

## Genetic Variability and Correlation Analysis in Different Genotypes of Pea (*Pisum sativum* L.) under Vindhyanchal Plateau of (M.P.)

Vaqaar Malik<sup>1\*</sup>, R.K. Jaiswal<sup>2</sup>, D.K. Raidas<sup>3</sup>, Praveen Kumar Singh Gurjar<sup>4</sup>, I.S. Naruka<sup>5</sup> and Harsha<sup>6</sup>

<sup>1</sup>Ph.D. Student, Department of Horticulture (Vegetable Science), Rajmata Vijayaraje Scindia Krishi Vishwavidyalaya-College of Agriculture, Gwalior (Madhya Pradesh), India.

<sup>2</sup>Principal Scientist, Department of Horticulture, Rajmata Vijayaraje Scindia Krishi Vishwavidyalaya - Fruit Research Station, Entkhedi Bhopal (Madhya Pradesh), India.

<sup>3</sup>Assistant Professor, Department of Plant Physiology, Rajmata Vijayaraje Scindia Krishi Vishwavidyalaya -RAK College of Agriculture, Sehore (Madhya Pradesh), India.

<sup>4</sup>Senior Scientist, Department of Horticulture, Rajmata Vijayaraje Scindia Krishi Vishwavidyalaya - College of Agriculture Gwalior (Madhya Pradesh), India.

<sup>5</sup>Professor & HOD, Department of Horticulture, Rajmata Vijayaraje Scindia Krishi Vishwavidyalaya - College of Agriculture Gwalior (Madhya Pradesh), India.

<sup>6</sup>Ph.D. Student, Department of Horticulture (Fruit science), Rajmata Vijayaraje Scindia Krishi Vishwavidyalaya - College of Agriculture, Gwalior (Madhya Pradesh), India.

(Corresponding author: Vaqaar Malik\*)

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**ABSTRACT:** The experiment was conducted with 22 germplasm and laid out in randomized block design with three replications. The analysis of variance for 22 genotypes showed significant differences for all the traits, representing a broad spectrum of variability among the genotypes. High heritability coupled with high genetic advance as percentage of mean was recorded for No. of nodes at 60 days, No. of nodes at 40 days and No. of nodes at harvest, whereas, high heritability coupled with moderate genetic advance as percentage of mean was recorded for No. of seeds per pod, No. of nodes at 20 days, plant height (cm) at 20 days, No. primary branches at 20 days, root nodules at 60 days, days to 50 % flowering, No. of pods per plant, pod yield q/ha, pod length (cm), days to picking 1, significant and positive correlation was observed for pod yield (q/ha) with pod yield (g/plant), shelling %, chlorophyll content, days to maturity, days to picking 2, pod length (cm), days to 50 % flowering, average pod weight (g), No. primary of branches at harvest, root nodules at 60 days, plant height (cm) at 40 days and days to picking 1. Contribution of individual traits towards the total divergence was found maximum for pod yield q/ha, pod yield (g/plant), No. of leaves at 60 days, days to picking 2, Pod length (cm), No. of seeds per pod and dry of 100 seed (g).

**Keyword:** ANOVA, Variability, Heritability, Correlation, Chlorophyll content, Genetic advance as %, Garden pea.

### INTRODUCTION

Pea (*Pisum sativum* L.) is a cool season crop and it is mainly grown as winter crop in plains and summer crop in hills of India. The consumers have a special preference for pea from plain regions because of its characteristic flavour, sweetness, freshness and good quality produce. The crop has great potential in the domestic and export market. It is grown in practically all temperate regions worldwide (Vavilov, 1926). It is the fourth-most widely grown pulse crop in the world, with three types of farmed peas: dry peas, green peas, and foraging peas. The most widely grown crop is dried pea, which was once mostly used as animal feed but is now often consumed by humans. It is a crop with a great deal of protein (27%) for human nutrition. Green peas are the vegetable with the highest protein level, with a protein content of 6-7% on a fresh weight basis. In recent years, both the utility of peas as a food crop

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and as fodder has surged. All of the necessary amino acids required for optimal cellular function are present in pea protein. According to Ceyhan and Avci, pea protein is high in lysine and other essential amino acids but low in sulfur-containing amino acids like cysteine and methionine. Vitamins A, B, and C, as well as minerals, dietary fiber, and antioxidant compounds are all found in pea (Sharma, 2010). As a component of a nutritious eating routine, particularly for kids and the old, green peas are truly significant when consumed in new, canned or frozen structure. The seeds and immature pods of green peas contain the most vitamins. The pea is a good predecessor to other crops as it enriches the soil with the nodule bacteria which live in its roots and it fixes nitrogen which live in its roots and it fixes nitrogen which becomes available to other plants (Rudnicki and Avci 2002). Genetic variability, heritability and genetic advance are

prerequisite for improvement of any crop for selection of superior genotypes and improvement of any traits (Prabhu *et al.*, 2009). Yield is a complex character influenced by several genetic factors interacting with environment. Therefore, success of any breeding programme for its improvement depends on the existing genetic variability in the base population and on the efficiency of selection (Kumari *et al.*, 2012). Heritability indicates the proportion of phenotypic variance that is due to genotypes which is heritable. It serve as a useful guide to breeders as the selection for trait having high heritability will be effective and improvement will be brought through selection. The genetic advance is an improvement in the genetic value new population as compared to original one. It will be possible to decide various breeding programmes for improvement of different characters based on the study of heritability and genetic advance (Kumari *et al.*, 2008). Therefore, this study was done to assess the genetic variability, heritability, and genetic advances among 22 genotypes of pea.

## MATERIALS AND METHODS

The experiment was carried out in Randomized Block Design with three replications and experiment was conduct on 2021-22. The experiment was conducted with 22 germplasm. Data were recorded on days to 50 % flowering, Days to maturity, plant height (cm) at 20, 40, 60 days and at harvest, No. primary branches at 20, 40, 60 days and at harvest, No. of leaves per plant at 20, 40, 60 days and at harvest, No. of nodes at 20, 40, 60 days and at harvest, chlorophyll content, days to picking 1, days to picking 2, No. of pods per plant, pod length (cm), average pod weight (g), number of seeds per pod, dry of 100 seed (g), Shelling %, pod yield (g/plant) and pod yield q/ha. The mean values were subjected to statistical analysis to work out ANOVA for all the characters, as suggested by Panse and Sukhatme (1957). The phenotypic and genotypic coefficient of variation was calculated as per the procedure given by Burton (1952). Heritability in broad sense ( $h^2$ ) was estimated based on the formula proposed by Hanson *et al.* (1956). Correlation coefficient was computed by using formula given by Al-Jibouri *et al.* (1958) and genetic advance as per cent of mean was computed adopting the method given by Johnson *et al.* (1955).

## RESULTS AND DISCUSSION

### A. Analysis of Variance

The analysis of variance for 22 genotypes showed significant differences for all the traits, representing a broad spectrum of variability among the genotypes represented in (Table 1).

The technique for adopting any breeding programme depends upon the nature and magnitude of variability present in the available genotypes under study.

### B. Genetic Characteristics

Assessment of genetic variability of yield and its related traits in the available germplasm was an important purpose of the present investigation. Coefficient of

variation studied indicated that estimates of phenotypic coefficient of variation were slightly higher than the corresponding genotypic coefficient of variation for all the characters. Genotypic and Phenotypic Coefficient of Variation was recorded high for the characters viz., number of pods per plant, number of leaves per plant at 40 days, number of seeds per pod, number of nodes at 20 days, number primary branches at 20 days, plant height at 20 days, days to 50 % flowering, Pod yield q/ha, pod length, days to picking 1, plant height at 40 days, dry of 100 seed, number primary branches at 40 days, days to picking 2, Number of leaves at 60 days and number of leaves per plant at 20 days, whereas moderate Genotypic and Phenotypic coefficient of variation were recorded for the characters plant height at 40 days, pod length, days to picking 1, number primary branches at 40 days, days to picking 2, number primary branches at 60 days, days to maturity, plant height at 60 days, dry of 100 seed, length of inter nodes, plant height at harvest, average pod weight, number primary of branches at harvest and pod yield (g/plant) represented in (Table 2). Thus, the selection based on phenotypic performance will be reliable which is in agreement with the findings of Sharma and Sharma (2013) for days to maturity, plant height (cm) at 60 days, dry of 100 seed (g), length of inter nodes (cm), plant height at harvest for No. of seeds per pod, No. of nodes at 20 days, No. primary branches at 20 days, Plant height (cm) at 20 days, Root nodules at 60 days, for Days to 50 % flowering, pod yield q/ha, pod length (cm), days to picking 1, plant height (cm) at 40 days, dry of 100 seed (g), No. primary branches at 40 days, for No. of nodes at 60 days No. of nodes at 40 days, No. of nodes at harvest, No. of pods per plant, No. of leaves per plant at 40 days in their studies. These findings are in accordance with the earlier findings of Saxesena *et al.* (2014).

### C. Heritability and genetic advance Studies

Heritability is that portion of variability which is transferable to next generation which measures the variability that is due to genetic causes and is the ratio of genotypic variance to the phenotypic variance. Heritability estimates are valid strictly for the population from which they are derived and which can vary population to population for different traits. The heritability for the same trait may differ considerably for different populations (Al-Aysh *et al.*, 2015). Environmental variations play major role on heritability of character in addition to genetic cause. Differences in the estimation of heritability can occur due to genetic as well as environmental variances. In the present investigation high heritability observed for viz., days to 50 % flowering, days to maturity, plant height (cm) at 20 days, Plant height (cm) at 40 days, plant height (cm) at 60 days, plant height at harvest, No. primary branches at 20 days, No. primary branches at 40 days, No. primary branches at 60 days, No. primary of branches at harvest, No. of leaves per plant at 20 days, No. of leaves per plant at 40 days, No. of leaves at 60 days, No. of leaves at harvest, No. of nodes at 20 days, No. of nodes at 40 days, No. of nodes at 60 days, No. of

nodes at harvest, chlorophyll content, days to picking 1, days to picking 2, length of inter nodes (cm), No. of pods per plant, pod length (cm), average pod weight (g), No. of seeds per pod, dry of 100 seed (g), shelling %, pod yield (g/plant), pod yield q/ha. Similar findings were noted by earlier workers also revealed high heritability. Pod yield per plant, days to first flowering, days to fifty percent flowering, pod length, number of seeds perpod,100 seed weight, shelling per cent (Selvi *et al.*, 2014), days to first pod picking, (Katiyar *et al.*, 2014) and total sugars (Al-Aysh *et al.*, 2015) for No. of leaves per plant at 40 days, No. of leaves at 60 days, No. of leaves at harvest, No. of nodes at 20 days, No. of nodes at 40 days, No. of nodes at 60 days, No. of nodes at harvest, root nodules at 60 days. High heritability coupled with high genetic advance as percentage of mean was recorded for No. of nodes at 60 days, No. of nodes at 40 days and No. of nodes at harvest, whereas, high heritability coupled with moderate genetic advance as percentage of mean was recorded for No. of seeds per pod, No. of nodes at 20 days, plant height (cm) at 20 days, No. primary branches at 20 days, days to 50 % flowering, No. of pods per plant, pod yield q/ha, Pod length (cm), days to picking 1. Such results indicated, predominantly the presence of additive gene action in the expression of these traits and consequent chance of improving these traits through simple selection. These findings are in accordance with the earlier findings of Yatish *et al.* (2021).

#### D. Correlation Studies

In the present investigation significant and positive correlation was observed for pod yield (q/ha) with pod yield (g/plant), shelling %, chlorophyll content, days to maturity, days to picking 2, pod length (cm), days to 50 % flowering, average pod weight (g), No. primary of branches at harvest and days to picking 1. These traits showed stable performance in different environment seem to be major yield factors; hence selection of these traits will be effective for constructing plant type of Garden pea for improvement seed yield (Table 3).

These results indicated environmental factors influenced these associations, therefore these traits would not consider for improvement of seed yield. These findings showed close similarity with earlier work of Shilpa *et al.* (2017) for pod yield per plant days to 50% flowering and shelling percent, for pod yield (g/plant), days to 50 % flowering, for days to maturity, days to picking 2, for average pod weight (g), pod length (cm), for shelling %, for chlorophyll content, days to picking 1, for no. primary of branches at harvest, number of seeds per pod, for Shelling % , and pod yield (g/plant), days to 50 % flowering. These findings are in accordance with the earlier findings of Yadav *et al.* (2010). The presence of substantial genetic variation, positive and highly significant correlated traits can be exploited in breeding programs for the improvement of Garden pea. Hence, the traits having positive association might be very useful for selection of high yielding genotypes. The value of correlation coefficient cannot be constant everywhere. It varies considerably according with kind of material handled, mode of observations taken, cultural practices followed and environmental conditions in which material is grown. Even though the material used is same, the environment including plant population, cultural practices changes the value of correlation coefficient considerably. Abiotic factors *viz.*, temperature fluctuations, erratic rains, moisture and humidity in various plant growth stages affect the association results particular phenological traits.

The trait association analysis revealed that for increasing seed yield (q/ha) emphasis should be given on Pod yield (g/plant), days to 50 % flowering, days to maturity, days to picking 2, average pod weight (g), pod length (cm), shelling %, chlorophyll content, days to picking 1, No. of primary of branches at harvest and number of seeds per pod. Hence, these traits might be very useful for considering of high yielding ideotype in garden pea.

**Table 1: ANOVA for yield and contributing characters in Garden Pea genotypes.**

Source of Var.	df	DFP	DM	PHT (cm) at 20 days	PHT (cm) at 40 days	PHT (cm) at 60 days	PHT at harvest	NPB at 20 days	NPB at 40 days	NPB at 60 days	NPB at harvest	NLP at 20 days	NLP at 40 days	NLP at 60 days	NLP at harvest	NN at 20 days	NN at 40 days
Replicate	2	4.06	1.92	0.34	0.43	1.04	4.23	1.61	0.38	1.02	0.12	0.12	0.68	0.51	5.13	0.02	0.84
Treatments	21	27.11**	50.39**	1.99**	11.68**	25.17**	17.97**	2.07**	1.09**	2.14**	1.17**	1.92**	30.80**	36.17**	32.13**	1.39**	1.59**
Error	42	0.689	3.115	0.139	0.382	1.148	1.090	0.010	0.013	0.025	0.051	0.471	0.734	0.224	0.317	0.084	0.230

  

Source of Var.	df	NN at 60 days	NN at harvest	NRN at 60 days	CH	DP 1	DP 2	LIN (cm)	NP per plant	PL (cm)	APW (g)	NSPP	D100S (g)	S%	PY (g/plant)	PY q/ha
Replicate	2	1.11	0.45	0.02	7.33	3.24	9.43	0.47	1.37	0.10	0.37	0.12	0.27	0.54	4.54	1.65
Treatments	21	1.12**	1.87**	2.75**	21.09**	22.77**	41.54**	1.50**	3.18**	1.71**	1.13**	1.25**	1.63**	1.92**	3.94**	53.26**
Error	42	0.186	0.241	0.172	1.942	1.332	0.985	0.064	0.181	0.031	0.031	0.086	0.110	0.620	0.706	2.607

\* Significant at 5% \*\* highly significant at 1%

ANOVA: Analysis of Variance

DFP: Days to 50 % flowering, DM: Days to maturity, PHT: Plant Height, NPB: No. primary branches per plant, NLP: No. of leaves per plant

NN: No. of nodes, NRN: Root nodules, CH: Chlorophyll content, DP: Days to picking, LIN: Length of inter nodes, NP: No. of pods per plant

PL: Pod length, APW: Average pod weight, NSPP: Number of seeds per pod, D100S: Dry of 100 seed (g), S%: Shelling %, PY: Pod yield

**Table 2: Variability parameters for yield and its component traits in pea genotypes.**

Sr. No.	Characters	GCV (%)	PCV (%)	Heritability (%)	Genetic advance value % mean
1.	Days to 50 % flowering	20.90	20.97	94.50	26.99
2.	Days to maturity	18.75	18.87	90.80	22.49
3.	Plant height (cm) at 20 days	20.34	20.53	90.10	25.61
4.	Plant height(cm)at 40 days	20.05	20.13	93.70	25.23
5.	Plant height (cm) at 60 days	19.17	19.27	92.40	23.39
6.	Plant height at harvest	18.38	18.49	90.90	21.75
7.	No. primary branches at 20 days	24.61	25.38	82.70	33.31
8.	No. primary branches at 40 days	19.97	20.32	84.20	24.56
9.	No. primary branches at 60 days	18.71	19.07	80.10	21.96
10.	No. primary of branches at harvest	17.78	18.29	70.20	19.83
11.	No. of leaves per plant at 20 days	18.79	19.36	72.60	21.79
12.	No. of leaves per plant at 40 days	22.46	22.55	94.60	30.17
13.	No. of leaves at 60 days	21.80	21.82	96.40	28.96
14.	No. of leaves at harvest	20.69	20.72	96.00	26.97
15.	No. of nodes at 20 days	27.69	28.09	91.00	40.34
16.	No. of nodes at 40 days	21.66	22.19	82.60	27.68
17.	No. of nodes at 60 days	19.26	19.66	80.50	23.01
18.	No. of nodes at harvest	18.12	18.66	70.60	20.47
19.	Root nodules at 60 days	23.36	23.63	90.80	31.67
20.	Chlorophyll content	20.56	20.84	87.80	25.91
21.	Days to picking 1	18.82	18.93	91.20	22.63
22.	Days to picking 2	19.65	19.71	94.60	24.47
23.	Length of inter nodes (cm)	21.33	21.78	84.10	27.17
24.	No. of pods per plant	24.66	24.95	91.30	34.33
25.	Pod length (cm)	20.41	20.53	92.60	25.90
26.	Average pod weight (g)	17.69	18.06	74.20	19.87
27.	No. of seeds per pod	23.08	23.38	90.10	31.07
28.	Dry of 100 seed (g)	19.33	19.48	90.30	23.61
29.	Shelling %	21.73	21.98	86.65	31.64
30.	Pod yield (g/plant)	17.05	17.27	79.10	18.83
31.	Pod yield q/ha	22.40	22.59	92.10	29.86

**Table 3: Simple correlation coefficients between fifteen major characters in pea genotypes**

Sr. No.	Characters	DFP	DM	PHT at harvest	NPB at harvest	NLP at harvest	CH	DP 1	DP 2	NP per plant	PL (cm)	APW (g)	NSPP	S %	PY (g/plant)	PY (q/ha)
1.	DFP	1.0000	0.7514**	0.0597	0.0065	0.2981**	0.3015**	0.7494**	0.9063**	0.3184**	0.1547	0.2578*	0.0747	0.4271	0.2274	0.3686**
2.	DM		1.0000	0.1518	-0.1414	0.3003	0.6463**	0.4157**	0.6470**	0.3920**	0.2174	0.3397**	0.0082	0.2887	0.3905**	0.5539**
3.	PHT at harvest			1.0000	0.8232**	-0.0066	0.3793**	-0.1182	0.0060	0.3866**	-0.0950	-0.0506	-0.1528	0.2745	0.1239	0.2280
4.	NPB at harvest at harvest				1.0000	0.1134	0.0427	-0.1505	-0.0890	0.2321	-0.0822	0.2088	0.1098	0.1966	0.4248**	0.2602*
5.	NLP at harvest					1.0000	-0.0126	0.4356**	0.3359**	0.0238	-0.0151	0.0880	0.0686	0.1509	0.1117	-0.1463
6.	CH						1.0000	0.1747	0.4017**	0.3322**	0.2208	0.1462	-0.0566	0.1935	0.2627*	0.5569**
7.	DP 1							1.0000	0.9275**	0.2259	0.4997**	0.3054**	0.3917**	-0.2028	0.2965**	0.2335
8.	DP 2								1.0000	0.3448**	0.4996**	0.5182**	0.3312**	0.1459	0.4404**	0.451**
9.	NP per plant									1.0000	0.3086**	0.4824**	0.2984**	0.0468	0.4221**	0.2198
10.	PL (cm)										1.0000	0.8767**	0.7640**	0.0402	0.8618**	0.4412**
11.	APW (g)											1.0000	0.6839**	0.1850	0.9651**	0.2878*
12.	NSPP												1.0000	0.1521	0.7745**	0.1950
13.	S %													1.0000	0.7327**	0.5631**
14.	PY (g/plant)														1.0000	0.5826**
15.	PY q/ha															1.0000

\* Significant at 5%, \*\* Significant at 1%

DFP: Days to 50 % flowering, DM: Days to maturity, PHT: Plant Height, NPB: No. primary branches per plant, NLP: No. of leaves per plant  
 NN: No. of nodes, NRN: Root nodules, CH: Chlorophyll content, DP: Days to picking, LIN: Length of inter nodes, NP: No. of pods per plant  
 PL: Pod length, APW: Average pod weight, NSPP: Number of seeds per pod, S%: Shelling %, PY: Pod yield

**CONCLUSIONS**

Mean performance values showed that all the characters have significant difference for all the 31 characters of 22 genotypes of garden pea. Phenotypic coefficient of variance (PCV%) was higher than the genotypic coefficient (GCV%) of variation for all traits indicating that environmental factor influencing their expression and their susceptibility to environmental fluctuations slightly. Variability studies suggest that all the characters revealed that direct selection is more effective to improve all the characters in garden pea. Pod yield q/ha expressed highly significant and positive correlation with pod yield (q/ha) with pod yield

(g/plant), shelling %, chlorophyll content, days to maturity, days to picking 2, days to 50 % flowering, average pod weight (g), No. primary of branches at harvest and days to picking 1, which indicates that these characters play the significant role to increase the pod yield (q/ha.). It is concluded that Pusa Praghati, Kashi Nandini, sehore local, Arka Priya, murdi local, punjab 89, kashi Samarth, Sadan khedi local, Mungaoli local, Raipura local, Jamoniya local genotypes shows better result in terms of yield attributing characters. Therefore, these varieties can be used further in breeding improvement programme in garden pea.

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