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Study of Genetic variability in Pea (*Pisum sativum* L.) during *rabi* Season at Mid Hills of Himachal Pradesh

Priyam Thakur[1], Ritika Singh[2*], Alok Kumar[3], Anupam Kumar[4] and Shivani Kaundal[5]

[1]*M.Sc. Scholar, Department of Genetics and Plant Breeding,*
Abhilashi University Mandi (Himachal Pradesh), India.
[2]*Assistant Professor, Department of Plant Breeding and Genetics,*
Abhilashi University Mandi (Himachal Pradesh), India.
[3]*Assistant Professor, Department of Seed Science and Technology,*
Abhilashi University Mandi (Himachal Pradesh), India.
[4]*Assistant Professor, Department of Plant Pathology,*
Abhilashi University Mandi (Himachal Pradesh), India.
[5]*Assistant Professor, Department of Biochemistry and Crop Physiology,*
Abhilashi University Mandi (Himachal Pradesh), India.

(Corresponding author: Ritika Singh)*

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ABSTRACT: A field experiment was conducted on thirty genotypes including two checks were grown in a RBD with three replication during *rabi* 2022 at Research Farm School of Agriculture, Abhilashi University Chailchowk Mandi, Himachal Pradesh to estimate the parameters of variability and association of important characters with yield in pea. Analysis of variance showed significant differences among the genotypes for all the characters under study. The phenotypic coefficient of variation (PCV) was higher than corresponding genotypic coefficient of variation (GCV). The PCV and GCV both were observed high for number of pods per node, number of seed per pod, seed yield and harvest index. High heritability coupled with high genetic advance in percent of mean were recorded for secondary branches per plant, pod length, number of seed per pod and seed yield which indicated the presence of both additive and non additive gene action thus providing scope for improvement of these characters, through hybridization and selection. Therefore, from the above obtained results it can be concluded that the characters studied are governed by additive gene effect. Hence adoption for selection of elite genotypes on the basis of these characters will result in effective crop improvement for higher yield and yield attributing characters.

Keywords: Variability, ANOVA, Mean, PCV, GCV.

INTRODUCTION

Pea (*Pisum sativum* L.) is a major leguminous vegetable crop whose cultivation is confined to both temperate and subtropical areas of the world. It is self pollinated crop having diploid chromosome number (2n= 14). In Himachal Pradesh pea is available at time when it cannot be grown in nearby areas of Punjab, Haryana and Delhi. It is an important cash crop in the hilly regions of western Himalayas especially. In Himachal Pradesh, agroclimatic conditions favour the cultivation of pea as an important off-season vegetable crop. The green pods are available during the summer months which find ready market in the plains and provide lucrative returns to the growers. The produce of hills is high priced for its characteristics flavour, sweetness, tenderness and attractive pods. In Himachal Pradesh pea occupies an area of 336.10 ha with production of 2709.69mh and productivity of 328.80 tonnes, respectively (Anonymous, 2022). Among major constraints, lack of varieties with high and stable productivity, losses from several biotic factors are common. During the pea cultivation there are many problems that produce yield loss of pea. Peas are subject to a number diseases, several may cause serious injury or loss. Annual losses from diseases vary from year to year, depending often on local weather conditions. Identification and development of new varieties is very important to boost the production and productivity of the pea crop and protect the pea plant from diseases especially powdery mildew and insect pest attack. Evaluation of germplasm is the first step in this direction, since the improvement in any crop is proportional to the magnitude of genetic variability.

Estimates of variability, heritability and genetic advance are reliable indicators for improvement of characters in a particular genetic material through selection. Hence, genetic variability has been considered as an important factor that is also an essential prerequisite for crop improvement programs for obtaining high-yielding progenies. The greater variability in the initial genetic material, the better would be the chance of selecting a desirable type. The higher the heritable variation, the greater will the possibility of fixing the characters by selection methods (Sharma and Bora 2013). Therefore, to breed the new cultivars, success of any breeding programme depends on the existing genetic variability in the base population that could lead to effective selection to obtain high yielding progenies. A comprehensive knowledge on genetic variability, and genetic advance are pre requisite for improvement of any crop for selection of supervisor genotypes and improvement of any trait. Similarly, information on character association in peas is important for effective and rapid selection in crop improvement. The present study therefore, was taken up to estimate the parameters of variability and character association in pea so that the desired target are achieved.

MATERIALS AND METHODS

The experiment was carried out at the Research Farm School of Agriculture, Abhilashi University Chailchowk Mandi, Himachal Pradesh during *rabi* 2022. The experimental material for present investigation consisted of 28 pea genotypes procured from NBPGR regional station Shimla and 2 check varieties procured from CSKHPKV Palampur and College of Horticulture Thunag Mandi H.P. The genotypes along with their sources of availability have been presented in Table 1. Sowing was done manually in lines in the month of November, 2022 at spacing of row to row and plant to plant 30 cm and 10 cm, respectively. Each genotypes was planned in Randomized Block Design (RBD) with three replications. Besides the application of farm yard manure (FYM) at 20t/ha incorporated at the time of land preparation. The recommended dose of NPK (60:80:70: NPK kg/ha). During the experiment, all recommended cultural practices were followed for proper growth and stand of the crop as and when required. The observation were recorded on five randomly selected plants in each replication for recording the data on yield and quality related traits like days to 50 per cent flowering, days to pod harvesting stage, days to 75 per cent maturity, plant height (cm), number of primary branches per plant, number of secondary branches per plant, number of pods per plant, pod length (cm), number of pods per node, dry matter yield (g), number of seed per pod, seed yield (g), harvest index (%) and100 seed weight (g). The statistical analysis of mean data for the design (RBD) was worked out as per the method suggested by Panse and Sukhatme (1985). The variability, heritability and genetic advance was calculated as per the formula given by Burton and De Vane (1953); Johnson *et al.* (1955).

Table 1: List of pea genotypes studied along with their sources of availability.

Sr. No.	Accession	Source
1.	IC-208391	NBPGR regional station Shimla
2.	IC-218997	NBPGR regional station Shimla
3.	IC-208667	NBPGR regional station Shimla
4.	IC-107452	NBPGR regional station Shimla
5.	IC-212622	NBPGR regional station Shimla
6.	IC-208385	NBPGR regional station Shimla
7.	IC-208397	NBPGR regional station Shimla
8.	IC-208933	NBPGR regional station Shimla
9.	IC-98608	NBPGR regional station Shimla
10.	IC-269305	NBPGR regional station Shimla
11.	IC-199303	NBPGR regional station Shimla
12.	IC-204123	NBPGR regional station Shimla
13.	IC-208370	NBPGR regional station Shimla
14.	IC-208365	NBPGR regional station Shimla
15.	IC-269578	NBPGR regional station Shimla
16.	IC-268399	NBPGR regional station Shimla
17.	IC-208932	NBPGR regional station Shimla
18.	IC-109553	NBPGR regional station Shimla
19.	IC-208378	NBPGR regional station Shimla
20.	IC-212657	NBPGR regional station Shimla
21.	EC-269304	NBPGR regional station Shimla
22.	EC-6620	NBPGR regional station Shimla
23.	EC-16391	NBPGR regional station Shimla
24.	EC-269469	NBPGR regional station Shimla
25.	EC-33920	NBPGR regional station Shimla
26.	EC-268386	NBPGR regional station Shimla
27.	EC-269421	NBPGR regional station Shimla
28.	EC-269571	NBPGR regional station Shimla
29.	Check variety (HIM PALAM MATAR-1)	CSKHPKV Palampur H.P.
30.	Punjab 89 (P-89)	College of Horticulture, Thunag Mandi, H.P.

RESULT AND DISCUSSION

The analysis of variance revealed significant mean sum of square due to genotypes for all traits under study (Table 2) *viz*., days to 50 per cent flowering, days to pod harvesting stage, days to 75 per cent maturity, plant height (cm), number of primary branches per plant, number of secondary branches per plant, number of pods per nodes, pod length (cm), number of pods per plant, number of seed per pod, dry matter yield (g), seed yield (g), 100 seed weight (g) and harvest index (%) indicating thereby presence of sufficient genetic variability and scope of selection for these traits. Similar finding has also been reported by, Kumar *et al*. (2015), studied the analysis of variance (ANOVA) showed significant differences among the genotypes for all the morphological characters. Kumar *et al*. (2021) studied the analysis of variance that repeated the presence of variability among the genotypes for days to 50 per cent flowering, number of primary branches per plant, number of pods per plant, plant height, days to maturity, seed yield per plant, number of secondary branches per plant, number of seeds per pod and harvest index.

According to the mean performance, genotypes Palam matar-1, Punjab-89, IC-269558, IC-204123, IC-208933, IC-208667, IC-109303 and IC-109553 exhibited high mean performance for different characters (Table 3.) i.e. days to 50 per cent flowering, days to pod harvesting stage, days to 75 per cent maturity, pod length, number of pod per plant, plant height, number of primary branches per plant, number of secondary branches per plant, number of pods per nodes, 100 seed weight, pod length, number of seed per pod, dry matter yield, seed yield and harvest index were found to be superior. Pathak *et al.* (2019)studied on randomly selected plants for nine characters days to 50 per cent flowering, days to maturity, plant height (cm), number of branches per plant, number of seeds per plant, number of pods per plant, number of seeds per pod, test weight (1000-seed weight) (g) and seed yield per plant (g). The highest mean value was observed for test weight followed by days to maturity and plant height.

The phenotypic and genotypic coefficient of variation help in exposing the nature of variability in population and indicates the relative role of genotypic and environmental factors in the expression of a character. The phenotypic coefficient of variability was higher than the genotypic coefficient of variability which indicates that the environment plays considerable role in expression of these traits (Table 4). In present investigation high PCV were observed for primary branches per plant, number of pods per nodes, number of seed per pod, seed yield and harvest index. Moderate PCV for plant height, secondary branches per plant, pod length, number of pod per plant, dry matter yield & 100 seed weight. Low PCV for days to 50 per cent flowering, days to pod harvest stage, days to 75 per cent maturity. High GCV were observed for, number of pods per node, number of seed per pod, seed yield & harvest index. Moderate GCV for plant height, primary branches per plant, secondary branches per plant, pod length, number of pod per plant & dry matter yield. Low GCV for days to 50 per cent flowering, days to pod harvesting stage, days to 75 per cent maturity & 100 seed weight. Similar finding were reported by Lal *et al*. (2018) studied that the magnitudes of phenotypic coefficient of variance (PCV) for all the characters were slightly higher than their corresponding genotypic coefficient of variance (GCV), indicated environmental influence on the expression of the characters. The estimates of PCV and GCV values give only the extent of variability existing for various traits but, do not give any information about the heritable portion. Therefore, estimates of heritability and genetic advance would give better idea about the possible gain of selection. Burton and De Vane (1953) have suggested that a genetic coefficient of variability together with the heritability estimates would give the more reliable indication of the expected genetic gain by selection. Heritability in broad sense is tremendous significance to the breeders as its magnitude indicates reliability with which a genotype can be recognized by its phenotypic expression (Lush 1940). In the present study, high estimates of heritability were recorded for plant height, number of primary branches per plant, number of secondary branches per plant, number of pods per node, pod length, number of seed per pod, dry matter yield, seed yield and harvest index. Moderate estimates of heritability were recorded for days to pod harvesting stage, number of pod per plant and 100 seed weight. Low estimates of heritability were observed for days to 50 per cent flowering and days to 75 per cent flowering. For an effective selection programme, knowledge of the estimates of heritability alone is not sufficient and genetic advance if studied along with heritability is more useful (Johnson et al. 1955). The genetic advance has an added edge over heritability a guiding factor to breeders in various selection programme. Genetic advance expresses as percent of mean was observed to be high were recorded for plant height, primary branches per plant, secondary branches per plant, number of pods per node, pod length, number of pod per plant, number of seed per pod, dry matter yield, seed yield and harvest index. Moderate genetic advance were recorded for 100 seed weight. Low genetic advance were recorded for days to 50 per cent flowering, days to pod harvesting stage and days to 75 per cent maturity. High heritability coupled with high genetic advance in percent of mean were recorded for secondary branches per plant, pod length, number of seed per pod, seed yield which indicated the presence of both additive and non additive gene action thus providing scope for improvement of these characters, through hybridization and selection. Similar result reported by Gupta *et al.* (2020) evaluated high heritability was recorded for all the characters except width of pod (55.84 %) which had medium heritability. High heritability coupled with high genetic advance was observed for the traits viz. plant height, seed yield per plant, number of pods per plant, length of first fruiting node, days to 50 per cent flowering, number of first fruiting node, length of pod and number of seeds per pod which indicated presence of additive gene action and demands for population improvement by selection. Ban *et al*. (2019) studied high heritability and high genetic advance were observed for characters like plant height, number of primary branches per plant, days to initiation of first flowering, days to 50 per cent flowering, days to first picking, number of pickings, number of clusters per plant, number of pods per cluster, pod length, number of seeds per green pod, green pod yield per plant, green pod yield per plot and green pod yield per hectare.

Table 2: Analysis of variance (ANOVA) for fourteen characters in Pea.

	Mean sum of square (MSS)			
Sr. No.	**Characters**	**df**	**Genotypes**	**Error**
			29	**58**
1.	Days to 50% flowering		24.251**	11.737
2.	Days to pod harvesting stage		71.166**	9.901
3.	Days to 75% maturity		61.861**	14.096
4.	Plant height (cm)		87.281**	7.265
5.	Number of branches per plant primary branches		0.851**	0.06
6.	Number of Secondary branches		32.709**	1.012
7.	Number of pods per nodes		1.007**	0.037
8.	Pod length (cm)		1.926**	0.057
9.	Number of pod per plant		4.308**	0.517
10.	Number of seed per pod		6.624**	0.159
11.	Dry matter yield (g)		6.033**	0.585
12.	Seed yield (g)		10.831**	0.314
13.	100 seed weight (g)		9.68**	1.481
14.	Harvest index (%)		598.946**	27.858

*Significant at 5 percent level of significance;   ** Significant at 1 percent level of significance

Table 3: Mean performance of 30 genotypes for fourteen characters in pea (*Pisum sativum* L.).

Sr. No.	**Accession No.**	**Days to 50% flowering**	**Days to pod harvesting stage**	**Days to 75% maturity**	**Plant height (cm)**	**No. of primary branches per plant**	**No. of secondary branches per plant**	**Number of pods per nodes**	**Pod length (cm)**	**Number of pod per plant**	**Number of seed per pod**	**Dry matter yield (g)**	**Seed yield (g)**	**100 Seed Weight (g)**	**Harvest Index (%)**
1.	IC-208391	109	151.67	144	25.07	1.60	16.33	2.27	5.03	7.87	3.73	10.67	3.33	18.67	31.21
2.	IC-218997	105.67	151.67	141	32.40	2.40	18.73	2.33	4.80	6.53	4.47	10.33	4.63	19.67	45.22
3.	IC-208667	115.67	148.67	143	28.20	2.33	11.60	4.00	5.97	10.40	4.93	15.13	5.67	18.00	37.87
4.	IC-107452	105.33	151.67	144	34.33	3.27	12.07	2.53	5.67	7.60	3.60	10.13	4.67	15.00	46.04
5.	IC-212622	109.67	142	138	34.30	3.00	20.00	2.20	6.03	8.53	4.20	11.20	5.03	17.00	44.58
6.	IC-208385	109	143.33	138	25.27	2.33	17.87	1.67	5.13	8.47	3.33	11.40	4.97	20.67	44.35
7.	IC-208397	110.33	151.67	143	31.27	2.67	19.93	2.60	7.00	6.80	6.40	11.20	5.33	19.67	47.61
8.	IC-208933	105	151.67	144	31.93	2.93	21.27	2.13	6.10	7.00	5.27	11.73	4.33	20.67	36.95
9.	IC-98608	109	151.67	144	22.73	3.00	19.07	2.33	5.60	9.47	5.80	7.93	6.00	18.67	75.76
10.	IC-269305	111.67	155	145	34.53	2.60	20.60	2.53	6.43	6.20	4.40	10.6	3.67	19.67	34.62
11.	IC-109303	106.33	146.67	138	41.13	2.07	20.53	1.87	5.50	10.53	5.00	10.97	5.33	18.67	48.85
12.	IC-204123	103.67	148.67	141	31.73	4.00	19.87	2.53	5.87	6.80	3.47	10.60	4.67	15.67	44.33
13.	IC-208370	109	151.67	144	29.27	2.33	13.00	2.93	5.80	8.13	4.07	12.13	3.33	18.33	27.44
14.	IC-268365	106.67	148.67	143	25.60	2.00	18.00	1.60	5.73	8.00	4.13	11.93	3.63	17.67	30.89
15.	IC-269558	107.67	153.33	146	41.60	3.00	15.13	1.87	5.93	8.07	2.73	10.87	6.33	18.67	58.36
16.	IC-268399	105.67	141.67	138	26.00	3.00	20.33	1.73	5.73	7.13	3.40	11.67	4.33	19.00	37.09
17.	IC-208932	107.33	148.33	141	37.60	2.20	17.87	2.20	5.77	9.50	5.27	11.60	5.00	18.33	43.06
18.	IC-109553	105.67	148.33	141	25.40	2.20	14.33	1.53	6.00	9.13	5.87	11.93	5.63	21.67	47.67
19.	IC-208378	111.33	150	142	31.07	3.13	12.40	1.60	6.23	8.60	5.60	12.53	6.67	14.67	53.34
20.	IC-212657	109	151.67	144	38.13	2.80	12.00	2.87	4.83	8.33	3.40	12.47	4.03	18.67	32.08
21.	EC-269304	106.67	148.33	141	27.53	2.47	15.07	2.20	5.70	9.40	3.73	12.20	3.33	19.00	27.38
22.	EC-6620	108.67	151.67	144	21.27	2.00	13.13	2.60	5.30	7.40	5.20	10.80	5.63	19.00	52.38
23.	EC-16391	110.33	153.33	146	27.80	2.67	13.33	1.53	6.00	9.53	6.00	13.20	4.03	20.00	30.18
24.	EC-269469	109	148.33	141	32.67	3.13	18.47	1.60	5.63	8.73	5.60	12.60	5.63	18.67	45.37
25.	EC-33920	109	150	143	26.27	3.60	13.33	2.00	5.70	8.67	5.20	12.53	6.03	17.67	48.13
26.	EC-268386	105.67	145	138	26.60	3.20	19.47	2.00	6.63	7.93	4.80	11.27	4.03	14.67	35.40
27.	EC-269421	104	143.33	136	32.40	2.53	18.27	2.20	5.70	8.20	4.20	11.00	4.33	16.00	39.29
28.	EC-269571	105	140	133	30.40	3.20	16.60	3.00	6.23	7.13	3.27	9.60	3.33	17.33	34.90
29.	P.MATAR-1	103	136.67	128.33	21.73	2.33	12.40	3.20	8.13	6.47	9.80	13.33	11.47	19.67	86.05
30.	P-89	103.33	136.67	128.33	24.13	2.13	11.27	1.53	8.50	6.00	8.07	14.67	11.00	20.67	75.11
Mean		107.58	148.04	140.69	29.95	2.67	16.41	2.24	5.96	8.09	4.83	11.61	5.18	18.39	44.72
CV		3.18	2.13	2.67	9.00	9.19	6.13	8.57	4.01	8.89	8.25	6.59	10.81	6.62	11.80
SEm		1.98	1.82	2.17	1.56	0.14	0.58	0.11	0.14	0.42	0.23	0.44	0.32	0.7	3.05
CD at 5%		5.6	5.14	6.14	4.41	0.4	1.64	0.31	0.39	1.18	0.65	1.25	0.92	1.99	8.63
CD at 1%		7.45	6.84	8.16	5.86	0.53	2.19	0.42	0.52	1.56	0.87	1.66	1.22	2.65	11.48
Minimum		103	136.67	128.33	21.27	1.6	11.27	1.53	4.8	6	2.73	7.93	3.33	14.67	27.38
Maximum		115.67	155	146	41.6	4	21.27	4	8.5	10.53	9.8	15.13	11.47	21.67	86.04

Table 4: Estimation of parameters of variability.

Sr. No.	Characters	PCV (%)	GCV (%)	h2 (Broad Sense)	Genetic Advance as % of Mean 5%
1.	Days to 50% flowering	3.708	1.899	26.22	2.003
2.	Days to pod harvesting stage	3.72	3.052	67.349	5.16
3.	Days to 75% maturity	3.894	2.836	53.04	4.255
4.	Plant height (cm)	19.454	17.246	78.593	31.496
5.	Number of primary branches per plant	21.31	19.225	81.388	35.729
6.	Number of secondary branches per plant	20.736	19.809	91.258	38.982
7.	Number of pods per nodes	26.788	25.381	89.772	49.539
8.	Pod length (cm)	13.844	13.25	91.601	26.123
9.	Number of pod per plant	16.503	13.902	70.969	24.126
10.	Number of seed per pod	31.487	30.387	93.134	60.41
11.	Dry matter yield (g)	13.348	11.609	75.643	20.8
12.	Seed yield (g)	37.714	36.13	91.78	71.304
13.	100 Seed Weight (g)	11.164	8.99	64.851	14.914
14.	Harvest Index (%)	33.035	30.855	87.234	59.365

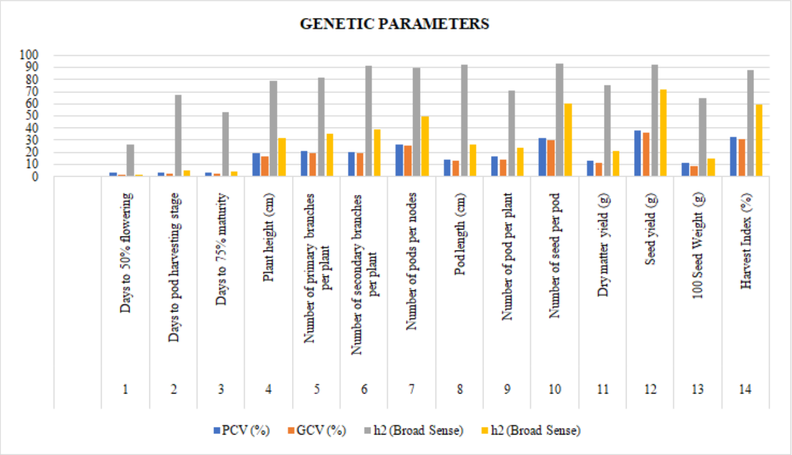

Fig. 1. Variability parameters for different quantitative traits in pea genotypes.

CONCLUSIONS

In conclusion, analysis of variance revealed significant mean sum of square due to genotypes for all traits under study. The genotypes Palam matar-1, Punjab-89, IC-269558, IC-204123, IC-208933, IC-208667, IC-109303 and IC-109553 exhibited high mean performance for different characters i.e. days to 50 per cent flowering, days to pod harvesting stage, days to 75 per cent maturity, pod length, number of pod per plant, plant height, number of primary branches per plant, number of secondary branches per plant, number of pods per nodes, 100 seed weight, pod length, number of seed per pod, dry matter yield, seed yield and harvest index were found to be superior for mean performance. The PCV and GCV both were observed high for number of pods per node, number of seed per pod, seed yield and harvest index. Thus these characters provide good source of variation and hence they are useful in crop improvement. High heritability were recorded for plant height, number of primary branches per plant, number of secondary branches per plant, number of pods per node, pod length, number of seed per pod, dry matter yield, seed yield and harvest index. High genetic advance as per cent mean were recorded for plant height, number of primary branches per plant, number of secondary branches per plant, number of pods per node, pod length, number of pod per plant, number of seed per pod, dry matter yield, seed yield and harvest index. On the basis of overall finding of the present study, out of twenty eight genotypes, seven genotypes *viz*, IC-269558, IC-204123, IC-208933, IC-208667, IC-109303, IC-109553, IC-208667were found to be superior for yield characters. Further, these germplasm accessions could be utilized in the breeding programme to develop high yielding genotypes.

FUTURE SCOPE

According to mean performance Palam matar-1, Punjab-89, IC-269558, IC-204123, IC-208933, IC-208667, IC-109303, IC-109553 and IC-208667, were found to be superior for yield characters. These could be used in further breeding programme and these genotypes will be best for yield characters.

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Conflict of interest. None.

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