

RESEARCH ARTICLE

STUDIES OF VARIABILITY, HERITABILITY AND GENETIC ADVANCEMENT FOR FIELD PEA (*PISUM SATIVUM* L.) IN SATNA DISTRICT, M.P.

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Abstract: Twenty diverse cultivars of pea grown in a Completely Randomized block design (CRBD) at AKS University, Satna, during *Rabi* season on November 2022. Data were collected for ten quantitative traits and estimated for variance, genetic variability, heritability and genetic advance. The design of the experiment indicated highly significant differences for all the characters due to treatments. The analysis of variance indicated the existence of sufficient amount of variability among genotypes for all the studied characters. The maximum GCV along with PCV was observed in number of pod per cluster followed by seed yield per plant, 100 seed weight (g), number of seed per pod and number of pods per plant. Higher estimates (h^2b) >80% were observed for Seed yield per plant followed by 100 seed weight (g), plant height (cm), days to maturity, days to 50 % flowering, pod length, shelling (%) and number of seed per pod. High estimate of expected genetic advance at 5% were found for number of pod per cluster followed by seed yield per plant, 100 seed weight (g), number of seed per pod and number of pods per plant. High heritability coupled with high genetic advance indicated the predominance of additive gene action in the expression of these traits.

Keywords: Field pea, Variance, Variability, Heritability, Genetic advance

INTRODUCTION

Pea (*Pisum sativum* L.) belongs to circle of relatives *Leguminosae* or *Fabeaceae* and is an essential legume vegetable grown all-around the world for the duration of cool season. Its miles a self pollinated crop having diploid chromosome number $2n=14$ and $n=7$ chromosome found in reproductive gametes. Pea is of Mediterranean origin, the Near East and Ethiopia are considered as its secondary centres of origin. Peas are used alone and combined with different veggies. It's also utilized as a pulse. Occasionally, pea is grown for fodder, cover crops, green manure and the pods are occasionally fed to livestock.

According to the actual integrated taxonomic information system database, the *Pisum* genus has only two species: *P. fulvum* and *P. sativum* L. According to same data, the *P. sativum* L. species has five varieties: *P. sativum* var. *arvense* (L.) Poir. (Austrian winter pea), *P. sativum* var. *elatius*, *P. sativum* var. *macrocarpon* Ser, *P. sativum* var. *pumilio* Meikle, *P. sativum* var. *sativum* L. (garden pea).

For the advancement of any crop, genetic variability is the primary requirement (Azmat *et al.*, 2011). Abundant genetic variation is to be had in *Pisum sativum*. For the improvement of genetic behaviour of the crop, expertise of genetic variability is wanted for distinct characters which form an essential device

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for identification of appropriate genes and their nature of adherence (Nwangburuka *et al.*, 2011). For development of improved cultivars, type of genetic variability, among the genotype is treasured for preservation and further acquisition of germplasm as an accession from different origin is necessary as parent stock (Amurrio *et al.*, 2007). It is going to be possible to decide various breeding programmes for advancement of different characters on the basis of heritability and genetic advance estimates (Kumari *et al.*, 2012).

MATERIALS AND METHODS

The present investigation was conducted during *Rabi*, 2022-23 at Research farm, Genetics and Plant Breeding, AKS University, Sherganj, Satna, Madhya Pradesh. The material consists of 20 varieties/strains of Pea (*Pisum sativum* L.) germplasm comprising indigenous genotypes, evaluated in Completely Randomized Block Design. The entire experimental field divided in 3 blocks of equal size and each block had 20 plots. Each plot was consisted of three rows 2 meters length, following row to row spacing of 40 cm. and plant to plant spacing of 10 cm.

Ten observations on yield and yield contributing characters were recorded. In each plot, five competitive plants were randomly selected for recording observations for all the ten quantitative characters, which were recorded on the plot basis.

The data were recorded for days to 50 % flowering, plant height (cm), days to maturity, no. of pods per plant, pod length, no. of cluster per plant, no. of pod per cluster, number of seed per pod, 100 seed weight (g), and seed yield per plant.

The analysis of variance for the design of the experiment was carried out according to the procedure outlined by Panse and Sukhatme, (1967). The genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV) and environmental coefficient of variation (ECV) was estimated by the formula suggested by Burton and de Vane, (1953). Heritability in broad sense (h^2b) was estimated using the formula suggested by Burton and de Vane, (1953). Genetic advance was calculated by the method suggested by Johnson *et al.*, (1955).

RESULTS AND DISCUSSION

The analysis of variance for the design of the experiment involving 20 strains/varieties of pea was evaluated in Randomized Block Design with three replications for the ten quantitative characters. The design of the experiment indicated highly significant differences for all the characters presented in Table: 1. indicating thereby the presence of sufficient genetic variability in the genotypes. The analysis of variance exhibited that mean sum squares due to genotypes were significant for all the growth parameters, yield contributing traits, indicating thereby the presence of sufficient genetic variability in the genotypes. Earlier researchers namely Gudadinni *et al.* (2017); Khan *et al.* (2017); Barcchiya *et al.*, (2018); Kumawat (2018); Ali *et al.* (2018); Bishnoi *et al.* (2021); Ertiro (2022); and Kumar *et al.*, (2022) have also reported significant amount of variability in the genetic material for all the characters studied in field pea.

The mean performance, grand means, range, GCV, and PCV of 20 genotypes of mustard for 12 quantitative characters are presented in Table: 2 and Table:3. The magnitude of GCV ranged from number of pod per cluster (37.68) to days to maturity (7.19). The magnitude of PCV ranged from number of pod per cluster (40.15) to days to maturity (7.25). The GCV along with PCV was observed in number of pod per cluster followed by seed yield per plant, 100 seed weight (g), number of seed per pod and number of pods per plant. This is an indicative of less amenability of these characters to environmental fluctuations and hence, greater emphasis should be given to these traits. Earlier researchers also observed high amount of PCV and GCV values for number of primary branches per plant per plant Singh *et al.*, (2014); internodal length Guleria *et al.*, (2009); pod yield per plant days to first flowering, plant height and days to fifty per cent flowering Ali *et al.*, (2018); plant height, number of pods per plant, number of effective nodes, number of seeds per plant, harvest index, 100- seed weight and yield per

plant Bishnoi *et al.*, (2021), days to maturity and thousand seed weight g/ha Ertiro, (2022).

Heritability estimates are used to predict expected advance under selection so that breeders are able to anticipate improvement from different of selection intensity. The major function of heritability estimates is to provide information on transmission of characters from parents to the progeny. Such estimates facilitate evaluation of hereditary and environmental effect in phenotypic variation and thus aid in selection. Burton and De Vane (1953) suggested that the GCV along with heritability estimate could provide better picture of the genetic advance to be expected by phenotypic selection. Heritability h^2 (Broad Sense), h^2 (Broad Sense)%, Genetic Advancement @ 5%, Genetic Advancement @1%, Genetic Advance as % of Mean 5%, and Genetic Advance as % of Mean 1%, was estimated for all the characters and has been presented in Table: 4.

Higher estimates (h^2b) >80% were observed for all the characters except number of pods per plant. The heritability value ranged from number of pods per plant (76.40%) to seed yield per plant (98.90%). High heritability estimates were found for Seed yield per plant followed by 100 seed weight (g), plant height (cm), days to maturity, days to 50 % flowering, pod length, shelling (%) and number of seed per pod suggested that the characters are least influenced by the environmental factors and also indicates the dependency of phenotypic expression which reflect the genotypic ability of strains to transmit the gene to their progenies. Similar results were reported earlier by Katoch *et al.*, (2016); Lal *et al.*, (2018a); Kumar *et al.*, (2018); Kumar *et al.*, (2019) and Meena *et al.*, (2022). Heritability estimate was moderate for were also reported by Habtamu and Million, (2013); Ahmad *et al.*, (2014); and Meena *et al.*, (2022).

Genetic advance is a measure of genetic gain under selection which depends upon main factors viz., genetic variability, heritability, and selection index Allard RW, (1960). The expected genetic advance as percent of mean at 5% ranged from days to maturity (14.68%) to number of pod per cluster (72.84%). High estimate of expected genetic advance as percent of mean at 5% were found for number of pod per cluster followed by seed yield per plant, 100 seed weight (g), number of seed per pod and number of pods per plant. High heritability coupled with high genetic advance observed for seed yield per plant, number of pod per cluster and 100 seed weight (g), number of seed per pod, number of pods per plant indicating that these characters could be prominently governed by additive gene action. So the selection of these traits could be more effective for desired genetic improvement. High degree of heritability estimate along with high genetic advance of genetic advance was also revealed Pathak and Jamwal, (2002); Lavanya *et al.*, (2010); Pal and Singh,

(2013); Iqbal *et al.*, (2015); Katoch *et al.*, (2016); Gautam *et al.*, (2017); Gudadinni *et al.*, (2017); Ali *et al.*, (2018); Barcchiya *et al.*, (2018); Gupta *et al.*, (2018); Kumar *et al.*, (2018); Ertiro, (2022); Kumar *et al.*, (2022); Meena *et al.*, (2022) in their respective studies.

CONCLUSION

The design of the experiment indicated highly significant differences for all the characters among treatments. Wide range of variation was found for all the studied characters of pea. The GCV and PCV was observed in number of pod per cluster followed by seed yield per plant, 100 seed weight (g), number of seed per pod and number of pods per plant. The high PCV were also recorded for number of pod per cluster followed by seed yield per plant, 100 seed weight (g), number of seed per pod and number of

pods per plant. High heritability coupled with high genetic advance observed for seed yield per plant, number of pod per cluster and 100 seed weight (g), number of seed per pod, number of pods per plant indicating that these characters could be prominently governed by additive gene action. So the selection of these traits could be more effective for desired genetic improvement.

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Table 1. Analysis of variance for 10 quantitative characters in Pea.

S.N.	Traits	Replications (df = 2)	Treatments (df = 19)	Error (df = 38)
1	Days to 50 % flowering	1.50	208.76**	6.56
2	Plant height (cm)	3.73	242.31**	3.04
3	Days to maturity	5.73	167.89**	2.88
4	No. of Pods per plant	285.25	127.29**	30.02
5	Pod length	0.01	1.94**	0.06
6	Shelling (%)	1.42	60.49**	5.01
7	No. of pod per cluster	3.14	4.66**	0.56
8	Number of seed per pod	1.03	8.62**	0.83
9	100 seed weight (g)	11.17	141.82**	1.69
10	Seed yield per plant	16.07	701.19**	7.94

*Significant at 5% probability level.

**Significant at 1% probability level.

Table 2. Mean performance of 10 characters of pea genotypes.

S.N.	Genotypes	DFP	PH	DM	NPP	PL	SP	NPC	NSP	HSW	SYP
1	US Green11	60.17	52.96	96.36	34.28	8.47	51.06	2.30	6.38	18.23	48.56
2	Karil	61.54	70.84	102.86	30.89	7.22	44.81	3.37	5.10	25.42	42.50
3	TOPS10	63.32	72.48	112.35	35.68	8.56	48.10	2.32	6.91	16.77	56.43
4	S10	56.64	61.20	109.44	39.88	9.40	51.87	3.72	9.48	17.41	59.66
5	Green Wood	64.01	68.53	114.74	37.19	9.38	51.16	3.02	7.35	17.27	63.02
6	Woonder10	65.14	62.13	103.35	29.34	9.68	47.75	2.51	5.64	17.59	35.82
7	GS10	48.00	70.71	91.52	23.14	8.46	53.76	5.24	6.29	23.86	24.29
8	Suhana1010	44.07	60.86	96.75	45.11	8.73	50.08	1.89	8.67	23.51	62.19
9	Hans	46.06	67.20	109.20	27.44	9.43	50.84	2.58	7.90	22.38	25.26
10	KSP110	57.38	67.98	95.50	36.16	9.53	51.83	5.74	7.32	24.30	55.34
11	Greendew	53.92	56.01	111.03	24.84	10.51	49.94	2.20	10.33	16.62	43.76
12	Tiger	56.04	62.49	99.11	36.20	9.56	46.58	5.07	7.60	18.71	54.13
13	4009	63.31	45.18	96.77	24.45	9.33	42.72	1.91	9.90	35.08	28.14
14	NS1100	63.65	49.53	108.87	33.44	9.68	36.23	1.94	9.43	34.87	41.14
15	Kiwi101	68.29	37.78	110.84	35.81	9.65	43.45	2.43	8.50	38.80	55.06
16	JK124	68.54	64.36	104.99	26.41	8.48	52.27	2.29	6.13	29.70	22.77
17	KN5	46.62	63.26	91.86	25.46	7.54	49.60	2.48	4.30	29.24	21.57
18	Kashi Nandini	45.78	59.34	102.54	43.03	8.20	40.59	5.20	8.64	29.96	68.87
19	R1012	46.42	60.32	94.47	24.24	8.52	50.79	2.31	5.39	31.18	28.01
20	PSM3	48.30	66.88	111.50	30.09	9.46	46.58	3.60	8.25	24.45	34.97

DFP= Days to 50 % flowering, PH= Plant height (cm), DM= Days to maturity, NPP= No. of Pods per plant, PL= Pod length, SP= Shelling (%), NPC= No. of pod per cluster, NSP= Number of seed per pod, HSW= 100 seed weight (g), SYP= Seed yield per plant

Table 3. Mean, Range, Genotypic, Phenotypic and environmental variances, and coefficient of variation for 10 quantitative characters in pea.

S.N.	Characters	Grand mean	Range		GCV	PCV	ECV	C.D. @ 5%
			Max	Min.				
1	Days to 50 % flowering	56.36	68.54	44.07	14.57	14.80	4.54	4.23
2	Plant height (cm)	61.00	72.48	37.78	14.64	14.73	2.86	2.88
3	Days to maturity	103.20	114.74	91.52	7.19	7.25	1.65	2.81
4	No. of Pods per plant	32.15	45.11	23.14	17.71	20.26	17.04	9.06
5	Pod length	8.99	10.51	7.22	8.82	8.96	2.74	0.41
6	Shelling (%)	48.00	53.76	36.23	8.96	9.36	4.67	3.70
7	No. of pod per cluster	3.11	5.74	1.89	37.68	40.15	24.03	1.23
8	Number of seed per pod	7.48	10.33	4.30	21.55	22.68	12.22	1.51
9	100 seed weight (g)	24.77	38.80	16.62	27.59	27.76	5.26	2.15
10	Seed yield per plant	43.57	68.87	21.57	34.89	35.09	6.47	4.66

Table 4. Heritability (%) in broad sense, Genetic advance and genetic advance as percent of mean for 10 quantitative characters in pea.

S.N.	Characters	Heritability (h ² b)	Heritability (h ² b %)	Genetic Advancement 5%	Genetic Advancement 1%	Gen. Adv. as % of Mean 5%	Gen. Adv. as % of Mean 1%
1	Days to 50 % flowering	0.969	96.90	16.65	21.33	29.53	37.85
2	Plant height (cm)	0.987	98.70	18.28	23.43	29.97	38.41
3	Days to maturity	0.983	98.30	15.15	19.41	14.68	18.81
4	No. of Pods per plant	0.764	76.40	10.25	13.14	31.89	40.87
5	Pod length	0.969	96.90	1.61	2.06	17.88	22.92
6	Shelling (%)	0.917	91.70	8.48	10.87	17.68	22.65
7	No. of pod per cluster	0.881	88.10	2.26	2.90	72.84	93.35
8	Number of seed per pod	0.903	90.30	3.16	4.04	42.20	54.08
9	100 seed weight (g)	0.988	98.80	14.00	17.94	56.50	72.41
10	Seed yield per plant	0.989	98.90	31.14	39.90	71.46	91.58

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