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Studies genetic divergence for yield and its component traits in pea (*Pisum sativum* L.) in sodic condition

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Abstract

Pea (*Pisum sativum* L.) $2n = 2x = 14$, belongs to the family *Fabaceae*. It originated in central Asia, the Near East, Abyssinia and Mediterranean. In India huge range of variability is available in the land races or cultivars, in terms of qualitative as well as quantitative characters of pea.

Analysis of Variance in the present investigation indicated that the genotypes evaluated differed significantly among all the treatment for all the twelve traits. The 35 genotypes of pea were grouped into 6 clusters. The different clusters showed considerable differences in intra-cluster group means for 12 characters. Maximum cluster mean for green pod yield per plant was observed in cluster VI followed by cluster III. All the cluster from cluster I and VI had in general medium mean performance for most of the characters exhibiting extreme cluster means for none of the characters under study. Maximum cluster means for green pod yield per plant was observed in cluster III followed by cluster I and VI. All cluster showed maximum mean values for plant height. The minimum group mean value showed for branches per plant in all the clusters. The minimum inter-cluster distance was recorded between cluster III and I (51.922). The higher inter cluster distance indicated greater genetic divergence between the genotypes of those clusters, while lower inter-cluster values between the clusters suggested that the genotype of the clusters were not much genetically diverse from each other.

Keywords: Pea, Genetic Divergence, Intra-cluster, Variability, Variance

Introduction

The pea (*Pisum sativum* L.) is one of the earliest human foods crops belong to the family *Fabaceae*. The exact origin and progenitor of pea is unknown, but it is one of the oldest cultivated plants. Vavilove listed central Asia, the Near East, Abyssinia and Mediterranean as the centre of origin based on the genetic diversity. The possibility of improvement in any crop is measured by available variability in the crop. On other hand, yield is a complex character and is associated with some yield contributing characters. Yield is not only a polygenically controlled trait, but it is also directly or indirectly constituted by the associated yield characters. Instead of above parameters Mahalanobis D^2 analysis was also utilized into the assessment of genetic diversity among the genotypes and the contribution of each character to the total diversity. The genetic divergence (D^2) was analysed using Mahalanobis statistics. The genotypes are grouped in clusters according to their performance.

Methods and Materials

The experimental material consisting of thirty five pea genotypes was sown during Rabi season of 2009-10 to assess genetic divergence for yield and its component traits in pea (*Pisum sativum* L.) in sodic condition. The experimental field had sandy loam soil, low in organic carbon, nitrogen, medium in phosphorous, potash, and slightly sodic in nature with pH 8.5, Electronic Conductivity (EC) 04 and exchangeable sodium percentage (ESP) 29.9. The experimental material for the present investigation comprised 35 genotypes of Pea collected from different places in India and being maintained at main experiment station in the Department of Vegetable Science, N.D. University of Agriculture & Technology, Narendra Nagar (Kumarganj), Faizabad (U.P.) Table 1. The experiment was conducted in Randomized Block Design with three replications to assess the performance of 35 genotypes. Seed of each genotype were sown in a plot measuring 3.0 X 0.90 meter at spacing of 30 cm and 10 cm were maintained between row to row and plant to plant, respectively. Analysis of variance was computed using method suggested by Panse and Sukhatme and D^2 analysis was done by using method suggested by Mahalanobis (1928) [2].

Results and Discussion

The identification of donor parents for important characters, assessment of genetic variation and diversity in the available genotypes and the information about characters association are required for successful breeding programmes. The findings of present investigation consisting of thirty five genotypes of pea are discussed as follows for twelve characters. The analysis of variance for different characters is presented in table 1. The mean sum of square due to replication was non-significant for all the characters but pod length and seeds per pod were significant. The variation due to treatment was highly significant for all characters except nod at 1st pod appear and seeds per pod. In other words the performances of the genotypes with respect of these characters were statistically different; suggesting that, there is ample scope for selection present in different traits for pea improvement.

The studies of genetic divergence among the 35 genotypes of pea genotypes were carried out by using Mahalanobis D² statistics. In present investigation 35 genotypes of pea were grouped in six distinct non-overlapping clusters using Mahalanobis' D² statistics (Table 2). This indicated presence of considerable diversity in the genotypes. The major clusters in the above mentioned genetic divergence analysis contained frequently the genotypes of heterogeneous origin. Although, the genotypes of same origin or geographic region were also found to be grouped together in the same cluster, the instances of grouping of genotypes of different origin or geographic region in same cluster were frequently observed. This suggested that there is no parallelism between genetic and geographic diversity.

Table 3 reveals that the clustering pattern of the 35 genotypes was grouped into 6 different non-overlapping clusters. Cluster (III) had highest number of genotypes (11) followed by cluster I (9), II(6), and VI(6), and cluster IV had only two genotypes, where as cluster V had presented only one entry of genotype. The minimum intra-cluster distance was found for cluster V (0.000) and maximum was recorded for cluster II (45.321). the maximum inter-cluster distance were calculated between cluster V and VI (1000.943), which suggested that members of these two clusters are genetically very diverse to each other. The inter cluster values between IV and V (633.55) I and V (537.665) and cluster III and IV (477.752) were high. These results are supported by Sharma and Singh (2001)^[5] and Dixit *et al.* (2002)^[11]. The minimum inter-cluster distance was recorded between cluster III and I (51.922). the higher inter cluster distance indicated greater genetic divergence between the genotypes of those clusters, while lower inter-cluster values between the clusters suggested that the genotype of the clusters were not much genetically diverse from each other. A perusal showed (Table 4) that cluster means for different traits indicated considerable differences between the clusters. All the cluster from cluster I and VI had in general medium mean performance for most of the characters exhibiting extreme cluster means for none of the characters under study. These results were also found by Rao *et al.* (1994)^[4] and Singh and Gumber (1996)^[6]. Maximum cluster means for fruits yield was observed in cluster III followed by cluster I and IV. It is similar to the result of Yadav *et al.* (2009)^[8]. All cluster showed maximum mean values for plant height. The minimum group mean value showed for branches per plant in all the clusters. These results are in similar fashion of the study of Singh *et al.* (2007)^[7].

Table 1: Analysis of variance (mean sum of square) for 12 characters in pea genotypes (2009-10).

Characters D.F.	Source of variation		
	Replication	Treatment	Error
	2	34	68
Days to 50% flowering	1.03	241.47**	4.13
Plant height (cm)	1.29	245.34**	4.29
Nodes/ plant	0.58	12.37**	1.23
Internodal length (cm)	0.003	0.25**	0.04
Node At First Pod Appears	0.12	7.06*	0.39
Branches/ Plant	0.20	0.81**	0.28
Pods/ Plant	2.17	11.20**	1.23
Pod length (cm.)	0.57*	0.42**	0.11
Shelling %	0.83	5.50**	0.98
Seeds/ Pod	1.62*	0.59*	0.33
100 Seed Weight (gm)	0.23	2.16**	0.13
Green Pod Yield/ Plant (gm)	1.08	18.82**	2.48

Table 2: Average of intra and inter- cluster D² values for six clusters

	1 Cluster	2 Cluster	3 Cluster	4 Cluster	5 Cluster	6 Cluster
1 Cluster	36.266	59.048	51.922	105.938	537.665	254.26
2 Cluster		45.321	54.639	94.405	378.947	309.81
3 Cluster			31.783	69.777	477.752	320.79
4 Cluster				15.965	633.355	352.06
5 Cluster					0.000	1000.94
6 Cluster						39.53

Table 3: Clustering pattern of 35 genotypes on the basis of Mahalanobis D² statistics

Cluster Number	No. of genotypes	Genotypes
I	9	DPP-9411, NDVP-92, VRP-7, VP-5, DPP-62, PH-1, P-88-7, VP-9003, IP-3
II	6	PHPMR-1, NDVP-117, CHPMR-1, NDVP-8, AP-1, JP-19
III	11	CHP-1, VP-7906, KS-221, VRPMR-9, DPP-68, VL-3, Bonneville, KS-216, DPP-4, CHPMR-2, JP-83
IV	2	NDVP-250, NDVP-10
V	1	JP- 501
VI	6	NDVP-24, Arkel, NDVP-12, NDVP-19, PMR-19, NDVP-7

Table 4: Intra- cluster group means for 12 characters in Pea.

Cluster	Days to 50% flowering	Plant height (cm)	Nodes/ plant	Internodal length (cm)	Node At first pod appears	Branches/ plant	Pods/ plant	Pod length (cm.)	Shelling %	Seeds/ pod	100 Seed weight (g)	Green Pod yield/ plant (g)
I	60.667	82.951	23.233	3.678	12.717	1.500	10.117	8.088	44.267	6.800	17.027	27.150
II	39.111	73.347	19.111	3.299	9.056	0.500	8.167	7.994	42.861	6.722	16.044	22.550
III	60.500	80.183	23.611	3.659	12.722	1.556	11.889	8.428	44.550	7.500	16.967	28.161
IV	55.667	91.700	24.000	3.943	10.333	1.333	10.667	8.200	42.567	7.000	16.267	26.233
V	67.333	93.233	24.667	4.180	13.667	2.000	12.333	7.433	45.733	6.667	16.100	26.767
VI	66.333	122.733	27.667	4.327	13.667	1.333	11.333	7.767	44.233	7.000	16.100	26.900

Conclusion

All the 35 genotypes of pea showed significant genetic diversity. Based on *per se* performance for green pod yield per plant and other characters taken into consideration, genotype NDVP-10 was considered as the best genotype for green pod yield per plant followed by NDVP-250 and NDVP-8. Significant differences were revealed by the Mahalanobis D² statistic, the varieties could be grouped into six clusters. There was no consistent relationship between genetic divergence and geographical distribution but the results suggested that crosses between selected genotypes from widely separated clusters are most likely to give desirable recombinants.

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