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DIVERSITY ANALYSIS AND IDENTIFICATION OF PROMISING LINES FOR HYBRIDIZATION IN FIELD PEA (*PISUM SATIVUM* L.)

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ABSTRACT

In the present study, twenty one advanced breeding lines and two varieties (HUDP 15 and IPFD 1-10) as check were evaluated for assessing genetic divergence for exploitation in a breeding programme aimed at improving yield potential of field pea by using Mahalanobis D^2 statistics. The intra-cluster D^2 value ranged from 0.00 to 65.10 while inter-cluster D^2 value ranged from 101.389 to 763.200 indicated that the selected advance breeding lines were highly divergent. The maximum intra cluster distance was recorded for cluster I (65.109) while cluster IV and V (0.00) showed no intra-cluster distance values revealed homogenous nature of the genotype within the cluster. The genetically more divergent advanced breeding lines present in cluster II and V as indicated by inter-cluster distance value (763.200). Selecting lines of these clusters probably provide promising recombinants and better segregants for future breeding programme.

INTRODUCTION

Pea (*Pisum sativum* L.) is the oldest crop of the world; approximately 9000 years ago it was cultivated along with cereals like barley and wheat (McPhee, 2003). Due to its very old history of domestication, versatile use as vegetables, pulses and feed, it is important food legumes in the world (Choudhury *et al.*, 2006). Highly proteinaceous used as rotation crop with cereals and oil seeds. Pea is grown mainly as winter pulse crop of West Europe, North America, India, Australia, Pakistan and South America. It is one of the four important cultivated legumes after soybean, groundnut and beans (Husle, 1994). Field pea is a good source of dietary protein and energy. Protein content varies from 15.5-39.7% (Thaler and Stein, 2003) and also having low fat (0.8g) while soluble carbohydrate (mostly starch) is high. It has twice as much as fibre (5.6%) as maize. Due to its nutritional quality, the market demand increasing day by day, this can be achieved by enhancing the production of field pea with the help of improved varieties.

To develop a new variety there is need of the magnitude of genetic variability in the base material and the vast of variability for desired characters. A good knowledge on genetic diversity or genetic similarity could be helpful in long term selection gain in plants (Kumar *et al.,* 2012). Hence, genetic variability and diversity is of prime interest to the plant breeder as it plays a key role in framing and successful breeding programme. The genetically diverse parents are always able to produce high heterotic effects and great frequency of desirable segregants in further generation as already reported by earlier workers (Kumar *et al.,* 1994). D^2 statistic is a useful tool to measure genetic divergence among genotypes in any crop developed by Mahalanobis (1936). However, in the present study, an attempt has been made to identify genetic divergent lines in advanced generation, so as to select the potential parents for breeding programme to attain the anticipated improvement in grain yield of field pea.

MATERIALS AND METHODS

The experimental materials included 21 advanced breeding lines of field pea and two local checks namely HUDP 15 and IPFD 1-10. These advanced breeding lines were received from Indian Institute of Pulses Research (IIPR), Kanpur under All India Co-ordinated Research Project on Improvement of MULLaRP crops during 2008-09. These experimental materials were grown under randomized complete block design (RCBD) with three replications at Genetics and Plant Breeding Research Farm of Allahabad Agricultural Institute, Deemed University, Naini, Allahabad (U.P.). The experimental field was divided into 3 blocks of equal size and each block possesses 23 plots. Each advanced breeding line was accommodated in a six rows of 4 m length, row to row distance was at 30 cm with an approximate plant to plant distance of 10 cm. Fertilizers and manures were applied as per recommended dose. Recommended agronomic practices

Table 1: Analysis of variance for different quantitative traits in field pea

Characters	Treatments (df = 22)	CV%
Days to emergence (days)	1.391*	10.63
Number of primary branches per plant	0.195**	12.69
Days to 50% flowering (days)	167.528**	2.59
Plant height (cm)	856.546**	5.41
Number of pods per plant	21.385**	11.89
Number of clusters per plant	3.223**	10.11
Pod length (cm)	1.144**	5.19
Number of seeds per pod	1.821**	9.08
Days to maturity (days)	54.119**	1.54
100 seed weight (g)	10.106**	7.14
Yield per plant (g)	12.156**	6.70

** Significant at 0.01 level of significance;* Significant at 0.05 level of significance

Table 2: Distribution of 21field pea advanced breeding lines and two local checks in five different clusters

Cluster	No. of Advanced Breeding Lines	Advanced Breeding Lines included
I	12	FP8-211,FP8-214,FP8-219, FP8 -220,FP8-223,FP8-227, FP8-228,FP8-229,FP8-236, FP8-237,FP8-239,FP8-240
II	3	FP8-216,HUDP 15,IPFD 1-10
III	6	FP8-215,FP8-217,FP8-226, FP8-232,FP8-233,FP8-241
IV	1	FP8-242
V	1	FP8-225

Table 3: Intra (diagonal) and inter-cluster average distances for different quantitative characters in field pea

Cluster number	I	II	III	IV	V
I	65.109	101.389	120,000	280.964	626.657
	-8.06	-10.06	-10.95	-16.76	-25.03
II		33.675	190.194	327.687	763.200
		-5.8	-13.79	-18.1	-27.62
III			64.691	169.436	649.819
			-8.04	-13.01	-25.49
IV				0	598.238
				0	-24.45
V					0
					0

were followed to raise a good crop. Necessary weeding was done to keep the crops free from weeds. Flood irrigation was given to the plants at particular growth stages. Observations were recorded on five randomly selected competitive plants for eleven quantitative characters viz., Day to emergence, Number of primary branches per plant, Days to 50% flowering, Plant height (cm), Number of pods per plant, Number of clusters per plant, Pod length (cm), Number of seeds per pod, Days to maturity, Hundred seed weight (g) and Seed yield per plant (g). In each entry of each replication for all the characters except days to emergence, days to 50% flowering and days to maturity which were recorded on plot basis. Analysis of variance was carried out as suggested by Panse and Sukhatme (1964). Genetic divergence was estimated by using D^2 statistics of Mahalanobis (1936) and clustering of genotypes was done according to Tocher's method as described by Rao (1952). The per cent contribution of characters towards genetic divergence was calculated according to Singh and Chaudhary (1997).

RESULTS AND DISCUSSION

The analysis of variance revealed that the significant differences were present for all the characters studied and the experimental materials were genetically divergent from each other (Table 1). This indicates that there is ample scope for selection of promising lines from the present gene pool aimed at enhancing genetic yield potential of field pea. All the twenty one advanced breeding lines and two local checks were grouped into five clusters following Tocher's methods (Table 2). Cluster I constitutes of 12 advanced breeding lines, forming the largest cluster followed by cluster III (6) and cluster II (3). Clusters IV and V were ungrouped, comprising single advanced breeding line. The pattern of group constellation proved the existence of significant amount of variability.

The intra-cluster D^2 value ranged from 0.00 to 65.10 while inter-cluster D^2 value ranged from 101.389 to 763.200 indicated that the selected advance breeding lines were highly divergent (Table 3 and Fig. 1). The maximum intra cluster distance was recorded for cluster I (65.109) followed by cluster III (64.691) and cluster II (33.675) while cluster IV and V (0.00) showed no intra-cluster distance values as they were solitary cluster indicating comparatively homogenous nature of the genotype within the cluster. The maximum inter-cluster D^2 value was observed between cluster II and V (763.200) followed by cluster III and V (649.819), cluster I and V (626.657) and cluster IV and V (598.238) suggesting that the advanced breeding lines belonging to these clusters may be used as parents for hybridization programme to develop desirable type because crosses between genetically divergent lines will generate heterotic segregants (Sureja and Sharma, 2001 and Yadav *et al*., 2009). As heterosis can be best exploited and chances of getting transgressive segregants are maximum when generating diverse lines are crossed (Pratap *et al.,* 1992 and Lal *et al.,* 2001). The maximum contribution to genetic divergence was made by days to 50% flowering (39.53) followed by yield per plant (17.39), plant height (16.21) and days to maturity (9.09) had the greater contribution to genetic diversity therefore necessary attention is required to be focused on these characters (Shrivastava *et al.,* 2012).

The comparison of cluster means revealed considerable differences among the clusters of different quantitative characters (Table 4). Cluster I showed high mean value for days to 50% flowering (70.67), pod length (7.06), number of seeds per pod (5.48) and days to maturity (109.72). Cluster II showed highest mean value for days to 50% flowering (74.89), number of pods per plant (19.78), number of clusters per plant (7.24) and days to maturity (111.67) while high for days to emergence (7.44), number of primary branches per plant (1.91) and yield per plant (12.98). Cluster III recorded high mean value for days to emergence (7.39), number of pods per plant (16.32) and pod length (7.07). Cluster IV gained highest mean value for days to emergence (8.33), number of primary

Table 4: Cluster mean values for different quantitative characters in field pea

Cluster Characters	I	II	III	IV	V	% Contribution
Days to emergence (days)	7.25	7.44	7.39	8.33**	6.00*	0.00
Number of primary branches per plant	1.53*	1.91	1.64	1.93**	1.73	1.19
Days to 50% flowering (days)	70.67	74.89**	59.61	56.67	56.33*	39.53
Plant height (cm)	67.70	62.80	61.64	58.47*	139.33**	16.21
Number of pods per plant	14.90	19.78**	16.32	14.40*	19.20	1.58
Number of clusters per plant	5.26	7.24**	5.22*	5.567	6.80	3.95
Pod length (cm)	7.06	6.69	7.07	7.39**	6.10*	5.93
Number of Seeds per pod	5.48	5.08	5.47	5.70**	4.60*	1.98
Days to maturity (days)	109.72	111.67**	105.78	92.67*	106.67	9.09
100 seed weight (g)	15.86	15.63	15.68	19.63**	14.61*	3.16
Yield per plant (g)	9.79*	12.98	10.42	15.09**	12.21	17.39

* Lowest mean value among different clusters. ** Highest mean value among different clusters.

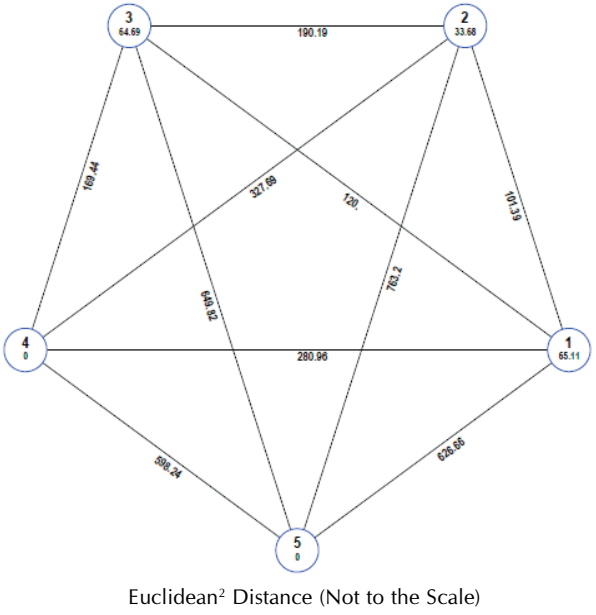

Figure 1: Intra and inter-cluster distance diagram for different quantitative characters in field pea

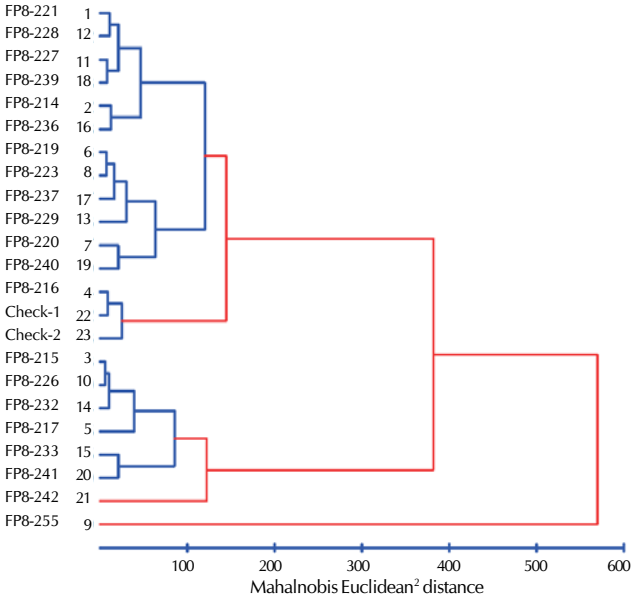

Figure 2: Euclidean average linkage dendrogram

branches per plant (1.93), pod length (7.39), number of seeds per pod (5.70), 100 seed weight (19.63) and yield per plant (15.09). Cluster V contained single advanced breeding lines with highest mean value for plant height (139.33) and high for number of primary branches per plant (1.73), number of pods per plant (19.20), number of clusters per plant (6.80) and yield per plant (12.21).

On the basis of yield performance, maximum inter cluster distance and some specialized characters, advanced breeding line FP8- 225 from cluster V and advanced breeding line FP8-216 of cluster II, whereas FP8-225 of cluster V and FP8-241, FP8-217 of cluster III may be selected as being the most diverse and high yielding lines. The lines fall into same cluster having lowest degree of divergence from each other (Fig. 2) and crosses among these lines of the same cluster unable to produce any transgressive segregants. While, the lines belonging to different clusters having maximum divergence and can be successfully utilize in hybridization programmes to get desirable transgressive segregants.

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