moisture Regime	Environment
C.C.S. University, Meerut	2004-2005	Irrigated Rainfed	I II
	2005-2006	Irrigated Rainfed	III IV
Kisan (P.G.) College,Simbhaoli, Ghaziabad	2004-2005	Irrigated Rainfed	V VI
	2005-2006	Irrigated Rainfed	VII VIII

Table 2. Distribution of 30 genotypes of pea in different clusters under eight environments.

Environment 1		
Cluster No.	No. of genotypes	Name of genotypes
I	10	Pusa Prabhat, Ph-3, Bonniville, Pusa Pragati, Pusa Panna, DDR-1, Pusa Mukta, KPMR-157, P-1863, HVP-11.
II	7	PSG-3, Arkel, PSH-2, PSG-4, Pusa Kiran, JM-6, PSG-1
III	3	Pusa-10, EC-6, P-1540
IV	10	L-116, P-1852, DMR-4, DMR-7, Rachna, DMR-11, PMRK-1, T-163, Kinnouri-1, PMR-3
Environment 2		
I	6	Pusa Prabhat, Bonniville, P-1540, Rachna, PSG-4, DMR-11
II	6	Ph-3, DMR-4, Arkel, Pusa Pragati, DDR-1, P-1863
III	9	PSG-3, L-116, P-1852, EC-6, PSH-2, Kinnouri-1, Pusa Mukta, JM-6, KPMR-157
IV	9	Pusa-10, DMR-7, PMRK-1, T-163, PMR-3, Pusa Kiran, Pusa Panna, HVP-11, PSG-1
Environment 3		
I	5	Pusa Prabhat, L-116, P-1852, Pusa-10, Ph-3
II	6	PSG-3, EC-6, DMR-4, Arkel, PSH-2, Kinnouri-1
III	6	DMR-7, Bonniville, Rachna, PMR-3, Pusa Panna, Pusa Mukta
IV	5	PSG-4, DMR-11, PMRK-1, Pusa Pragati, PSG-1
V	8	P-1540, T-163, Pusa Kiran, DDR-1, JM-6, KPMR-157, P-1863, HVP-11
Environment 4		
I	8	Pusa Prabhat, PSH-2, Bonniville, PSG-4, Pusa Panna, Pusa Pragati, Pusa Mukta, PSG-1
II	3	PSG-3, Arkel, JM-6
III	3	Pusa-10, EC-6, P-1540
IV	6	Ph-3, PMR-3, Pusa Kiran, DDR-1, KPMR-157, HVP-11
V	10	L-116, P-1852, DMR-4, DMR-7, Rachna, DMR-11, PMRK-1, T-163, Kinnouri-1, P-1863
Environment 5		
I	10	Pusa Prabhat, Pusa-10, Bonniville, P-1540, Rachna, PSG-4, PMR-3, Pusa Panna, Pusa Mukta, KPMR-157
II	2	L-116, DMR-11
III	6	Pusa Kiran, DDR-1, JM-6, P-1863, HVP-11, PSG-1
IV	12	PSG-3, P-1852, Ph-3, EC-6, DMR-4, Arkel, PSH-2, DMR-7, PMRK-1, T-163, Kinnouri-1, Pusa Pragati

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Environment 6		
I	7	L-116, Pusa-10, Ph-3, DMR-7, Bonniville, PSG-4, PMRK-1
II	2	Pusa Prabhat, PSH-2
III	12	Rachna, DMR-11, T-163, Kinnouri-1, PMR-3, Pusa Panna, Pusa Pragati, Pusa Mukta, KPMR-157, P-1863, HVP-11, PSG-1
IV	8	PSG-3, P-1852, EC-6, DMR-4, Arkel, P-1540, Pusa Kiran, DDR-11
V	1	JM-6
Environment 7		
I	6	Pusa Prabhat, Pusa-10, EC-6, Pusa Panna, Pusa Mukta, JM-6
II	7	Arkel, PSG-4, Pusa Pragati, DDR-1, KPMR-157, P-1863, HVP-11
III	5	DMR-11, Ph-3, Bonniville, P-1540, PSG-1
IV	11	L-116, P-1852, DMR-4, PSH-2, DMR-7, Rachna, PMRK-1, T-163, Kinnouri-1, PMR-3, Pusa Kiran
V	1	PSG-3
Environment 8		
I	4	Bonniville, PSG-4, Pusa Mukta, KPMR-157
II	5	DMR-11, Pusa Kiran, Pusa Panna, JM-6, HVP-11
III	12	Pusa Prabhat, Pusa-10, DMR-4, Arkel, P-1540, Rachna, PMRK-1, T-163, Kinnouri-1, PMR-3, DDR-1, PSG-1
IV	8	PSG-3, L-116, P-1852, EC-6, PSH-2, DMR-7, Pusa Pragati, P-1863
V	1	Ph-3

Table 3. Estimatation of intra and inter-cluster distance in eight environments for thirty genotypes in pea.

Environmental 1					
Cluster No.	I	II	III	IV	
I	2.880				
II	2.849	2.510			
III	5.031	5.723	3.786		
IV	4.261	4.751	5.261	2.931	
Environmental 2					
Cluster No.	I	II	III	IV	
I	2.641				
II	5.531	2.489			
III	4.734	3.899	3.409		
IV	3.133	4.236	4.058	3.011	
Environmental 3					
Cluster No.	I	II	III	IV	V
I	2.553				
II	3.335	3.065			
III	4.486	3.661	2.764		
IV	5.066	4.411	4.046	2.608	
V	6.226	4.802	4.010	4.287	2.546
Environmental 4					
Cluster No.	I	II	III	IV	V
I	2.665				
II	4.212	3.282			
III	4.972	5.639	2.699		
IV	3.302	4.385	4.743	2.494	
V	4.538	5.087	5.949	3.585	2.963
Environmental 5					
Cluster No.	I	II	III	IV	
I	2.944				
II	5.107	3.020			
III	3.401	5.398	2.684		
IV	4.021	5.249	4.653	3.227	
Environmental 6					
Cluster No.	I	II	III	IV	V
I	2.888				
II	5.022	2.667			
III	3.304	5.543	2.726		
IV	4.584	4.886	3.751	3.008	
V	8.477	8.648	8.021	8.307	0.000

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Environmental 7					
Cluster No.	I	II	III	IV	V
I	2.948				
II	4.504	2.764			
III	3.925	3.184	2.726		
IV	4.995	3.224	3.305	2.798	
V	9.771	9.437	8.711	8.323	0.000
Environmental 8					
Cluster No.	I	II	III	IV	V
I	2.472				
II	3.887	2.895			
III	4.649	3.254	2.903		
IV	5.684	4.600	2.910	2.833	
V	10.010	9.512	8.544	8.456	0.000

were grown and two-meter row length and row-to-row spacing were kept at 30cm. Recommended agronomic and plant protection measures were taken. Eight environments, four in each year were created (Table 1). The data were collected on 16 characters. Observations were recorded on individual plant basis on 5 randomly selected plants of the middle row excluding the border plants. Their mean was used for statistical analysis. D^2 analysis was conducted using Mahalanobis Generalised Distance and clustering was done according to Tocher's method, as suggested by Rao (1952).

RESULTS AND DISCUSSION

Genetic divergence among the parental lines, especially in respect of the character in which improvement is sought, is a foundation for any crop improvement programme to the successful. Mahalanobis (1936) has suggested D^2 analysis, which is a powerful tool for determining genetic divergence within a population. Thirty genotypes of pea in the present study were grouped in 4 clusters in E1, 4 clusters in E2, 5 clusters in E3, 5 clusters in E4, 4 clusters in E5, 5 clusters in E6, 5 cluster in E7 and 5 cluster in E8 (Table 2).

Perusal of Table 3 revealed that the genotypes of the same cluster have little divergence of each cluster with respect to aggregate effects of the characters studied. The hybridization between the genotypes of same cluster, thus, may not provide good recombination and the crosses may be attempted between genotypic clusters of having large inter cluster distances. This is likely to give desirable transgressive segregants. The highest inter cluster distance was noted between cluster II and cluster III in E_1, in E_2 between cluster I and cluster II, in E_3 between cluster I and IV cluster, in E_4 between cluster II and III cluster, in E_5 between cluster II and III cluster, in E_6 between cluster II and V cluster, in E_7 between cluster I and cluster V and in E_8 between cluster I and cluster V. The greater the genetic distance between the clusters, showed higher genetic divergence among genotypes, and this helps in crop improvement. The intra cluster distance varied from 2.50(II) to 3.786 (III) in E1, 2.489 (II) to 3.409 in E2 (III), 2.546(V) to 3.065 (II) in E3, 2.494 (IV) to 3.282 (II) in E4, 2.684 (III) to 3.020 (II) in E5, 0.000 (II) to 3.008 (IV) in E6, 0.000 (V) to 2.948 (I) in E7 and 0.000 (V) to 2.903 (III) in E8. The data on cluster means (Table 4) indicated the existence of appropriate variation for various yield components. Therefore, selection of genotypes from different groups and using them in hybridization would prove fruitful in crop improvement program (Singh, 2002). Sirohi *et al.,* 2006, Singh *et al.,* 1998 and Gupta *et al.*, 1992 have also reported the similar findings in pea. The diversity among different genotypes measured by inter cluster distance (D value) play a vital role for improvement of pea by hybridization and selection (Singh and Mishra, 2008).

The pattern of distribution of genotypes from different geographical regions into different clusters followed a different preposition in each environment. This tendency of genotypes occurring in clusters cutting across geographical isolation is not the only factor causing genetic diversity. The results revealed that clustering pattern of genotypes was not consistence over environments. Number of clusters as well as number of genotypes in the cluster differed from environment to environment. Different methods for selection of parents for a hybridization programme have been suggested in the past for several crops. Usually, it is suggested that parents must be selected on the basis of D^2 analysis of Mahalanobis (1936). This is a useful tool in quantifying the degree of divergence between populations and also helps in the choice of genetically diverse parents to obtain recombinants in the segregating generations in the present study.

Table 4. Mean values of sixteen characters in different clusters under eight environments for thirty genotypes of pea.

Cluster No.	Days to 50% flowering	Days to maturity	Plant height	Leaf area index	Time of pod filling at interval	No. of pod/ plant	Pod length	Nodules weight	No. of nodules/ plant	No. of seed/ plant	Seed yield/ plant	Biological yield/ plant	100-seed weight	Harvest index	Protein content	Sugar content
Environment 1																
I	87.07	106.27	36.95	0.11	10.27	5.86	6.02	0.26	30.52	4.74	2.24	8.14	12.42	27.84	20.60	0.16
II	87.38	105.29	34.74	0.08	10.17	10.78	6.32	0.28	30.87	4.05	2.12	9.37	13.24	21.93	19.75	0.68
III	84.78	106.78	36.96	0.10	21.44	5.78	7.29	0.48	54.22	5.73	2.78	9.22	18.44	32.51	19.79	0.16
IV	92.13	107.00	82.75	0.16	9.95	13.68	6.32	0.36	38.47	4.76	5.37	18.31	15.40	30.03	20.28	0.19
Environment 2																
Cluster No.	Days to 50% flowering	Days to maturity	Plant height	Leaf area index	Time of pod filling at interval	No. of pod/ plant	Pod length	Nodules weight	No. of nodules/ plant	No. of seed/ plant	Seed yield/ plant	Biological yield/ plant	100-seed weight	Harvest index	Protein content	Sugar content
I	83.44	104.50	32.29	0.10	10.81	4.37	5.99	0.24	29.93	4.28	2.00	6.99	12.29	27.81	20.40	0.23
II	91.44	107.61	91.67	0.18	9.86	13.91	5.74	0.33	34.39	3.92	5.08	20.07	16.47	25.89	21.15	0.22
III	90.56	108.52	52.10	0.12	10.64	9.81	6.58	0.39	46.52	5.02	4.52	14.44	17.97	31.73	19.66	0.19
IV	89.78	107.81	38.17	0.09	9.72	10.71	5.82	0.28	29.73	4.09	2.37	11.01	13.18	21.60	20.26	0.46
Environment 3																
Cluster No.	Days to 50% flowering	Days to maturity	Plant height	Leaf area index	Time of pod filling at interval	No. of pod/ plant	Pod length	Nodules weight	No. of nodules/ plant	No. of seed/ plant	Seed yield/ plant	Biological yield/ plant	100-seed weight	Harvest index	Protein content	Sugar content
I	81.87	104.40	27.10	0.10	10.63	4.12	5.79	0.22	28.08	4.33	2.06	6.95	12.25	28.73	20.12	0.25
II	92.16	108.17	37.58	0.10	9.39	8.31	6.12	0.24	26.68	4.60	2.49	9.69	13.92	24.69	20.19	0.47
III	88.00	108.89	51.48	0.09	10.61	12.33	5.27	0.33	34.94	3.43	3.43	15.69	14.46	20.42	20.84	0.32
IV	88.00	110.13	37.44	0.11	11.05	7.73	5.99	0.42	51.03	4.31	3.92	12.60	20.43	32.21	20.29	0.29
V	94.00	108.58	89.78	0.19	9.85	14.26	5.70	0.35	38.37	4.14	5.99	21.23	17.59	28.68	20.30	0.15
Environment 4																
Cluster No.	Days to 50% flowering	Days to maturity	Plant height	Leaf area index	Time of pod filling at interval	No. of pod/ plant	Pod length	Nodules weight	No. of nodules/ plant	No. of seed/ plant	Seed yield/ plant	Biological yield/ plant	100-seed weight	Harvest index	Protein content	Sugar content
I	86.33	107.58	38.69	0.08	11.14	10.33	5.27	0.34	37.61	3.36	3.68	13.86	14.49	25.37	20.60	0.25
II	88.78	107.22	33.29	0.10	9.69	11.56	6.10	0.31	29.62	4.33	2.78	12.36	15.94	22.26	20.33	0.97
III	88.89	109.78	35.33	0.10	11.18	6.02	6.31	0.47	54.98	4.44	3.42	11.87	21.48	30.61	19.79	0.19
IV	92.69	110.56	39.91	0.12	10.77	10.33	5.46	0.33	37.78	3.79	5.54	14.98	17.10	36.63	20.34	0.48
V	93.80	108.70	89.24	0.17	9.72	13.71	5.61	0.34	36.63	4.08	5.85	21.29	16.94	27.83	20.62	0.18

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Environment 5

Cluster No.	Days to 50% flowering	Days to maturity	Plant height	Leaf area index	Time of pod filling at interval	No. of pod/ plant	Pod length	Nodules weight	No. of nodules/ plant	No. of seed/ plant	Seed yield/ plant	Biological yield/ plant	100-seed weight	Harvest index	Protein content	Sugar content
I	85.17	107.20	33.38	0.08	10.97	8.15	5.30	0.34	38.05	3.57	3.41	11.37	15.07	28.67	20.48	0.20
II	86.33	109.00	36.73	0.10	11.13	6.90	6.38	0.35	34.67	4.77	3.12	13.17	24.08	24.48	19.20	0.88
III	87.06	108.11	39.84	0.07	9.29	8.62	5.72	0.29	31.41	4.83	1.98	9.79	13.49	20.68	20.79	0.11
IV	94.28	109.39	72.63	0.16	9.98	12.52	5.69	0.34	36.40	4.12	5.80	18.07	16.53	32.29	20.18	0.28

Environment 6

Cluster No.	Days to 50% flowering	Days to maturity	Plant height	Leaf area index	Time of pod filling at interval	No. of pod/ plant	Pod length	Nodules weight	No. of nodules/ plant	No. of seed/ plant	Seed yield/ plant	Biological yield/ plant	100-seed weight	Harvest index	Protein content	Sugar content
I	82.14	106.52	26.91	0.08	11.00	6.04	5.65	0.33	34.50	4.16	2.39	9.10	14.74	26.21	19.99	0.39
II	85.17	106.67	37.90	0.07	11.07	13.80	5.07	0.37	45.70	3.13	4.97	16.43	14.38	27.67	21.02	0.23
III	87.94	108.50	45.12	0.08	9.12	9.04	5.83	0.28	30.35	4.63	2.49	10.26	14.19	23.70	20.69	0.10
IV	93.50	109.96	54.48	0.14	9.93	10.02	5.56	0.31	32.38	4.04	5.12	14.62	15.81	34.82	19.78	0.33
V	88.33	107.00	37.93	0.07	8.87	10.00	5.33	0.30	36.47	4.33	4.63	13.20	34.33	9.57	21.30	1.13

Environment 7

Cluster No.	Days to 50% flowering	Days to maturity	Plant height	Leaf area index	Time of pod filling at interval	No. of pod/ plant	Pod length	Nodules weight	No. of nodules/ plant	No. of seed/ plant	Seed yield/ plant	Biological yield/ plant	100-seed weight	Harvest index	Protein content	Sugar content
I	80.78	105.50	22.47	0.07	11.13	5.11	5.46	0.31	32.57	3.71	1.73	6.83	13.42	25.59	20.74	0.21
II	89.19	108.00	34.51	0.07	9.45	8.05	5.78	0.21	23.61	4.86	2.43	8.12	13.64	29.87	21.06	0.12
III	85.47	107.87	33.01	0.07	9.30	9.05	6.23	0.29	31.39	4.59	1.77	8.68	13.48	20.17	20.53	0.43
IV	87.45	109.48	55.82	0.10	9.16	9.82	5.67	0.29	30.87	4.45	3.27	11.80	14.62	27.31	20.28	0.06
V	88.33	107.00	37.93	0.07	8.87	10.00	5.33	0.30	36.47	4.33	4.63	13.20	34.33	9.57	21.30	1.13

Environment 8

Cluster No.	Days to 50% flowering	Days to maturity	Plant height	Leaf area index	Time of pod filling at interval	No. of pod/ plant	Pod length	Nodules weight	No. of nodules/ plant	No. of seed/ plant	Seed yield/ plant	Biological yield/ plant	100-seed weight	Harvest index	Protein content	Sugar content
I	80.25	105.08	23.41	0.06	10.83	4.92	5.31	0.33	35.42	3.28	1.55	6.08	11.63	25.66	20.88	0.08
II	84.67	105.07	24.05	0.07	10.67	6.27	5.98	0.25	26.21	4.88	1.27	7.08	12.72	18.54	20.37	0.26
III	88.28	108.31	43.37	0.07	9.05	8.63	5.69	0.24	25.63	4.47	2.44	9.45	13.73	26.22	21.19	0.20
IV	88.79	109.12	53.59	0.12	9.27	9.97	6.02	0.29	31.44	4.67	3.42	11.54	14.89	29.10	19.59	0.10
V	88.33	107.00	37.93	0.07	8.87	10.00	5.33	0.30	36.47	4.33	4.63	13.20	34.33	9.57	21.30	1.13

From the above discussion, certain conclusion regarding the use of information on genetic divergence for breeding programmes can be made. It is well known that in any breeding programme for high yielding and stable varieties, diveregent parents should be selected. One would also like that the parents of a crossing programme should be high yielding and stable, but divergent at the same time. On the contrary, this really suggests the need of studying divergence in varying environmental conditions, when the parents are to be selected after the study of divergence in different environment, two different approaches may be followed: (a) one may select the parents on the basis of divergence exhibited in the rich and most productive environment, like environment 6, 7 and 8 in the present study, high yielding and stable genotypes may selected from different clusters preferably having a high inter-cluster distance. (b) Selection of parents can also be made on the basis of divergence, across the environments, and can be considered as the reliable estimates of genetic divergence. It can be seen from Table 1 that the genotypes (JM-6, Pusa Prabhat, PSH-2 in E_6; PSG-3, DMR-11, PH-3, Bonniville, P-1540, PSG-1in E_7 and PH-3, Bonniville, PSG-4, Pusa Mukta, KPMR-157 in E_8) showed consistency as divergent parents for future hybridization programme.

REFERENCES

Gupta, V.B. *et al.* (1992). *Crop Imp.* **19(1):**18-22.

Mahalanobis, P.C. (1936). *Proc. Natl. Inst., India.* **2:**49-55.

McPhee, K. (2003). *Food, Agri. Environ.* **1(1):** 64-69.

Rao, C.R. (1952). *Advanced Statistical Methods in Biometrical Research*. John Wiley and Sons, New York.

Singh, D. and Mishra, V.K. (2008). *Agri. Sci. Digest*, **28(1):**77-79.

Singh, N. (2002). *Indian J. Pulse Res.*, **15:**70-72.

Singh, S.K. *et al.* (1998). *Genetika,* **30(1):**41-50.

Sirohi, S.P.S. *et al.* (2006). *Plant Archives* **6(2):**799-801.