



Genetic Diversity Studies in Field Pea (*Pisum sativum* var. *arvense* L.) Germplasm

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Authors' contributions

This work was carried out in collaboration between both authors. All authors read and approved the final manuscript.

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ABSTRACT

The present study entitled “Genetic diversity Studies in Field Pea Germplasm (*Pisum sativum* var. *arvense* L.)” was carried out to estimate the genetic variability for yield and yield contributing traits, study the relationship between yield and yield attributing traits on seed yield and its component traits and to assess direct and indirect of yield attributing traits on seed yield. The experimental material was consisting of 41 Field Pea genotypes. The experiment was laid out in Randomized complete block design with three replications. The observations were recorded on five randomly selected plants from each treatment and replication for 12 different quantitative traits Days to 50% flowering, Days to 50% pod setting, Plant height (cm), Number of branches per plant, Number of Pods per plant, Number of seeds per pod, Pod length (cm) days to maturity, biological yield (gm), Harvest Index, Seed Index (gm), Seed yield per plant (gm). Based on the mean performance, high seed yield per plant were identified for the genotype zimndal (11.59) followed by Matar-23 (10.76). The higher phenotypic and genotypic coefficient of variations were observed for number of primary branches per plant (33.92 & 24.56), seed yield per plant (29.84 & 25.67) and number of seeds per pod (28.61 & 22.64). High heritability coupled with high genetic advance as percent of mean was observed for plant height (84.43 & 40.55), days to 50% flowering (77.30 & 34.92) and pod length (71.55 & 32.55). Based on Mahalanobis D² values 41 genotypes grouped into 8 clusters. Among 8

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clusters cluster I had more number of genotypes (25) followed by cluster II (8 genotypes), cluster VIII (3 genotypes). The maximum intra cluster distance was observed in cluster VIII (10.26) followed by cluster II (8.59) and cluster I (7.72). The highest inter cluster distance observed between cluster I and cluster VI (24.07) followed by cluster I and cluster IV (22.25), cluster I and cluster III (21.41). Therefore, genotypes present in these clusters may be used as parents to produce the transgressive segregants. The cluster IV (12.57) had significant and higher cluster mean for seed yield per plant. The trait number of primary branches per plant (25.12%) had maximum contribution towards to genetic divergence followed by harvest index (21.95%), biological yield per plant (19.39%), seed yield per plant (19.15%).

Keywords: Field pea, genetic variability; heritability; genetic advance; genetic diversity; harvest index; intra cluster distance; inter cluster distance.

1. INTRODUCTION

Field pea (*Pisum sativum L.*) belongs to family Leguminosae (Fabaceae). It is important legume vegetable grown during cool season. Being a cool season crop, it is most extensively grown in the temperate region throughout the world. Field pea is a rich source of protein, amino acids and carbohydrates. In world field pea consists 6.27 million hectares area, 11.16 million tons production with the productivity of 1779 kg/ha. In India field pea covers 0.76 million hectares area, 0.84 million tons production with the productivity of 1100 kg/ha. In Uttar Pradesh it covers 0.3 million hectares area, 0.38 million tons production with the productivity of 1495 kg/ha. Accomplishment in an improvement programme for selection is directly related with the presence of variability and efficiency of selection in the sample population [1]. Heritability indicates the portion of phenotypic difference that is due to genotypes which can be inherited from one generation to next generation. It serves as a valuable steer to breeders as the selection for trait having high heritability is favourable. It will be possible to decide various breeding programmes for improvement of different characters on the basis of heritability and genetic advance estimates[2].

The method of surveying hereditary difference is the D^2 measurement proposed by Mahalanobis in 1936. In this method, forces of differentiation at two levels (intra and inter cluster levels) are screened out, and thus play an effective part in the selection of genetically divergent parents for utilization in any hybridization programme [3].

2. MATERIALS AND METHODS

The Experimental materials for the present study were obtained from the Department of Genetics and Plant Breeding, Naini Agricultural

Institute, Sam Higginbottom University of Agriculture, Technology & Sciences, Prayagraj (UP), during Rabi-2020-2021. The experimental materials comprising of 41 genotypes with one check variety was grown under Randomized Block Design (RBD) with three replications. The observations were recorded on five randomly selected plants in each entry of each replication for all the characters. Days to 50% flowering, Days to 50% pod setting, Plant height (cm), Number of branches per plant, Number of Pods per plant, Number of seeds per pod, Pod length (cm), days to maturity, biological yield (gm), Harvest Index, Seed Index (gm), Seed yield per plant (gm), except days to emergence, days to maturity were recorded on plot basis. The experimental data was analyzed statistically to find out the significance of mean difference between varieties and different genetic parameters were estimated. Analysis of variance was performed to test the significant of difference among the genotypes for the characters studied. Mahalanobis D^2 technique (Mahalanobis, 1936) was used to analyze genetic diversity.

3. RESULTS

41 genotypes of field pea showed that significant differences among all characters under study.

The trait number of primary branches per plant (25.12%) had maximum contribution towards to genetic divergence followed by harvest index (21.95%), biological yield per plant (19.39%), seed yield per plant (19.15%).

The parameters of genetic variability revealed (Table 1) that high GCV and PCV values for seed yield per plant (25.67) followed by number of primary branches per plant (24.56), harvest index (23.74) and number of seeds per pod (22.64), indicating that these traits would be

great help to breeder in evolving a selection program for genetic improvement of crop plant. Similar results were reported by Singh *et al.* [4], Katocha *et al.* [5], Barcchiya *et al.* [6]. High heritability with high genetic advance was recorded for seed yield per plant (92.58 & 1.05) followed by days to 50% pod setting (89.40 & 13.67) and plant height (84.30 & 31.13). Genetic advance was varied from (0.361) number of

primary branches per plant 31.13 (plant height). The high genetic advance was observed for plant height (31.13) and moderate genetic advance was observed for days to 50% pod setting (13.671), days to maturity (13.652) and days to 50% flowering (13.3). Genetic advance as per cent of mean was varied from 1.476 (number of primary branches per plant) to 40.555 (plant height). The traits having high

Table 1. Genetic parameters for 12 biometrical traits of Field Pea

Parameters/Traits	GCV	PCV	h ² (Broad sense)	GA 5%	GAM 5%
Days to 50% flowering	21.80	23.97	77.3	13.30	34.92
Days to 50% pod setting	8.66	9.22	89.4	13.67	18.83
Plant height (cm)	21.43	23.34	84.3	31.13	40.55
No. of primary branches per plant	24.56	33.92	21.22	0.36	1.47
Pod length	18.75	19.25	71.55	1.85	32.55
No. of pods per plant	21.55	27.48	55.9	2.76	31.67
No. of seeds per pod	22.64	28.61	62.6	2.64	36.90
Days to maturity	11.82	12.65	71.6	13.65	17.12
Biological yield per plant (g)	11.40	14.08	65.6	10.20	19.02
Harvest index (%)	23.74	26.35	82.56	5.59	12.65
Seed index (gm)	7.50	8.97	49.10	2.82	10.83
Seed yield per plant (g)	25.67	29.84	92.58	1.057	9.31

PCV: Phenotypic Coefficient of Variation, GCV: Genotypic Coefficient of Variation, GA: Genetic Advance, GAM: Genetic Advance as Percent of Mean

Table 2. distribution of 41 genotypes of field pea in different clusters

Cluster	Number of genotypes	Genotypes included
I	25	Rachana, Sourabha-check, Dashrath, Paras, Vikas, Matar-215, KS-10, VS-10, BNS-10P10, Boniville, Swathi, Ronaldo-10, KSP-110, Suneetha, Maxima-3636, Sourabha, Prachi-10, BNR ruche, Green Pearls-10, Jindal, Hortus, PS-1100, Icarus, JK-124, GR-333
II	8	Indam Green wood, GS-10, Pusa Pragathi, Aruna-10, Arka Sampurna, Zimndal-10, Matar-09, Matar-23
III	1	Matar-203
IV	1	Matar-01
V	1	Matar-229
VI	1	Arka Pramodh
VII	1	Aman
VIII	3	Kadapa local-1, Jawahar matar-s4, Azad pea-9

Table 3. Inter cluster and intra cluster distances of 8 clusters of Field pea

Cluster	I	II	III	IV	V	VI	VII	VIII
I	7.72	14.43	21.41	22.25	19.26	24.07	19.83	14.75
II		8.59	13.31	14.88	13.4	17.71	14.13	16.87
III			0	4.39	6.26	10.26	7.31	16.12
IV				0	5.01	6.22	9.01	16.44
V					0	8.04	10.52	14.68
VI						0	13.9	18.92
VII							0	12.77
VIII								10.26

Table 4. Cluster mean of 12 biometrical characters of 41 Field Pea genotypes

Characters/Clusters	DF50	DP50	PH	NPBP	PL	NPP	NSP	DM	BYP	HI	SI	SYP
Cluster-1	36.00	69.47	67.65	20.5	6.08	8.3	6.86	73.87	48.84	27.21	26.66	11.18
Cluster-2	36.04	72.75	72.09	21.89	5.47	7.14	6.12	91.83	59.68	25.84	25.22	10.89
Cluster-3	52.33	86.67	107.6	35.8	3.80	11.03	7.93	92.47	69.73	25.88	22.17	11.73
Cluster-4	53.00	85.00	115.33	40.00	5.50	10.50	8.67	94.60	69.93	27.67	25.42	12.57
Cluster-5	58.00	86.67	106.00	38.67	3.73	10.07	6.73	91.83	61.91	31.43	25.55	11.77
Cluster-6	54.00	87.67	111.33	45.33	7.27	11.79	9.13	97.00	70.2	30.46	28.65	15.35
Cluster-7	42.33	75.33	112.73	42.13	3.67	13.71	10.27	88.20	65.04	25.04	21.90	11.27
Cluster-8	37.78	78.78	108.73	37.62	4.76	12.11	10.27	74.29	54.71	25.17	25.85	11.93
% Contribution	1.22	2.44	0	25.12	1.95	2.07	4.02	0	19.39	21.95	2.68	19.15

DF50: Days to 50% Flowering, DP50: Days to 50% Pod Setting, PH: Plant Height, NPBP: Number of Primary Branches per Plant, PL: Pod Length, NPP: Number of Pods per Plant, NSP: Number of Seeds per Pod, DM: Days to Maturity, BYP: Biological Yield per Plant, HI: Harvest Index, SI: Seed Index, SYP: Seed Yield per Plant.

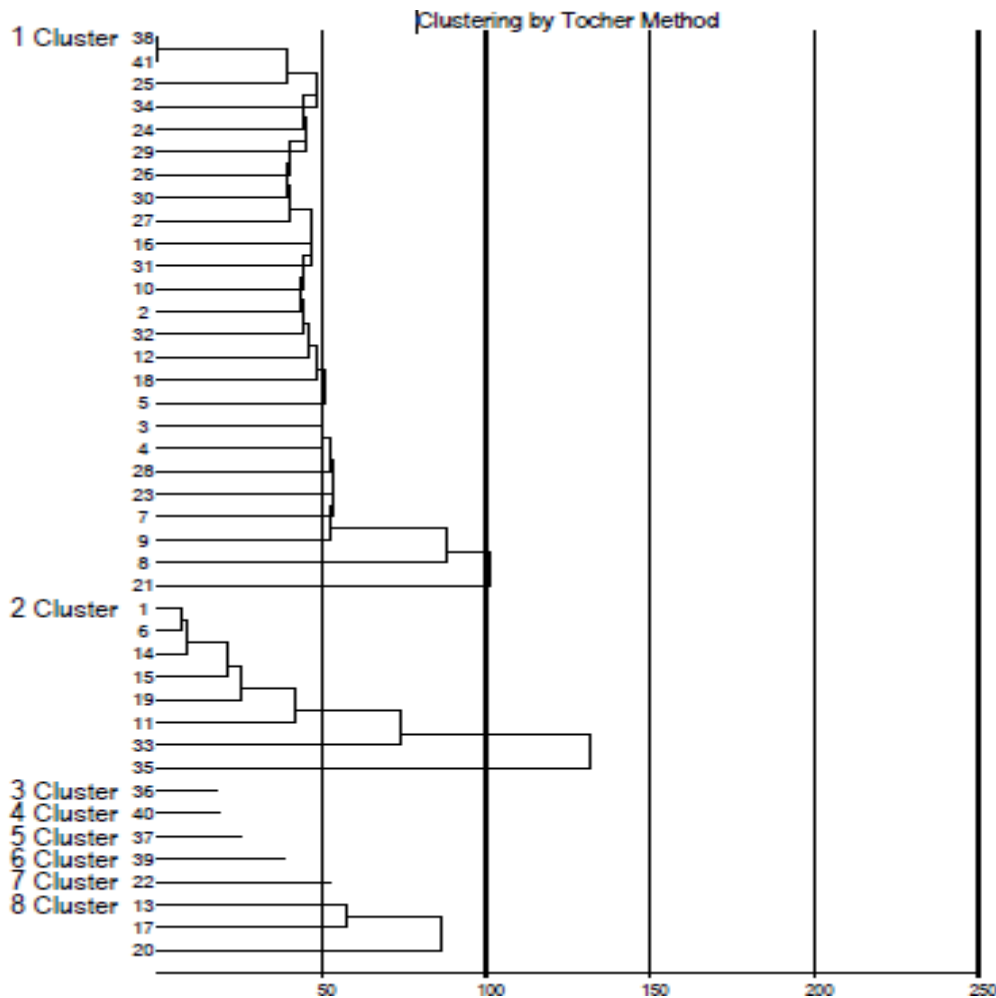


Fig. 1. Dendrogram for 12 biometrical traits of 41 Field Pea genotypes towards genetic divergence

genetic advance as per cent of mean was recorded for plant height (40.555), number of seeds per pod (36.905), days to 50% flowering (34.924), pod length (32.557) and number of pods per plant (31.674), it indicates that most likely heritability is due to the additive gene action. Similar results were reported by Georgieva *et al.* [7], Barcchiya *et al.* [6].

4. DISCUSSION AND CONCLUSION

Based on D^2 values 41 genotypes grouped into 8 clusters (Table 2 & Fig. 1), among 8 clusters cluster I had more number of genotypes (25) followed by cluster II (8 genotypes), cluster VIII (3 genotypes), cluster III, IV, V, VI, VII had (1 genotype) each.

The intra cluster values ranged from 0 to 10.26. (Table 3) The maximum intra cluster distance were observed in cluster VIII (10.26) followed by

cluster II (8.59) and cluster I (7.72) The minimum intra cluster distance for cluster III, IV, V, VI, VII exhibited zero. The inter cluster distance differ from 4.39 (between III and IV) to 24.07 (between I and VI). Other inter cluster distance were between these values. The highest inter cluster distance observed between cluster I and cluster VI (24.07) followed by cluster I and cluster IV (22.25), cluster I and cluster III (21.41), cluster I and cluster VII (19.83), cluster I and cluster V (19.26), cluster VI and cluster VIII (18.92). The minimum intercluster distance observed between cluster III and IV (4.39), cluster IV and cluster V (5.01), cluster IV and cluster VI (6.22). Similar results were reported by Kumar *et al.* [8], Singh and Mishra [9], Siddika *et al.* [10], Saha *et al.* [11], Gupta *et al.* [15].

Cluster means were found highest for different characters (Table 4) cluster IV showed highest mean performance for plant height (115.33),

cluster V showed highest mean performance for days to 50% flowering (58.00), cluster VI showed highest mean performance for days to 50% pod setting (87.67), number of primary branches per plant (45.33), pod length (7.27), days to maturity (97.00), biological yield per plant (70.20), harvest index (30.46), seed index (28.65), seed yield per plant (15.35). Cluster VII showed highest mean performance for number of pods per plant (13.71) and number of seeds per pod (10.27). based upon D² values, percent contribution of different characters obtained. Among the 12 characters studied the most important characters contributing to the divergence were number of primary branches per plant (25.12%) had maximum contribution towards to genetic divergence followed by harvest index (21.95%), biological yield per plant (19.39%), seed yield per plant (19.15%), number of seeds per pod (4.02%), seed index (2.68%), days to 50% pod setting (2.44), number of pods per plant (2.07%). Similar results were reported by Muhammad *et al.* [13], Rahman *et al.* [14], Saha *et al.* [11] and Prakash *et al.* [16]

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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