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Research Article

Genetic analysis in advanced breeding lines of field pea (*Pisum sativum* L.)

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Abstract
The present study investigated genetic diversity among 47 advanced field pea breeding lines. For all of the traits investigated, ANOVA revealed significant differences between the lines. The highest PCV, GCV and high heritability as well as a high genetic advance per cent of mean were recorded for the number of primary branches/plants, clusters/plant and pods/plant. The present collection of 47 lines was sorted into seventeen clusters after a genetic divergence analysis using Mahalanobis's D^2 analysis. Cluster XII and XIII (43.62) had the greatest average inter-cluster distance, while cluster VII had the greatest intra-cluster distance (12.66). The highest percentage contribution of features to divergence was biological yield/plant, followed by the number of primary branches/plants. For most of the genotypes, clusters XV and XVII had higher cluster means. As a result, lines corresponding to these clusters can be utilised in the breeding programme in the future.

Keywords: Heritability, field pea, genetic advance, genetic divergence, cluster distance.

INTRODUCTION

Pea (*Pisum sativum* L.) is a temperate annual self-pollinated legume in the Leguminosae (Fabaceae) family with a diploid chromosome number of 2n=2x=14. It has a Mediterranean origin, with secondary places of origin in the Near East and Ethiopia (Blixt, 1974). Field pea is a high-yielding *rabi* pulse crop that is used not only for human consumption but also for animal feed. After *Phaseolus vulgaris* L., it is the world's second most significant food legume (Tar'an *et al.,* 2005). It is grown in Uttar Pradesh, Madhya Pradesh, Jharkhand, Assam, Maharashtra and Bihar are among the states in India. In Manipur, it is grown in an area of about 15.95 thousand hectares, with a production of 14.69 thousand tonnes and productivity of 921 kg/ha (Anonymous, 2020). The essential necessity for improving any crop is genetic variability (Azmat *et al.,* 2011). In *Pisum sativum*, there is a lot of genetic diversity (Blixt, 1974). Knowledge of genetic variability for distinct traits is required for improving crop genetic behaviour and it serves as an important tool for identifying relevant genes and their nature of adherence (Nwangburuka *et al.,* 2011). Genetic diversity refers to the genetic variation that exists among different cultivars of a crop species. Variability differs from diversity in that variability exhibits observable phenotypic differences, whereas diversity may or may not exhibit observable phenotypic differences, depending on the context. The D^2 measurement, introduced by Mahalanobis in 1936, is a way of measuring genetic differences. Forces of differentiation are screened out at two levels (intra and inter-cluster levels) in this procedure, and so play an important role in the selection of genetically divergent lines for use in any crossing programme (Singh, 1983). The current study was conducted with the goal of determining the genetic divergence among field pea breeding lines.

MATERIALS AND METHODS

The experiment was conducted on 47 field pea advanced breeding lines (**Table 1**) at Andro Research Farm, Central Agricultural University, Imphal, Manipur during

Table 1. List of Field pea breeding lines and their source of origin

S. No.	Lines	Pedigree	Sources
1.	CAU-FP-1	Prakash × Rachna	AICRP(MULLaRP) CAU, Imphal
2.	CAU-FP-2	HFP 9426 × Rachna	AICRP(MULLaRP) CAU, Imphal
3.	CAU-FP-3	Makhayatmubi × Makuchabi	AICRP(MULLaRP) CAU, Imphal
4.	CAU-FP-4	RFP 2011 × Rachna	AICRP(MULLaRP) CAU, Imphal
5.	CAU-FP-5	Makuchabi × Prakash	AICRP(MULLaRP) CAU, Imphal
6.	CAU-FP-6	Makuchabi × Pant 217	AICRP(MULLaRP) CAU, Imphal
7.	CAU-FP-7	Makhayatmubi × Prakash	AICRP(MULLaRP) CAU, Imphal
8.	CAU-FP-8	Prakash × Pant P 217	AICRP(MULLaRP) CAU, Imphal
9.	CAU-FP-9	HFP 1024 × Makhayatmubi	AICRP(MULLaRP) CAU, Imphal
10.	CAU-FP-10	KPMR 939 × Pant P 42	AICRP(MULLaRP) CAU, Imphal
11.	FPT-20-16	(RFP 4 × DFP 74) × PF 1029	RARS, Durgapura
12.	FPT-20-17	IPF 5-19 × VRP 22	IIPR, Kanpur
13.	FPT-20-18	-	IIPR, Kanpur
14.	FPT-20-19	IPFD 5-19 × HFP 530	Pantnagar
15.	FPT-20-20	BMR 7 × P 163	Tripura
16.	FPT-20-21	P 725 × P 1795	IIPR, Kanpur
17.	FPT-20-22	HFP 4 × VP 2003-19	VPKAS, Almora
18.	FPT-20-23	RFPH 192 × K 516-2010-1	Raipur
19.	FPT-20-24	KPMR 84-2 × EC 109195	HAU, Hisar
20.	FPT-20-25	Makhyachamubi × TRCP-8	Agartala
21.	FPT-20-26	HFP 554 × HFP 9907B	CCS HAU, Hisar
22.	FPT-20-27	IPFD 1-10 × EC 8495	IIPR, Kanpur
23.	FPT-20-28	T 163 × DMR 7	Tripura
24.	FPT-20-29	Rachna × HFP 8909	CSAUA&T, Kanpur
25.	FPT-20-30	HFP 530 × HFP 9426	CCS HAU, Hisar
26.	FPT-20-31	VL Matar 1 × P 388	Almora
27.	FPT-20-32	RFPH 94-26 × A 2010-4	Raipur
28.	FPT-20-33	IPFD 5-19 × HFP 530	Pantnagar
29.	FPT-20-34	(RFP 4 × DFP 74) × PF 1029	RARS, Durgapura
30.	FPT-20-35	IPFD 5-19 × HFP 530	Pantnagar
31.	HFP 1574	HFP 9907B × Pant P 25	CCS HAU, Hisar
32.	IPF 19-11	IPF 99-25 × Pant P 14	IIPR, Kanpur
33.	IPF 19-15	IPF 99-25 × EC 1	IIPR, Kanpur
34.	IPF 19-18	IPF 99-25 × P01544-4	IIPR, Kanpur
35.	KPMR 957	T 163 × HFP 9426	CSAUA&T, Kanpur
36.	Makhayatmubi	Landrace	Manipur
37.	Pant P 473	HFP 530 × Pant P 31	Pantnagar
38.	Pant P 474	IPFD 5-19 × RFP 19	Pantnagar
39.	Pant P 476	HFP 9702 × Pant P 66	Pantnagar
40.	RFPG 144	KPMR 400 × Ambika	RARS, Durgapura
41.	RFPG 151	RFP 4 × HFP 4	RARS, Durgapura
42.	RFPG 170	RFP 4 × FP 10-112	RARS, Durgapura
43.	RFP 2010-21	KPMR 516 × Rachna	Raipur
44.	RFP 2012-122-1	RFPH 9907 × A-2010-3	Raipur
45.	VL 70	VP 283 × FC 1	VPKAS, Almora
46.	VL 71	Rachna × VL 52	VPKAS, Almora
47.	WBFP-14-S-9	JVP 11 × VL 37	Berhampore (WB)

Rabi, 2020-21, following RCBD with 3 replications. The research farm is located at 24^0 46´ N and 94^0 03´ E. Each genotype is planted in a single 4 m row with a 30 cm x 10 cm gap between and within the rows. All the recommended packages of practices were followed to raise a good crop during the experiment. For data collection, ten plants were chosen at random from each genotype in each replication.

Days to 50% flowering, days to maturity, plant height (cm), the number of primary branches/plant, the number of clusters/plant, the number of pods/plant, pod length (cm), the number of seeds/pod, the number of seeds/plant, 100 seed weight (g), seed yield/plant (g), biological yield/plant (g) and harvest index were recorded. To identify the significant effects of treatments, the standard RBD analysis method was used (Rangaswamy, 2010). GCV and PCV were calculated according to Burton and De Vane (1953). Heritability is the proportion of genetic variation to total observable variance in a population that is calculated using Allard's formula (1960). Each character's GA was calculated according to Burton and De Vane (1953) and Johnson *et al.* (1955). The genetic divergence among the genotypes was assessed using Mahalanobis's (1936) D^2 statistical analysis.

RESULTS AND DISCUSSION

The ANOVA for the design of the experiment understudy was calculated separately for each trait. The mean sum of squares based on ANOVA of 47 field pea lines for 13 traits indicated the presence of a high amount of variability among themselves. It was detected that estimated ANOVA (**Table 2**) revealed that variance present in various lines for all the studied traits were highly significant.

The Genotypic Coefficient of Variation (GCV) was observed to be lower than the Phenotypic co efficient of variation (PCV) for all the traits under study. It indicates the effect of environment in the character expression. Lal *et al*. (2018) and Pathak *et al.* (2019) observed similar results in field pea. Maximum PCV and GCV recorded for the number of primary branches/plant (58.43, 56.32 %) followed by the number of clusters/plant (37.30, 35.55 %), the number of pods/plant (23.44, 22.69 %) and the number of seeds/plant (22.08, 21.60 %) (**Table 3**). These results are in agreement with Kumar (2008), Jeberson *et al*. (2016), Jeberson *et al*. (2017), Kumar *et al.* (2019), Bhardwaj *et al*. (2020) and Pujari *et al.* (2021) in pea.

Among the thirteen characters studied, heritability of biological yield/plant showed the highest value (98.22%) followed by the number of seeds/plant (95.67 %), seed yield/plant (93.68 %), the number of pods/plant (93.68%), the number of primary branches/plant (92.92%), plant height (91.59%), the number of clusters/plant (90.84%), harvest index (85.32%), the number of seeds/pod (82.68%), pod length (70.26%) and 100 seed weight (67.26%) (**Table 3**). These findings were corroborated with the work of Yadav *et al.* (2010) and Gautam *et al.* (2017) in pea. The high heritability coupled with high GA per cent of mean was recorded for the number of primary branches/plant, the number of clusters/plant, the number of pods/plant, the number of seeds/plant, seed yield/plant, biological yield/plant, the number of seeds/pod and harvest index indicating the substantial contribution of additive gene action. Similar result was found by Dar *et al.* (2013), Ahmad *et al.* (2014), Jeberson *et al*. (2016) in pea and Ranjani *et al.* (2021) in pigeon pea.

In plant breeding, genetic diversity is crucial because F_1s between lines of different origins have more heterosis than F_1s between closely related lines (Singh, 1983).

Table 2. ANOVA for 13 different traits in 47 lines of field pea

Source of variation	Degrees of freedom	DF	DM	PH	PBR	CPP	PPP	PL
Replication	2	8.00	48.43	15.67	0.02	0.11	0.06	0.11
Genotypes	46	13.01**	10.03**	210.30**	0.25**	0.79**	3.12**	0.61**
Error	92	4.07	3.24	6.24	0.01	0.03	0.07	0.08
C.V. (%)		2.82	1.74	3.04	15.29	11.29	5.89	4.84

Source of variation	Degrees of freedom	SPP	SPPL	100 SW	SYP	BY	HI
Replication	2	0.05	1.34	4.01	0.02	0.09	5.70
Genotypes	46	1.29**	34.47**	14.84**	0.79**	5.16**	51.89**
Error	92	0.08	0.51	2.07	0.02	0.03	2.82
C.V. (%)		5.84	4.60	7.06	4.67	2.24	4.66

**** 1% level of significance**

DF- Days to 50% flowering, DM- Days to maturity, PH- Plant height PBR- Number of primary branches/plant, CPP- Number of clusters/plant, PPP- Number of pods/plant, PL- Pod length, SPP- Number of seeds/pod, SPPL- Number of seeds/plant, 100 SW- 100 seed weight, SYP- Seed yield/plant, BY- Biological yield/plant and HI-Harvest index.

Table 3. Genetic variability parameters for 13 different traits in 47 field pea breeding lines

S.No.	Characters	Mean	Minimum	Maximum	GCV (%)	PCV (%)	Heritability (%)	Genetic advance	GA as per cent of mean
1	Days to 50% flowering	71.52	67.34	75.34	2.41	3.71	42.25	2.31	3.23
2	Days to maturity	103.69	100.34	107.00	1.45	2.26	41.18	1.99	1.92
3	Plant height	82.06	56.54	96.27	10.05	10.50	91.59	16.26	19.81
4	Number of primary branches/plant	0.50	0.20	1.20	56.32	58.43	92.92	0.56	111.84
5	Number of clusters/plant	1.42	0.60	2.67	35.55	37.30	90.84	0.99	69.79
6	Number of pods/plant	4.44	2.27	7.14	22.69	23.44	93.68	2.01	45.24
7	Pod length	5.68	4.48	6.68	7.45	8.89	70.26	0.73	12.86
8	Number of seeds/pod	4.97	3.27	6.67	12.77	14.04	82.68	1.19	23.92
9	Number of seeds/plant	15.58	10.00	24.60	21.60	22.08	95.67	6.78	43.52
10	100 seed weight	20.40	16.64	25.44	10.12	12.34	67.26	3.49	17.09
11	Seed yield/plant	2.82	1.52	4.26	18.01	18.60	93.68	1.01	35.91
12	Biological yield/plant	7.86	5.26	11.30	16.63	16.78	98.22	2.67	33.95
13	Harvest index	35.10	25.29	49.07	11.24	12.16	85.32	7.70	21.38

Table 4. Clustering of Field pea lines into different groups

Cluster	Number of lines	Name of lines
I	29	FPT-20-23, CAU-FP-7, RFPG 151, CAU-FP-4, FPT-20-34, FPT-20-28, IPF 19-11, FPT-20-16, HFP 1574, IPF 19-18, CAU-FP-1, RFPG 144, RFP 2010-21, FPT-20-31, FPT-20-35, FPT-20-18, WBFP-14-S-9, FPT-20-25, RFP 2012-122-1, CAU-FP-10, CAU-FP-8, CAU-FP-3, FPT-20-17, CAU-FP-6, CAU-FP-2, IPF19-15, FPT-20-29, FPT-20-33 and Makhayatmubi
II	1	FPT-20-27
III	1	Pant P 474
IV	1	RFPG 170
V	1	FPT-20-20
VI	1	CAU-FP-5
VII	3	FPT-20-26, FPT-20-30 and FPT-20-24
VIII	1	VL 71
IX	1	CAU-FP-9
X	1	FPT-20-21
XI	1	Pant P 473
XII	1	FPT-20-32
XIII	1	FPT-20-19
XIV	1	FPT-20-22
XV	1	Pant P 476
XVI	1	VL 70
XVII	1	KPMR 957

Mahalanobis's generalised distance, calculated using the D^2 statistic (Rao, 1952), is a unique method for differentiating populations based on a set of characteristics rather than morphological similarities and phylogenetic links.

Forty-seven field pea lines were grouped into 17 clusters on the basis of observed distances among the lines within and among clusters (**Table 4**). Cluster I contained a maximum number of lines *i.e.,* 29 followed by 3 in cluster VII and one line in each of the other clusters. From **Table 5** it is evident that the inter-cluster distances were greater than the intra-cluster distances revealing considerable diversity among the lines. At intra-cluster level maximum values were recorded for cluster VII (12.66) followed by cluster I (12.52) this indicated a wide genetic diversity among the lines of these clusters. In other clusters, intra-cluster distances were zero (0.00) because there was only one line present in these clusters. The average inter-cluster values were maximum between cluster XII and cluster XIII (43.62) followed by cluster XII and cluster XVII (40.14) and cluster XII and XV (38.94), minimum between cluster V and VI (7.40) followed by cluster II and VI (9.10), cluster II and V (10.26) and Cluster

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Table 5. Average intra (Bold values) and inter-cluster D^2 values in 47 lines of field pea

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV	XV	XVI	XVII
I	**12.52**	15.61	16.00	15.04	16.57	15.46	18.77	16.31	17.95	15.41	15.64	22.17	27.31	23.86	24.08	19.78	27.36
II		**0.00**	12.91	16.54	10.26	9.10	21.96	23.92	10.26	17.42	14.68	28.45	18.43	20.11	23.50	24.77	28.66
III			**0.00**	13.10	14.14	14.04	22.61	20.49	17.98	22.74	17.51	27.16	19.76	14.95	21.75	24.05	20.81
IV				**0.00**	12.55	12.27	24.23	14.11	19.84	21.92	14.65	29.97	20.48	17.43	15.45	24.89	18.53
V					**0.00**	7.40	27.57	19.85	17.72	19.21	14.74	32.47	14.49	15.22	14.83	26.84	21.78
VI						**0.00**	24.09	20.22	13.08	16.71	16.71	30.77	15.64	15.70	19.37	25.71	23.58
VII							**12.66**	26.02	18.14	20.81	23.49	17.05	36.36	32.89	36.72	22.41	38.31
VIII								**0.00**	27.64	19.93	18.80	27.34	30.47	23.44	20.68	21.70	22.68
IX									**0.00**	18.43	19.30	27.37	24.08	25.25	29.98	26.37	33.99
X										**0.00**	21.69	21.28	31.05	28.09	28.26	24.41	33.01
XI											**0.00**	29.41	25.76	24.90	22.28	20.85	29.10
XII												**0.00**	43.62	37.90	38.94	27.69	40.14
XIII													**0.00**	14.72	20.86	35.40	23.71
XIV														**0.00**	20.07	31.14	16.81
XV															**0.00**	34.88	14.97
XVI																**0.00**	35.66
XVII																	**0.00**

Table 6. The cluster-wise mean values for yield and its contributing traits in 47 lines of field pea

Cluster	DF	DM	PH	PBR	CPP	PPP	PL	SPP	SPPL	100 SW	BY	HI	SYP
I	71.38	103.53	82.40	0.50	1.51	4.46	5.64	4.96	15.37	20.23	7.57	36.61	2.77
II	74.00	104.00	92.53	0.30	0.60	3.20	6.40	5.50	13.67	24.97	8.78	33.46	2.94
III	74.67	103.67	81.33	1.03	0.87	4.13	5.83	5.87	16.80	21.07	8.81	33.89	2.99
IV	75.33	106.33	75.67	0.40	1.67	5.27	5.79	5.47	20.33	18.30	9.08	38.64	3.51
V	68.67	104.67	95.47	0.20	1.13	4.33	6.03	5.33	17.53	20.73	9.63	34.74	3.35
VI	72.33	106.33	86.80	0.20	1.40	4.33	5.75	4.47	15.13	22.83	9.43	32.28	3.04
VII	72.67	104.89	64.62	0.54	0.94	3.30	5.92	4.70	10.91	19.34	6.35	31.91	1.99
VIII	69.67	101.33	77.93	0.50	1.87	7.13	4.71	4.53	20.07	19.23	7.53	39.96	3.01
IX	73.33	106.33	76.48	0.20	0.70	2.27	5.92	4.33	10.13	25.43	8.53	33.86	2.89
X	68.33	105.00	93.73	0.20	1.50	4.80	4.96	3.27	10.13	25.03	7.42	30.62	2.27
XI	73.67	104.67	87.07	0.20	0.60	3.73	6.18	5.80	20.67	21.20	7.77	43.14	3.35
XII	69.67	101.00	76.93	1.00	1.13	3.53	5.29	4.13	10.13	16.63	5.63	27.02	1.52
XIII	71.67	103.33	91.00	0.20	1.20	4.20	6.32	6.67	17.47	22.77	11.30	32.16	3.63
XIV	67.33	100.33	80.53	0.80	1.00	5.40	4.99	4.40	18.13	19.47	10.45	29.78	3.11
XV	69.67	102.00	96.20	0.30	2.00	5.87	6.41	5.67	23.80	20.20	10.56	40.29	4.25
XVI	73.00	102.00	77.20	0.80	1.83	4.87	5.65	5.30	15.00	17.90	5.39	49.07	2.64
XVII	72.00	105.33	84.53	1.20	2.67	6.67	5.56	4.93	24.60	18.27	10.71	35.48	3.80

DF- Days to 50% flowering, DM- Days to maturity, PH- Plant height (cm), PBR- Number of primary branches/plant, CPP- Number of clusters/plant, PPP- Number of pods/plant, PL- Pod length (cm), SPP- Number of seeds/pod, SPPL- Number of seeds/plant, 100 SW- 100 seed weight (g), BY- Biological yield/plant (g), HI-Harvest index (%) and SYP- Seed yield/plant (g).

II and IX (10.26). These findings were corroborated with the work of Gupta and Singh (2006), Singh and Mishra (2008) and Rahman *et al*. (2013) in pea.

The cluster mean of different characters (**Table 6**) indicated that clusters XV and XVII had higher cluster mean for most of the traits. Cluster XV had a maximum cluster mean for plant height (96.20 cm), pod length (6.41 cm) and seed yield/plant (4.25 g). Cluster XVII had a maximum cluster mean for the number of primary branches/plant (1.20), the number of clusters/plant (2.67) and the number of seeds/plant (24.60). Cluster XIII had a maximum cluster mean for the number of seeds/pod (6.67) and biological yield/plant (11.30 g). Cluster IX had a maximum cluster mean for 100 seed weight (25.43 g). Cluster XIV had a minimum cluster mean for days to 50% flowering (67.33) and days to maturity (100.33). Cluster VIII had a maximum cluster mean for the number of pods/plant (7.13). Maximum cluster mean for harvest index (49.07) was observed in cluster XVI.

Table 7. Per cent contribution of yield and its contributing traits towards genetic divergence

S. No.	Characters	Contribution (%)
1	Days to 50% flowering	0.00
2	Days to maturity	0.00
3	Plant height	10.92
4	Number of primary branches/plant	11.47
5	Number of clusters/plant	6.85
6	Number of pods/plant	11.01
7	Pod length	1.85
8	Number of seeds/pod	1.20
9	Number of seeds/plant	11.01
10	100 seed weight	0.09
11	Seed yield/plant	3.61
12	Biological yield/plant	39.87
13	Harvest index	2.13

Per cent contribution of yield and its contributing traits towards divergence (**Table 7**) indicated that biological yield/plant (39.87) contributed maximum followed by the number of primary branches/plant (11.47), the number of pods/plant (11.01), the number of seeds/plant (11.01), plant height (10.92), the number of clusters/plant (6.85), seed yield/plant (3.61), harvest index (2.13), pod length (1.85), the number of seeds/pod (1.20) and 100 seed weight (0.09). Sharma *et al*. (2013) in garden pea and Srivastava *et al*. (2018) in field pea also found similar results.

In this study, the maximum PCV and GCV were recorded for the number of primary branches plant, clusters per plant, pods per plant and seeds per plant. Seed yield per plant, biological yield per plant, seeds per plant, pods per plant, primary branches per plant, plant height, clusters per plant, harvest index, seeds/pod, pod length and 100 seed weight showed high heritability, indicating a little environmental impact. Seed yield per plant, biological yield per plant, the number of branches per plant and harvest index had high heritability along with high GA as per cent of mean indicated additive gene action played a substantial influence. The lines were diversified, as revealed by inter-cluster distances and cluster means, demonstrating their suitability for crop improvement through hybridization.

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