International Journal of Chemical Studies

P-ISSN: 2349–8528
E-ISSN: 2321–4902
IJCS 2018; 6(6): 2288-2291

Received: 19-09-2018
Accepted: 21-10-2018

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Evaluation of Field pea (*Pisum sativum* L. var. arvense) genotypes for genetic variability and divergence

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Abstract
The experiment was carried out with ninety genotypes and four check varieties to estimate extant of genetic divergence, genotypic coefficient of variance and phenotypic coefficient of variance for different traits, for this purpose data on various quantitative characters was taken out. Analysis of variance revealed highly significant differences among all the genotypes for majority of the traits except pod length, this indicates good amount of genetic variation in the experimental material under investigation. Moderate to high level of genotypic and phenotypic coefficient of variance were observed among the genotypes. Phenotypic coefficients of variance were found slightly higher than genotypic coefficient of variance this indicates very less environmental influence on the expression of the characters. Higher estimates of GCV (22.84) were recorded for pod length (cm) followed by number of pods per plant (20.96), number of primary branches per plant (20.78) and plant height (17.40) this indicates that pod length, number of pods per plant, number of primary branches per plant and plant height may be utilized as selection parameters. Genetic divergence through Non-hierarchical Euclidean cluster analysis includes TOCHER's and WARD methods. Through the WARD's method all the genotypes were grouped into 10 non-overlapping clusters in which cluster number IV and X were found largest including 12 genotypes while cluster IX was found smallest having 2 genotypes namely Pant P 223 and NDP 14-11. The higher inter cluster distance were observed between cluster number II and VIII (84.837) and between cluster II and V (75.302), this indicates that the genotypes belonging to these clusters are more genetically divergent from each other and Intermating between such genotypes would produce more heterotic F_1 progeny.

Keywords: Field pea (*Pisum sativum* L. *var. arvense*), genetic variability, genetic

Introduction
Pea (*Pisum sativum* L.) is an important legume grown as a field crop throughout the temperate regions of the world. Pea is an important plant in human and animal nutrition because of its high protein level 23- 33%. The major field pea producing state are M.P, U.P, Jharkhand, Rajasthan, Assam, Bihar, Chhattisgarh, Maharastra with production of 362.9, 314.00, 40.40, 30.90, 27.70, 18.20, 10.30, 9.60 thousand tonnes respectively in 2014-15 (Anonymous 2016) [1].
Among various grain legumes grown, field pea (*Pisum sativum* L. var. arvense), is one of the most important pulse crop of India, grown in winter season and belonging to tribe- Vicieae, order- fabales, family–leguminosae (fabaceae), sub-family- papilionaceae, genus– *Pisum* and species– *sativum* with chromosome number 2n = 14. Pea has versatile uses as food, feed and fodder. Pea (*Pisum sativum* L.) besides pulse residues are nutritious feed for livestock and milch cattle and thus, offer an added advantage to the poor farmer families.
The choice of potential genetically diverse parents for use in hybridization programme is based on the hypothesis that crosses involving divergent parents offer greater possibility of obtaining desirable segregants in the segregating generation. Several workers have emphasized need of parental diversity in optimum magnitude to obtain superior genotypes in the segregating generations. Therefore, effort should be needed to increase the wider use of existing diversity from germplasm collection.
The improvement in field pea is mainly based on exploiting the natural sources of germplasm by means of selection or hybridization followed by selection (Zohary & Hopf, 2000) [11]. Genetic variability is considered as important factor which is essential prerequisite for crop improvement program for obtaining high yielding progenies (Tiwari & Lavanya, 2012) [10].

The most important task for pea breeding is to develop high yielding varieties with stable productivity and sufficiently good resistance to disease and unfavorable environmental conditions, increase protein content, essential amino acids and favorable ration among them. Taking these recommendations in consideration, the present investigation was done to estimate genetic variability and divergence among the genotypes.

Materials and Methods

The present investigation was carried out during *Rabi* 2016-17 using Augmented Block Design at Genetics and Plant Breeding Research Farm of Narendra Deva University of Agriculture and Technology, Narendra Nagar, Kumarganj, Faizabad (U.P.). Narendra Nagar is situated between 26.47 ^{0}N latitude, 82.12 ^{0}E longitudes and at an altitude of 113 m above the mean sea level. The climate of district Faizabad is semi-arid with hot summer and cold winter. Nearly 80% of total rainfall is received during the monsoon (only up to September) with a few showers in the winter. The soil type of experimental site was sandy loam, rich in potash and low in organic carbon, nitrogen and phosphorus.

A collection of 90 genotypes of fieldpea comprising exotic as well as indigenous and 4 check varieties *viz*. Rachna, HFP-4, HFP-8909 and HUDP-15 constituted the experimental material for this study, were obtained from Indian Institute of Pulse Research (IIPR), Kanpur and Pulse Section of the University. The whole experimental field was divided into 6 blocks of equal size and each block consist 19 plots in which four plots were randomly allotted to the four check varieties, while remaining 15 plots of a block were used for accommodating the un-replicated test genotypes. Each plot was consist of a single row of 4 m length, following inter and intra row spacing 30 cm and 10 cm respectively. Observations were recorded on randomly selected five competitive plants from each genotypes for nine characters, *viz*., Plant height (cm), number of primary branches per plant, number of pods per plant, pod length (cm), number of seeds per pod, 100-seed weight, biological yield per plant, harvest index and seed yield per plant (g), while two characters *viz*., days to 50 per cent flowering, days to maturity were recorded on the plot basis. In order to study genetic divergence these data were subjected to D2 analysis and their estimates are presented in Table 1, 2, 3 and 4. Analysis employed TOCHER's and WARD's methods so as to group the genotypes into different clusters.

Result and Discussion

The success of any breeding programme depends on the extant of genetic variability present in the germplasm. Genetic variability in parental lines is much more essential to obtain more heterotic performance in the F_1 generation. Therefore the present investigation was done to estimate extant of genetic variability and genetic divergence available in the germplasm lines. An analysis of variance for Augmented Block Design accommodating ninety germplasm lines and four checks in six blocks was carried out for each of the eleven characters in field pea. The mean squares due to blocks, checks, and error for all the characters are presented in Table-4.1

The variation due to checks was highly significant for majority of the traits except Pod length (cm). Mehta *et al*. (2005), Kumar *et al.* (2013) and Georgieva *et al*. (2016) [3] also noted that the genotypes differed significantly for all the traits except the Pod length (cm).

The estimates of genotypic and phenotypic coefficients of variation for 11 characters are given in Table 2. The magnitude of phenotypic coefficient of variation (PCV) was higher than the genotypic coefficient of variation (GCV) for all the characters. Same results also reported by Jaiswal *et al*. (2013) [4], Basir *et al*. (2017) [2] and Kanhaiya Lal *et al*. (2018) [6]. High PCV coupled with high GCV was found for pod length (25.30 %) followed by number of pods per plant (21.02 %).

The highest coefficient of variation were found for number of pods per plant (22.835) followed by number of primary branches per plant (22.511) and plant height (20.219), while lowest CV was found for days to maturity (3.715).

The selection of suitable diverse parents for hybridization is an important feature of any crop improvement programme for getting desired recombinants. The importance of genetic divergence in plant breeding has been emphasized by several researchers.

Table 1: Analysis of variance of augmented block design for 11 characters in field pea genotypes

S.V.	D.F.	Days of 50% flowering	Days to maturity	Plant height (c)	Number of Pods/ plant	Pod length (cm)	Number of Primary branches/ plant	Number of Seeds/ Pod	100-Seed weight (g)	Biological yield/ plant (g)	Seed yield (g)	Harvest index (%)
Block (ignoring Treatments)	5	42.58**	15.02	481.78**	3.189**	18.207**	0.224**	0.962**	7.637**	4.343**	2.238**	37.89**
Checks	3	41.38**	24.78*	7631.9**	4.463**	0.051	0.230**	0.128**	2.113**	2.0553**	0.441**	35.10**
ERROR	15	4.48	4.78	4.83	0.0167	0.158	0.001	0.0045	0.118	0.0820	0.009	0.848

*,** Significant at 5% and 1% probability level respectively

Table 2: Range, mean, coefficient of variation and least significant differences for 11 character of field pea

Characters	Range (Min-Max)	Mean Value	Coefficient of variation (%)			Range of parameters			
			GCV (%)	PCV (%)	Coefficient of variation (%)	LSD_1 5%	LSD_2 5%	LSD_3 5%	LSD_4 5%
Days to 50% flowering	70.292-88.792	79.746	4.99	5.66	5.892	2.604	6.378	7.130	5.446
Days to maturity	122.583-142.583	133.067	2.99	3.41	3.715	2.691	6.591	7.369	5.628
Plant height (cm)	39.550-137.68	87.370	17.40	17.58	20.219	2.70	6.62	7.40	5.65
Number of primary branches plant^{-1}	1.292-3.11	2.091	20.78	20.83	22.511	0.039	0.096	0.108	0.082
Number of pods plant^{-1}	4.181-12.88	7.688	20.96	21.02	22.835	0.159	0.389	0.435	0.333
Number of seeds pod^{-1}	2.049-5.16	3.527	13.37	13.51	14.439	0.083	0.203	0.227	0.174
Pod length (cm)	2.626-4.88	3.650	22.84	25.30	11.796	0.489	1.198	1.339	1.023
100-seed weight (g)	16.620-28.50	19.230	7.62	7.83	8.445	0.423	1.037	1.159	0.886
Biological yield plant^{-1}(g)	3.405-6.77	4.923	11.434	11.646	17.154	0.352	0.863	0.965	0.737

Harvest index (%)	8.494-15.43	12.953	9.53	9.83	12.609	1.134	2.777	3.104	2.371
Seed yield/plant(g)	28.702-46.63	37.960	15.96	16.08	10.445	0.118	0.288	0.322	0.246

- LSD1 = difference between two check means. GCV = genotypic coefficient of variance
- LSD2 = difference between adjusted yield of two genotype in the same block. PCV = phenotypic coefficient of variance.
- LSD3 = difference between adjusted mean of two genotypes in the different block.
- LSD4 = difference between adjusted yield of genotype and check mean

Table 3: Clustering pattern of 94 field pea genotypes on the basis of non-hierarchical Euclidean cluster analysis

Cluster No.	Number of genotypes	Genotypes
I	8	FP 13-97, PANT P-101, HUP 2, PANT 269, LFP 431, ADARSH, Pant P-137,FP 2009-4
II	10	KPMR 936, IPLK 112, EC 384275, HFP 1125, IPF 2014-13, KPF 1024, HUDP 11, IPF 12-17, HFP 529, EC 5117
III	9	IPF 13-13, PANT P-217, PANT P 247, PANT P 266, VL 58, IPF 13-14, EC 548810, HFP 1010, IPFD 13-4
IV	12	IPLK 85,NDP 11-101,EC 281864,FP 868, PANT P-138,IPF 11-15, VL 82, KPMR 4,HUP 2, HUDP 11, KPMR 902,KPF 1024
V	6	PANT P 222,PANT P 195,VL 61,IPF 2014-16,KPMR 970,KPMR 853
VI	10	IPFD 2014-2, VL-42, DMR 63, VL 56, KPF 1023, IPFD 1-10, JPP 3, EC 392177, HFP 4, HFP 8909
VII	10	EC 386742, HFP 554, IPLK 85, SKUA P-8, IPLK 109, RFP 61, P 1089, KPMR 931, NDP 12-102, RACHNA
VIII	8	PRAKASH, KPF 1036, AMAN,FP 34, EC 588004, VL 55, RFPG 79, KPF 1023
IX	2	PANT P 223, NDP 14-11
X	12	PANT P 244,RFG 79,KPMR 916,VL 37,HUDP-17,PLK 108,IPFD 12-2,RFP 2009-2-1,KPF 12-04,KFP 2009-2,VL 202,HUDP 15,

Table 4: Estimates of average intra-and inter-cluster distances for 10 clusters in field pea germplasm

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII	Cluster IX	Cluster X
Cluster I	11.529	43.316	20.182	22.041	29.645	19.470	24.387	37.840	25.045	35.081
Cluster II		9.67	49.754	49.841	75.302	61.321	52.176	84.873	58.821	67.276
Cluster III			12.002	19.286	18.23	19.509	17.820	27.991	19.618	39.156
Cluster IV				12.787	27.632	21.655	30.226	42.472	33.488	54.888
Cluster V					10.9	16.942	29.049	18.553	16.553	39.710
Cluster VI						10.555	22.590	17.649	15.481	25.061
Cluster VII							9.486	24.109	16.223	24.813
Cluster VIII								8.365	13.053	18.522
Cluster IX									7.536	20.266
Cluster X										8.865

- Bold figures indicate the intra-cluster distance

Table 5: Cluster means for different characters in field pea germplasm

Characters	Days to 50% flowering	Days to maturity	Plant height (c)	Number of primary branches/ plant	Number of Pods/ plant	Number Of seeds/ Pod	Pod length (cm)	100-Seed weight	Biological yield/ plant	Harvest index (%)	Seed yield/plant(g)
Cluster I	73.337	125.356	94.509	2.316	8.565	3.728	3.297	19.526	14.494	39.676	5.744
Cluster II	71.292*	127.333	84.150	2.500	10.145	3.708	4.136	28.504**	14.515	44.345**	6.436**
Cluster III	82.461	135.006	106.036**	2.245	8.658	3.837	3.687	19.560	13.585	41.018	5.562
Cluster IV	79.492	132.633	84.755	2.844**	11.40**	3.425	3.929	18.421	14.611**	42.180	6.170
Cluster V	85.617**	138.858**	94.715	2.243	8.336	3.090	3.141*	18.351	12.591	37.831	4.753
Cluster VI	77.708	131.483	80.475	2.403	8.197	3.106*	3.621	18.130	12.506	37.460	4.674
Cluster VII	79.117	133.008	92.450	1.610	6.687	4.196**	4.340**	19.620	13.751	37.851	5.191
Cluster VIII	83.181	136.417	70.767	1.746	6.104	3.340	3.652	18.135*	10.519	36.022	3.766
Cluster IX	81.461	135.143	80.837	1.802	6.310	3.438	3.572	20.205	13.165	33.938*	4.464
Cluster X	72.842	127.633*	66.675*	1.486*	4.730*	3.655	3.885	20.120	10.083*	36.851	3.693*

Table 6: Contribution of characters towards genetic divergence

Source	Times Ranked Ist	Contribution %
1. Days to 50% flowering	302.000	6.91
2. Days to maturity	430.000	9.84
3. Plant height (cm)	3285.000	75.15
4. Number of primary branches/plant	0.000	0.01
5. Number of pods/ plant	17.000	0.39
6. Number of seeds/ pod	0.000	0.01
7. Pod length (cm)	0.000	0.01
8. 100-seed Weight (gm)	16.000	0.37
9. Biological Yield/ Plant (gm)	0.000	0.01
10. Harvest index (%)	12.000	0.27
11. Seed yield/ plant (gm)	309.000	7.07

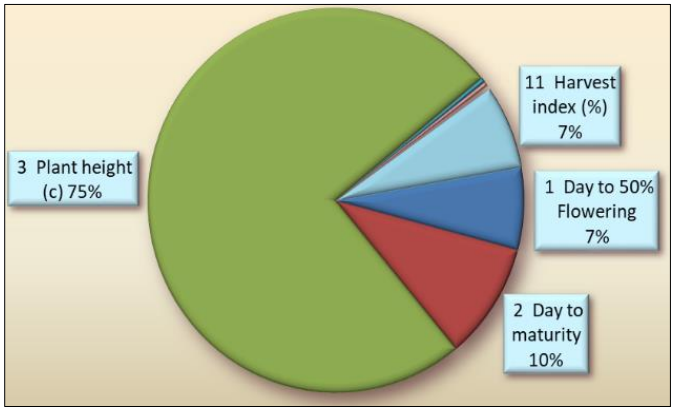

Fig 1: Contribution% towards Divergence

Ninety genotypes of field pea along with four checks were grouped in ten distinct non-overlapping clusters using Non-hierarchical Euclidian cluster analysis in which Cluster IV and X had higher number of genotypes (12) followed by cluster II, cluster VI & VII (10), cluster III (9), cluster I& VIII (8), cluster V (6) and cluster V had lowest number of genotypes *(2)*. The highest intra cluster distance was observed in cluster IV (12.787) followed by cluster III (12.002), cluster I (11.529), cluster V (10.9), cluster VI (10.555), cluster VII (9.486) While, the lowest values recorded in case of cluster X (8.865), cluster VIII (.8.365) and cluster IX (7.536).

The maximum inter cluster distance was recorded between cluster II and VIII (84.837) followed by cluster II and V (75.302), cluster II and VI (61.321), cluster II and X (67.276), cluster II and IX (58.821), cluster IV and X (54.888) which suggested that members of these two clusters are genetically very diverse to each other. The inter cluster distance between cluster VIII and cluster IX (13.053) was lowest. This indicated presence of considerable diversity in the germplasm collections, evaluated in the present study. Parihar *et al.* (2014) [7] also assessed one hundred forty genotypes of field pea to the genetic divergence for various agronomic traits and stated that all the accessions were significantly different for the traits and a wide range of variability exists for most of the traits.

The genotypes of Cluster I had average mean values for all characters. The genotypes of Cluster II had highest mean values for 100-seed weight, harvest index, seeds yield per plant and lowest mean value for days to 50% flowering.

The genotypes of cluster III had highest mean value for plant height (106.036 cm). The genotypes of cluster IV had highest mean value for number of primary branch/plant (2.844) as well as number of pod per plant (11.4) and biological yield per plant (14.611). The genotypes of cluster V had highest for days to 50% flowering (85.617) as well as days to maturity (138.858) and lowest mean value for pod length (3.141 cm).

The genotypes of cluster VI had lowest mean value for number of seeds per pod (3.106). The genotypes of cluster VII had highest value for number of seed/pod (4.668). The genotypes of cluster VIII had highest mean value for number of seeds per pod (4.196) as well as pod length (4.34 cm). The genotypes of cluster VII had lowest mean value for 100-seed weight.

The genotypes of cluster IX had lowest mean value for harvest index (33.938%). The genotypes of Cluster X had lowest mean values for number of days to maturity (127.633) as well as number of primary branches per plant (1.486), plant height (66.675cm), pods per plant (4.73), biological yield per plant (10.083 g) and seed yield per plant.

The analysis of character contribution towards genetic divergence between ninety four genotypes of field pea is given in Table 6. The maximum contribution in manifestation of total genetic divergence were made by plant height (75.15%) followed by day to 50% flowering (6.91%) pods per plant (0.39%), biological yield per plant (0.27%), 100 seed weight (0.37%),. The minimum contributions in manifestation of total genetic divergence were made by number of primary branches per plant, seeds per pod, pod length, seed yield per plant (0.01%).

The minimum contributions in manifestation of total genetic divergence were made by branches per plant, seeds per pod, pod length and seed yield per plant (0.01). Similar results were reported by Srivastava *et al*. (2012) [9].

The overall review of the result obtained by genetic diversity study in present investigation revealed that the crosses between the entries separated by the large inter-cluster distances and having high cluster mean values for one or other character to be improved is likely to be more useful. The results of Non-hierarchical Euclidian cluster analysis obtained under present study are also in agreement with the result of Parihar *et al.* (2014) [7] and Srivastava *et al.* (2012) [9].

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