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Variability, Heritability and Genetic Advance among Garden Pea (*Pisum sativum* L.) Genotypes at both Genotypic and Phenotypic Levels

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ABSTRACT: Peas is one of the important leguminous vegetables in India which has wide variability in different parameters with varied yields. The experiment was carried out at AICRP (Vegetable crops) research block, Kumbapur farm, Dharwad during 2020-21. The experimental material comprised of 38 genotypes which was laid out in Randomized complete block design (RCBD) with 3 replications. The observations were recorded on various growth, yield and quality parameters. The analysis of variance revealed that for all the characters investigated, there were significant differences among the genotypes and these germplasms had a higher degree of variability which indicates the presence of wide range of variability in the genotypes. A higher magnitude of PCV was observed than a corresponding GCV for all the characters, indicates that the genetic variation was not limited to genotypic effect alone but also affected by environmental factors. High GCV and PCV (> 20 %) values were observed for number of branches per plant, number of leaves, days to first flowering, days to 50 per cent flowering, days to first pod picking and pod yield per plant (35.53 % PCV and 34.83 % GCV) which indicates the existence of broad genetic base. High heritability estimates coupled with a high GAM and high GCV and PCV values were observed for the traits such as number of branches per plant, pod yield per plant. This suggests that genetic improvement for these traits is possible by selecting germplasm that shows additive gene action. High heritability and GAM were detected for plant height, number of branches per plant, number of leaves, days to first flowering, average weight of green pod, shelling percentage, protein content in seeds, pod yield per plant (96.11 % h^2 and 70.35 % GAM), pod yield per plot and pod yield per hectare. This suggests that genotypic and phenotypic improvement for these traits would be possible by selection that shows additive gene action.

Keyword: Garden pea, Leguminaceae (Fabaceae), Coefficient of variation, Heritability(h^2), Genetic advance over per cent mean (GAM).

INTRODUCTION

Improvement of any crop involves studies on genetic variability which is the basic requirement of breeding programme (Azmat *et al.*, 2011). Change in environmental conditions leads to changes in phenotypic variability, while the genetic variability remain unchanged and which is more beneficial to a plant breeder for exploitation in the selection or hybridization and to estimate the heritability and genetic advance. Heritability is an index for the percentage transmission of a character from parents to their offsprings. It does not provide a complete picture of genetic improvement by selection. Hence, the study of genetic advance coupled with heritability is more helpful in predicting the resultant effect of selection. In comparison to the original population, a genetic advance is an improvement in the genetic value of a new population. Based on the analysis of heritability and genetic advance, it is possible to decide various breeding programme for improvement of different characters (Kumari *et al.*, 2012).

Garden pea (*Pisum sativum* L.) is an important vegetable crop which occupies an area of 5,68,000 ha in India with a production of 58,48,000 tonnes and the productivity of 10.30 tonnes per ha (NHB, 2020). Pea productivity has always been a major concern for scientists in the country and efforts were done to evaluate the cultivars with higher yields. In India, peas have a wide scope for year-round production off seasonally over wide range of environments. This necessitates a breeding programme in order to provide cultivars that are ideal for off season.

Keeping the above facts in view, the present research is conducted during *rabi* 2020 with an objective to evaluate the performance of garden pea genotypes for growth, yield and quality parameters.

MATERIAL AND METHODS

The experiment was carried out at AICRP (Vegetable crops) research block, Kumbapur farm, Dharwad during 2020-21. The experimental material comprised of thirty-eight genotypes, which were collected from different sources (Table 1). The experiment was laid out in Randomized complete block design (RCBD) with three replications. The treatments or genotypes were randomly assigned in each replication. The whole investigation was done under the scientific management practices. During the study, observations for plant height (cm), number of primary branches per plant, number of leaves per plant, days to first flowering, days to 50 % flowering, days to first picking, number of pods per plant, pod length (cm), pod width (mm), number of seeds per pod, average pod weight, Shelling percentage, pod yield per plant, TSS and Protein content in seeds (Dhopte and Manuel 1989) were recorded by five randomly selected plants from each treatment.

The genotypic and phenotypic coefficients of variation were calculated as per the method was suggested by Burton and Devane (1953). Heritability in broad sense and expected genetic advance on the basis of percent of mean were worked out according to the method advocated by Robinson *et al.* (1953) and Johnson *et al.*, (1955), respectively.

RESULTS AND DISCUSSION

In order to determine the extent of observed variations which are attributed by genetic factors, such as range, mean, phenotypic variance (PV), genotypic variance (GV), phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), broad sense heritability (h^2), genetic advance (GA) and genetic advance over per cent mean (GAM) were estimated. The results shown that most of the characteristics analysed had a significant level of variability.

According to the analysis of variance, significant differences were found (both at p=0.01 and p=0.05) among the garden pea genotypes for growth, yield and quality parameters (Table 2). This has led to the findings that the garden pea genotypes have sufficient genetic variability for the various traits studied, which leads to considerable crop improvement. Hence, garden pea genotypes could be improved through the characters studied such as plant height, number of branches per plant, number of leaves per plant, number of days taken for first flowering, number of days taken for 50 per cent flowering, flower colour, number of days taken for first pod picking, number of pods per plant, average weight of green pod, pod length, pod width, pod yield per plant, pod yield per plot, pod yield per hectare, number of seeds per pod, shelling per cent, TSS and protein content in the seeds. These findings are in accordance with Afreen *et al*. (2017a); Singh and Dhall (2018); Kumar *et al*. (2019); Kalapchieva *et al*. (2020); Pujari *et al*. (2021).

For all the characteristics studied, a greater phenotypic variance existed than a genotypic variance (Table 3). PCV was ranged from 7.62 per cent (total soluble solids) to 40.10 per cent (number of branches per plant) and GCV was ranged from 6.42 (total soluble solids) to 38.48 per cent (number of branches per plant). The estimates of heritability ranged from 68.53 (pod length) to 96.11 per cent (pod yield per plant). Genetic advance ranged from 1.24 (average pod weight) to 48.34 (pod yield per plant) and genetic advance over per cent mean ranged from 11.17 (total soluble solids) to 76.07 per cent (number of branches per plant).

The data pertaining to variability, heritability, genetic advance and genetic advance over per cent mean for growth, yield and quality parameters of garden pea genotypes are depicted in Table 3.

Plant height at the time of pod maturity shown moderate estimates of GCV (14.05 %) and PCV (15.42 %). The high heritability (83.10 %) was observed along with moderate GA (11.25) and high genetic advance over per cent mean (26.39 %) were observed for the trait.

The Number of branches per plant shown that, estimates of PCV (40.10 %) were higher than GCV (38.48 %). High heritability (92.08 %) with very low GA (1.25) and high GAM (76.07 %) were recorded.

Number of leaves per plant shown higher estimates of PCV (23.31 %) than GCV (21.49 %). The high heritability (84.93 %) with moderate GA (19.21 %) and high GAM (40.79 %) were reported for the trait.

Number of days to first flowering shown higher estimates of PCV (31.35 %) than GCV (28.82 %). The high heritability (84.49 %) with moderate GA (18.12) and high GAM (54.57 %) were reported for the trait.

Days to 50 per cent flowering shown that, estimates of PCV (24.14 %) were higher than GCV (23.54 %). Higher estimates of heritability (95.07 %), GA (21.01) and GAM (47.28 %) were obtained for the trait.

Days to first pod picking shown higher estimates of PCV (21.33 %) than GCV (20.60 %) were observed. The higher estimates of heritability (93.32 %), GA (22.94) and GAM (41.00 %) were reported for the trait.

Number of pods per plant shown moderate estimates of GCV (18.56 %) and PCV (20.52 %) were observed. High heritability (81.76 %) and GAM (34.57 %) with low GA (5.91) were obtained.

The pod length of garden pea genotypes shown that, estimates of GCV (11.40 %) lower than the PCV (13.77 %). High heritability (68.53 %) with low GA (1.53) and moderate GAM (19.44 %) were observed for the trait.

The width of green pod shown lower GCV than the PCV (8.57 % and 10.08 %, respectively) value were observed. High heritability (72.39 %) with very low GA (2.03) and moderate GAM (15.03 %) were reported for this trait.

Pod yield per plant shown that, estimates of PCV (35.53 %) were slightly more than GCV (34.83 %). The very high estimates of heritability (96.11 %) coupled with high GA (48.34) and high estimate genetic advance as percent of mean (70.35 %).

Average pod weight shown that, moderate estimates of PCV (17.10 %) shown more than GCV (16.32 %) were observed. The estimation of high heritability (91.07 %) with low GA (1.24) and high GAM (32.09 %) were observed for this trait.

Number of seeds per pod shown that, estimates of GCV were lower than the PCV (10.03 % and 10.86 % respectively) was observed. The high heritability (85.30 %) with low GA (1.55) and moderate GAM (19.09 %) were obtained for the trait.

Shelling percentage shown that, moderate GCV and PCV (12.08 % and 12.72 %, respectively) were observed. The high heritability (90.20 %) with moderate GA (10.09) and high GAM (23.64 %) were reported for the trait.

Total soluble solids content of seeds shown low GCV and PCV (6.42 % and 7.62 %, respectively) were observed. The high estimated heritability (71.18 %) with low GA (1.34) and moderate GAM (11.17 %) were obtained for the trait.

Protein content in seeds shown that, moderate GCV (10.74 %) and PCV (11.21 %). The very high estimate of heritability (91.65 %) with low GA (4.57) and high GAM (21.17 %) were reported for the trait.

A higher magnitude of phenotypic coefficients of variation (PCV) was observed than a corresponding genotypic coefficient of variation (GCV) for all the characters, indicates that the genetic variation was not limited to genotypic effect alone but also affected by environmental factors. Therefore, care should be taken when selecting for these traits based on phenotypic performance. Similar findings have also been reported by Iqbal *et al.* (2015); Gudadinni *et al*. (2017); Devi *et al*. (2017); Meena *et al*. (2017); Barcchiya *et al.* (2018); Gupta *et al*. (2018).

In the current investigation, both GCV and PCV were similar for all the characters under study. High GCV and PCV (> 20 %) values were observed for number of branches per plant (Khan *et al*., 2017; Gour *et al.*, 2018; Yumkhaibam *et al*., 2019), number of leaves, days to first flowering, days to 50 per cent flowering, days to first pod picking and pod yield per plant (Guleria *et al*., 2009; Bhardwaj *et al*., 2020). This indicates that, there is substantial variability ensuring ample scope for the improvement of these traits through selection.

Moderate values of PCV and GCV were noticed for plant height (Tiwari and Lavanya 2012; Singh *et al*., 2013; Thakur *et al*., 2016; Mishra 2014), average weight of green pod (Abdulla *et al*., 2014; Saxesena *et al*., 2014; Lal *et al*., 2019), pod length, protein content in seeds (Katoch *et al.*, 2016), number of pods per plant (Kuksal *et al*., 1983; Afreen *et al*., 2017b), number of seeds per pod and shelling percentage (Sharma *et al*., 2007). In these characters, genes action is in additive and non-additive ways and are equally important.

Low PCV and GCV values were observed for TSS and pod width (Nawab *et al*., 2008; Jaiswal *et al*., 2013; Gautam *et al.*, 2017). This indicates the existence of a narrow genetic base.

Coefficients of variation reveal the degree of variability exists in the genotypes for different traits. However, heritability estimates are useful in predicting the response to selection. Any crop improvement programme must base its decisions on the extent of inherited traits. As a guide to breeding value, heritability is fundamental in the practicability of selection, as it is used to analyse the variability of phenotypic value.

It is possible to predict genetic gain using the estimation of heritability. On the basis of phenotypic performance with regard to quantitative characters, estimates of heritability with high values are useful in selecting superior genotypes. Heritability values alone are not sufficient to predict the resultant effect for selecting the best individual. Hence combined with genetic advance will help in the more accurate predictions. In general, characters which are highly heritable in broad sense with high genetic advance over per cent mean indicate the predominance of additive gene effect, and can be enhanced through mass selection, progeny selection, or by any other modification procedures as suggested by Panse (1957). Whereas, characteristics which have low heritability with low genetic advance can be improved through hybridization.

Very high estimate of heritability with high genetic advance over per cent mean were detected for plant height, number of branches per plant (Ali *et al*., 2018), number of leaves, days to first flowering, average weight of green pod (Nawab *et al*., 2008; Sharma and Bora 2013), shelling percentage (Ali *et al*., 2018), protein content in seeds (Ali *et al*., 2018; Lal *et al*., 2019), pod yield per plant (Nawab *et al*., 2008), pod yield per plot and pod yield per hectare (Thakur *et al.*, 2016; Ali *et al*., 2018; Lal *et al*., 2019; Ofga 2019).

High estimates of heritability coupled with moderate values of GAM were noticed for pod length, pod width, number of seeds per pod (Aziz-ur-Rahman and Sharma 2019, Yimam *et al*., 2020) and TSS. These traits can be exploited through heterosis breeding because of the prevalence of non-additive components. However, none of the parameter shown low heritability and low GAM.

High levels of additive components, such as a high heritability estimates coupled with a high GAM and high GCV and PCV values were observed for the traits such as number of branches per plant, pod yield per plant, pod yield per plot and pod yield per hectare which indicates additive gene action. This suggests that genetic improvement for these traits is possible by selecting germplasm that shows additive gene action.

Table 1: List of garden pea genotypes and their sources used in the experiment.

Sr. No.	Genotypes	Sources
1.	PEVAR-1	Collection from RHREC, Kumbapur farm, Dharwad, Karnataka
2.	PEVAR-2	Collection from RHREC, Kumbapur farm, Dharwad, Karnataka
3.	PEVAR-3	Collection from RHREC, Kumbapur farm, Dharwad, Karnataka
4.	PEVAR-4	Collection from RHREC, Kumbapur farm, Dharwad, Karnataka
5.	PEVAR-5	Collection from RHREC, Kumbapur farm, Dharwad, Karnataka
6.	PEVAR-6	Collection from RHREC, Kumbapur farm, Dharwad, Karnataka
7.	PEVAR-7	Collection from RHREC, Kumbapur farm, Dharwad, Karnataka
8.	PEVAR-8	Collection from RHREC, Kumbapur farm, Dharwad, Karnataka
9.	PEVAR-9	Collection from RHREC, Kumbapur farm, Dharwad, Karnataka
10.	PEVAR-10	Collection from RHREC, Kumbapur farm, Dharwad, Karnataka
11.	PEVAR-11	Collection from RHREC, Kumbapur farm, Dharwad, Karnataka
12.	PEVAR-12	Collection from RHREC, Kumbapur farm, Dharwad, Karnataka
13.	PEVAR-14	Collection from RHREC, Kumbapur farm, Dharwad, Karnataka
14.	PEVAR-15	Collection from RHREC, Kumbapur farm, Dharwad, Karnataka
15.	PEVAR-16	Collection from RHREC, Kumbapur farm, Dharwad, Karnataka
16.	PEVAR-17	Collection from RHREC, Kumbapur farm, Dharwad, Karnataka
17.	PMVAR-1	Collection from RHREC, Kumbapur farm, Dharwad, Karnataka
18.	PMVAR-2	Collection from RHREC, Kumbapur farm, Dharwad, Karnataka
19.	PMVAR-3	Collection from RHREC, Kumbapur farm, Dharwad, Karnataka
20.	PMVAR-4	Collection from RHREC, Kumbapur farm, Dharwad, Karnataka
21.	PMVAR-5	Collection from RHREC, Kumbapur farm, Dharwad, Karnataka
22.	PMVAR-6	Collection from RHREC, Kumbapur farm, Dharwad, Karnataka
23.	PMVAR-8	Collection from RHREC, Kumbapur farm, Dharwad, Karnataka
24.	Arka Apoorva	Collection from IIHR, Hesaraghatta, Banglore, Karnataka
25.	Arka Karthik	Collection from IIHR, Hesaraghatta, Banglore, Karnataka
26.	Arka Priya	Collection from IIHR, Hesaraghatta, Banglore, Karnataka
27.	Arka Sampoorna	Collection from IIHR, Hesaraghatta, Banglore, Karnataka
28.	Pusa Pragati	Collection from IARI, PUSA, New Delhi
29.	PB-89	Collection from UHF, Solan, Himachal Pradesh
30.	GS-10	Collection from UPL *ltd*., Indore, Madhya Pradesh
31.	AP-1	Collection from CSAUT, Kanpur
32.	AP-3	Collection from CSAUT, Kanpur
33.	KPV-1010	Collection from Kumar Bioseeds and Agro Products *pvt. ltd*., Pune, Maharashtra
34.	Aruna-10	Collection from Greens of Kerala, Thrissur
35.	Honnali Local-1	Collection from Honnali, Davangere, Karnataka
36.	Honnali Local-2	Collection from Honnali, Davangere, Karnataka
37.	Bailahongala Local-1	Collection from Bailahongala, Belagavi, Karnataka
38.	Bailahongala Local-2	Collection from Bailahongala, Belagavi, Karnataka

Table 2: Analysis of variance (Mean sum of squares) examined for growth, yield and quality parameters in different garden pea genotypes.

Sr. No.	Source of variation /characters	Replication MSS	Treatments MSS (Genotypes)	Error MSS	S.Em±	CD @ 5%	CD @ 1%
	Degrees of freedom	2	37	74			
A.	**Growth and flowering parameters**						
1.	Plant height (cm)	0.60	115.05**	7.30	1.56	4.40	5.83
2.	Number of branches per plant	0.01	1.24**	0.04	0.11	0.30	0.40
3.	Number of leaves per plant	40.16	325.28**	18.16	2.46	6.93	9.20
4.	Days to first flowering	27.04	291.45**	16.80	2.37	6.67	8.84
5.	Days to 50 per cent flowering	2.02	333.81**	5.68	1.38	3.88	5.14
6.	Days to first pod picking	4.30	408.25**	9.52	1.78	5.02	6.66
B.	**Yield parameters**						
7.	Number of pods per plant	0.98	32.40**	2.24	0.86	2.44	3.23
8.	Pod length (cm)	0.31	2.78**	0.37	0.35	0.99	1.31
9.	Pod width (mm)	0.10	4.55**	0.51	0.41	1.17	1.55
10.	Average Pod weight (g)	0.03	1.23**	0.04	0.11	0.32	0.43
11.	Pod yield per plant (g)	31.53	1741.92**	23.18	2.78	7.83	10.39
12.	Number of seeds per pod	0.23	2.09**	0.11	0.20	0.55	0.73
C.	**Quality parameters**						
13.	Shelling percentage	3.98	82.60**	2.89	0.98	2.76	3.67
14.	Total soluble solids (°Brix)	0.05	2.03**	0.24	0.28	0.80	1.06
15.	Protein content in seeds (%)	0.22	16.57**	0.49	0.40	1.14	1.51

**Significant at 1%; *Significant at 5%; S.Em± - Standard error of the mean; CD – Critical difference

Table 3: Mean, range and genetic parameters for growth, flowering, yield and quality parameters in garden pea genotypes.

Sr. No.	Characters	Grand mean	Range		GV	PV	GCV (%)	PCV (%)	h^2 (%)	GA	GAM (%)
			Min.	Max.							
A. Growth and flowering parameters											
1	Plant height (cm)	42.64±1.56	31.61	51.40	35.91	43.22	14.05	15.42	83.10	11.25	26.39
2	Number of branches per plant	1.65±0.11	1.00	3.00	0.40	0.44	38.48	40.10	92.08	1.25	76.07
3	Number of leaves per plant	47.09±2.46	30.80	60.22	102.37	120.54	21.49	23.31	84.93	19.21	40.79
4	Days to first flowering	33.20±2.37	19.70	51.73	91.55	108.35	28.82	31.35	84.49	18.12	54.57
5	Days to 50 per cent flowering	44.43±1.38	27.57	62.80	109.38	115.06	23.54	24.14	95.07	21.01	47.28
6	Days to first pod picking	55.96±1.78	41.53	74.57	132.91	142.43	20.60	21.33	93.32	22.94	41.00
B. Yield parameters											
7	Number of pods per plant	17.08±0.86	12.60	25.57	10.05	12.29	18.56	20.52	81.76	5.91	34.57
8	Pod length (cm)	7.87±0.35	6.17	9.52	0.81	1.17	11.40	13.77	68.53	1.53	19.44
9	Pod width (mm)	13.53±0.41	10.59	16.00	1.35	1.86	8.57	10.08	72.39	2.03	15.03
10	Average pod weight (g)	3.86±0.11	2.71	4.61	0.40	0.44	16.32	17.10	91.07	1.24	32.09
11	Pod yield per plant (g)	68.72±2.78	31.80	138.93	572.91	596.09	34.83	35.53	96.11	48.34	70.35
12	Number of seeds per pod	8.09±0.20	6.07	9.60	0.66	0.77	10.03	10.86	85.30	1.55	19.09
C. Quality parameters											
13	Shelling percentage	42.67±0.98	32.20	52.88	26.57	29.46	12.08	12.72	90.20	10.09	23.64
14	Total soluble solids (°Brix)	12.01±0.28	10.33	13.57	0.60	0.84	6.42	7.62	71.18	1.34	11.17
15	Protein content in seeds (%)	21.57±0.40	17.39	28.95	5.36	5.85	10.74	11.21	91.65	4.57	21.17

PV-Phenotypic variance; GV- Genotypic variance; h^2- Broad sense heritability; GCV- Genotypic coefficient of variation; PCV- Phenotypic coefficient of variation; GA- Genetic advance; GAM- Genetic advance over per cent mean

SUMMARY AND CONCLUSIONS

The analysis of variance revealed that for all the characters investigated, there were significant differences among the genotypes and these germplasms had a higher degree of variability.

High (>20 %) GCV and PCV were observed for number of branches per plant, number of leaves per plant, pod yield per plant, days taken for 50 per cent of flowering, days to first pod picking and days taken for first flowering. These findings indicate the existence of broad genetic base which helps in further crop improvement programme.

Moderate (10-20 %) GCV and PCV were observed for plant height, average weight of green pod, number of pods per plant, pod length, number of seeds per pod, shelling percentage and protein content in green seeds. Hence, there is moderate variability in these characters.

Low estimates of (0-10 %) GCV and PCV were observed for pod width and TSS. The narrow genetic base leads to divergent genotypes to recover transgressive segregants.

A high estimate of heritability (>60 %) was obtained for all the parameters of the garden pea genotypes. While none of the characters were shown moderate (30-60 %) to low (<30) heritability.

Very high estimate of heritability with high GAM were detected for plant height, number of branches per plant, number of leaves per plant, days to first flowering, days to 50 per cent flowering, days to first pod picking, average pod weight, pod yield per plant, shelling percentage and protein content in seeds. Direct selection would be more effective for these characters because they are dominated by additive components.

High estimates of heritability coupled with moderate values of GAM (20 %) were noticed for pod length, pod width, number of seeds per pod and TSS. It indicates that there is little response to selection for this trait due to the prevalence of non-additive components. While none of the traits were shown low GAM.

Conflict of Interest. None.

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