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RESEARCH ARTICLE

Genetic Studies based on Selected Morpho–physiological Parameters in Garden Pea (*Pisum sativum* L.)

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The experiment was planned to study genetic variability and association among different morpho-physiological traits. Forty five genotypes derived from five intervarietal crosses with variable plant and pod characteristics were evaluated in Randomized Complete Block Design with three replications during winter 2014–15 and 2015–16 at Palampur. Significant differences were observed among all genotypes for all the characters over years. High GCV and PCV along with high heritability (>60%) and genetic advance (>30%) were observed for pods/plant and pod yield/plant during respective years, suggesting additive gene inheritance and selection in early generations would be effective. Significant positive correlation of pod yield/plant was recorded with internodal length (0.235), seeds/pod (0.441), shelling percentage (0.306), pods/plant (0.885) and average pod weight (0.349). The positive association was mainly due to direct effects of these traits with pod yield/plant (0.90 and 0.43, respectively) and also indirectly contributed for positive association with other traits. Therefore, these traits provide an important criterion of selection procedures for achieving enhanced performance of garden pea genotypes for higher pod yield.

Key Words: Garden pea, Genetic parameters, Pod yield, Variability

Introduction

Garden pea (*Pisum sativum* L.) is a leading vegetable crop in the north–western Himalayan region of India comprising the states of Himachal Pradesh, Jammu and Kashmir, and Uttarakhand (Sharma *et al.*, 2010). It is an important source of proteins, vitamins, minerals and also lysine, a limiting essential amino acid in cereals (Sharma and Sharma, 2016). It is an important off–season vegetable crop of Himachal Pradesh, grown over the year and green pods are available during the period when its supply from plain areas almost ceases, and hence, provides lucrative returns to the growers.

The prime objective of breeding work is to increase the yield (Tyagi and Srivastva, 2002) and to prepare the background for the future research. High yield, desirable pod characteristics and resistance to biotic stresses are the main criteria, taken into consideration by the breeders for its genetic improvement. Despite continuous breeding efforts, the average yield of garden pea is low due to its narrow genetic base and consumer preference for some specific traits such as lush green well-filled pods. Also, genetic drift in the extensively grown age old few cultivars and emergence of new pathogen races also lead to low/stagnant yield. The age old varieties like 'Azad P–1', 'Lincoln', 'Arkel' etc., are still preferred by the growers due to desirable horticultural traits though the varieties have become vulnerable to a plethora of biotic and abiotic stresses (Sharma *et al.*, 2013).

Crop improvement with heritable characters, estimation of genetic parameters and their association is of prime importance in breeding (Ajmal *et al.*, 2009; Bozokalfa *et al.*, 2010). The estimate of heritability acts as a predictive instrument in expressing the reliability of phenotypic values (Unche *et al.*, 2008). Yield is highly influenced by the environment, hence selection based on yield alone may limit the improvement. On the other hand, the yield component traits are comparatively less complex in inheritance and are influenced to a lesser extent by the environment (Alkuddsi *et al.*, 2013). Thus, effective improvement in yield may be brought about through selection for yield component characters. Favourable associations between desirable attributes will help improvement in a joint manner whereas, unfavourable associations between the desirable attributes under selection may limit them. Hence, knowledge of associations between the yield components and also

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Table 1. Genotypes and their sources

Code	Genotype	Source	Code	Genotype	Source	Code	Genotype	Source
1	Palam Priya	CSK HPKV, Palampur	18	DPP-2011-SP-22	CSK HPKV, Palampur	35	DPP-2011-SN-16	CSK HPKV, Palampur
2	Pb 89	PAU, Ludhiana	19	DPP-2011-SP-23	CSK HPKV, Palampur	36	DPP-2012-SN-1	CSK HPKV, Palampur
3	Azad P-1	CSAUA&T, Kanpur	20	DPP-2011-SP-24	CSK HPKV, Palampur	37	DPP-2012-SN-2	CSK HPKV, Palampur
4	Palam Sumool	CSK HPKV, Palampur	21	DPP-2011-SP-25	CSK HPKV, Palampur	38	DPP-2012-SN-4	CSK HPKV, Palampur
5	Palam Triloki	CSK HPKV, Palampur	22	DPP-2011-SP-28	CSK HPKV, Palampur	39	DPP-2012-SN-7	CSK HPKV, Palampur
6	DPP-2011-SP-3	CSK HPKV, Palampur	23	DPP-2011-SP-29	CSK HPKV, Palampur	40	DPP-2012-SN-8	CSK HPKV, Palampur
7	DPP-2011-SP-6	CSK HPKV, Palampur	24	DPP-2011-SP-32	CSK HPKV, Palampur	41	DPP-2012-SN-9	CSK HPKV, Palampur
8	DPP-2011-SP-7	CSK HPKV, Palampur	25	DPP-2011-SP-33	CSK HPKV, Palampur	42	DPP-2012-SN-10	CSK HPKV, Palampur
9	DPP-2011-SP-8	CSK HPKV, Palampur	26	DPP-2011-SP-38	CSK HPKV, Palampur	43	DPP-2012-SN-11	CSK HPKV, Palampur
10	DPP-2011-SP-10	CSK HPKV, Palampur	27	DPP-2011-SN-1	CSK HPKV, Palampur	44	DPP-2012-SN-12	CSK HPKV, Palampur
11	DPP-2011-SP-11	CSK HPKV, Palampur	28	DPP-2011-SN-4	CSK HPKV, Palampur	45	DPP-2012-SA-1	CSK HPKV, Palampur
12	DPP-2011-SP-14	CSK HPKV, Palampur	29	DPP-2011-SN-5	CSK HPKV, Palampur	46	DPP-2012-SA-3	CSK HPKV, Palampur
13	DPP-2011-SP-15	CSK HPKV, Palampur	30	DPP-2011-SN-6	CSK HPKV, Palampur	47	DPP-2012-SA-4	CSK HPKV, Palampur
14	DPP-2011-SP-16	CSK HPKV, Palampur	31	DPP-2011-SN-8	CSK HPKV, Palampur	48	DPP-2011-ST-1	CSK HPKV, Palampur
15	DPP-2011-SP-17	CSK HPKV, Palampur	32	DPP-2011-SN-10	CSK HPKV, Palampur	49	DPPMR-09-1	CSK HPKV, Palampur
16	DPP-2011-SP-20	CSK HPKV, Palampur	33	DPP-2011-SN-13	CSK HPKV, Palampur	50	DPPMR-09-2	CSK HPKV, Palampur
17	DPP-2011-SP-21	CSK HPKV, Palampur	34	DPP-2011-SN-15	CSK HPKV, Palampur			

among themselves is essential for planning a sound breeding programme.

Simple correlation analysis that relates yield to a single variable may not provide a complete understanding of the importance of each component in determining pod yield (Dewey and Lu, 1959; Okuyama *et al.*, 2004). In such cases, it becomes necessary to use a method which takes into account the causal relationship between the variables, in addition to their magnitude. Path coefficient analysis permits a critical examination of specific factors that produce a given correlation and can be successfully employed in formulating an effective selection strategy. It allows separating the direct effect and their indirect effects through other attributes by apportioning the correlations (Wright, 1921) for better interpretation of cause and effect relationship. Similar studies were conducted by many researchers in various crops by using different genetic materials (Sharma *et al.*, 2016; Ashok *et al.*, 2018). Selection based on the detailed knowledge of magnitude and direction of association between yield and its attributes is very important in identifying the key characters, which can be exploited for crop improvement through suitable breeding programme. Keeping this in view, 45 F_7 progenies with variable pod and plant characteristics derived from five intervarietal crosses following pedigree method of selection were used to study the genetic variability along with five varieties recommended for cultivation in Himachal Pradesh.

Material and Methods

The present investigation was undertaken at the Research Farm, Department of Vegetable Science and Floriculture, CSK HPKV, Palampur (1290.8 m above mean sea level, with latitude 32º6’ N, longitude 76º3’ E). The soil of experimental field was clay loam with pH 5.7. The experimental material comprised 50 genotypes (Table 1 and Table 2) which were evaluated in Randomized Complete Block Design with three replications for two consecutive years (November to April 2014–15 and 2015–16). Each genotype was raised in two rows spaced at 45 cm with intra-plant distance of 10 cm. The observations were recorded on randomly selected ten plants of each genotype over the replications for 15 traits, viz., first flower node, days to flowering, days to first picking, number of branches, internodal length (cm), nodes/plant, plant height (cm) at final harvest,

Table 2. Intervarietal crosses attempted during 2006-07 and genotypes selected for evaluation during 2014-15 and 2015-16

S. No.	Crosses attempted	Coding of Genotypes	No. of genotypes in F7 for evaluation
1	Palam Sumool × Palam Priya	SP series	21
2	Palam Sumool × Pb-89	SN series	9
3	Palam Sumool × Azad P-1	SA series	12
4	Palam Sumool × Palam Triloki	ST series	1
5	VRPMR10 × Sugar Giant	DPPMR series	1
6	Green Pearl × DPP-9411	DPPMR series	1

pod length (cm), seeds/pod, shelling (%), pods/plant, pod yield/plant (g) and average pod weight (g). Besides, quality parameters such as total soluble solids (obrix) using hand refractometer and ascorbic acid (mg/100g fresh weight basis) as described by Ranganna (1979) were also estimated.

Statistical Analysis

Analysis of variance was performed for individual season and error variance was tested for homogeneity (Gomez and Gomez, 1983). The combined analysis of variance of two season's data was performed for each trait. The genotypic and phenotypic variations and heritability were calculated as per Burton and DeVane (1953). Heritability and genetic advance (GA) was calculated using formulae of Burton and DeVane (1953) and Johanson *et al.* (1955). Coefficients of correlation were calculated as suggested by Al–Jibouri *et al.* (1958) while path coefficients of different traits with pod yield/plant were carried out as per methodology suggested by Dewey and Lu (1959).

Results and Discussion

Phenotypic Coefficient of Variation (PCV) and Genotypic Coefficient of Variation (GCV)

An effective breeding programme for developing varieties of improved quality requires preliminary information on the nature and magnitude of genetic variability, degree of transmission of traits and their inter–relationship (Selvi *et al.*, 2016). The knowledge of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) is helpful in predicting the amount of variation present in the given genetic stock which in turn helps in formulating an efficient breeding programme. In this context, high values of PCV and GCV were recorded for pod yield/plant and pods/plant for both years and pooled years (Table 3). This indicates the existence of immense inherent variability that remains unaltered by environmental conditions among the genotypes, which in turn is more useful for exploitation in selection and hybridization programs (Jalal and Ahmed, 2012). Such high estimates of PCV and GCV for pods/plant and pod yield/plant were also reported in different studies using variable genetic material and environments (Sharma *et al.*, 2009). Moderate PCV and GCV estimates were observed for average pod weight during both years and pooled years while number of branches, nodes/plant, plant height, seeds/pod and ascorbic acid exhibited moderate PCV and GCV estimates during 2014–15 and 2015–16. Besides, moderate estimates of PCV were observed for internodal length and shelling (%) during 2014–15 and pooled years. Differences in the magnitude of PCV and GCV (high to moderate or moderate to low) for some of the traits in pool years indicated the role of environment in the manifestation of particular trait(s).

Heritability and Genetic Advance

Heritability of a trait is an index of transmission of

Table 3. Estimates of parameters of variability for different characters in garden pea during 2014-15, 2015-16 and pooled years

Traits	PCV (%)			GCV (%)			h2bs			GA (% of mean)		
	2014-15	2015-16	Pooled	2014-15	2015-16	Pooled	2014-15	2015-16	Pooled	2014-15	2015-16	Pooled
First flower node	9.17	7.68	8.63	7.88	6.72	5.90	73.80	76.63	46.60	13.94	12.12	8.29
Days to flowering	4.75	6.57	5.74	3.91	5.36	4.41	67.80	66.56	58.93	6.63	9.01	6.97
Days to first picking	4.51	2.98	3.86	3.89	2.51	2.81	74.21	70.74	53.11	6.90	4.35	4.23
Number of branches	12.81	14.57	13.71	10.00	11.33	6.84	59.70	60.46	24.86	15.76	18.14	7.02
Internodal length (cm)	12.56	9.95	11.47	12.42	9.37	8.76	97.78	88.54	58.35	25.29	18.16	13.78
Nodes/plant	14.81	13.65	14.33	14.04	10.67	8.43	89.88	61.07	34.68	27.41	17.17	10.24
Plant height (cm)	13.83	11.78	12.81	10.78	10.40	7.71	60.84	78.06	36.24	17.33	18.94	9.57
Pod length (cm)	9.70	8.80	9.27	8.75	7.60	7.77	81.50	74.59	70.19	16.28	13.52	13.42
Seeds/pod	13.36	11.36	12.28	12.03	10.26	9.00	81.07	81.67	53.78	22.32	19.09	13.60
Shelling (%)	12.79	9.72	11.12	10.01	7.79	7.75	61.20	64.33	48.52	16.13	12.88	11.12
Pods/plant	23.49	28.76	29.52	21.41	27.12	22.42	83.03	88.95	57.67	40.18	52.70	35.08
Pod yield/plant (g)	27.39	29.91	31.01	25.83	29.23	24.15	88.94	95.52	60.65	50.18	58.85	38.74
Average pod weight (g)	13.27	14.02	13.56	12.44	12.57	10.18	87.71	80.33	56.31	23.72	23.20	15.74
Total soluble solids (ºbrix)	8.45	5.01	7.03	6.84	4.73	4.19	65.64	88.95	35.59	11.41	9.19	5.16
Ascorbic acid (mg)	11.91	12.48	12.18	10.14	10.00	8.09	72.52	64.12	44.09	17.79	16.50	11.07

Abbreviations: GCV and PCV represent genotypic and phenotypic coefficients of variations, respectively,
h2bs: Heritability in broad sense,
GA (%): Genetic advance (%) of mean.

characters from parents to progeny (Bagati *et al.*, 2016). The estimates of heritability help the plant breeder in selection of elite genotypes from diverse genetic population, hence prior knowledge about the heritability of the traits is a prerequisite for the selection programme (Singh *et al.*, 2011; Bagati *et al.*, 2016). However, high heritability alone is not enough to make sufficient improvement through selection generally in advance generations unless accompanied by substantial amount of genetic advance (Bhargava *et al.*, 2003). Thus, genetic advance is yet another important selection parameter that aids breeder in a selection programme (Shukla *et al.*, 2004). On the same lines, high estimates of heritability (>60%) along with high genetic advance (>30%) were observed for pod yield/plant and pod/plant during 2014–15 and 2015–16 (Table 3) suggesting that these are simply inherited traits and the heritability is most likely due to additive gene effects and phenotypic selection may be effective in early generations for these traits (Katoch *et al.*, 2016; Shrimali *et al.*, 2017). High heritability along with moderate genetic advance was observed for pod length, first flower node, internodal length, nodes/plant, plant height, seeds/pod, shelling (%), average pod weight and ascorbic acid during 2014–15 and 2015–16 and for internodal length number of branches during 2015–16 which indicated the preponderance of additive and non–additive gene effects for their inheritance (Ranjan *et al.*, 2006; Saxesena *et al.*, 2016). High heritability and low genetic advance was observed for days to flowering and days to first picking during both the years and that of total soluble solids in 2015–16. Dar *et al.* (2013) and Habtamu and Million (2013) also reported such estimates for days to flowering indicating the role of non–additive gene action in their inheritance. As, in the present study expected genetic advance values were based on broad sense heritability, which incorporate both additive and non–additive components of gene action, much reliance cannot be placed on expected genetic advance. However, the traits, which had high heritability and also showed high expected genetic advance, could be substantially considered for making selections as these traits were mainly influenced by the major effects of additive gene action (Jalal and Ahmed, 2012).

Correlation and Path Analysis

For shifting the mean population under study in the desired direction, a thorough understanding of nature and extent of association between characters is essential. It would be very difficult to obtain the desired combinations, if negative association between characters is due to pleiotropic effects. However, if linkage is involved, special breeding programmes are needed to break these linkage blocks. Knowledge of the correlation that exists between important characteristics may facilitate the interpretation of results and provide the basis for planning more efficient breeding programs. It also helps to improve different characters simultaneously (Falconer, 1981). In this regard, pod yield/plant had shown a positive and significant correlation with pods/plant (0.885), seeds/pod (0.441), average pod weight (0.349), shelling percentage (0.306) and internodal length (0.235) during both the years, with pod length during 2014–15, and with number of branches, nodes/plant and plant height during 2015–16. Pooling of data over the years also revealed similar associations of these traits with pod yield suggesting that the selection on the basis of these traits might lead to higher yield. Earlier reports have also indicated significant and positive association for majority of these traits with variable magnitude in diverse breeding material (Kumar *et al.*, 2015; Katoch *et al.*, 2016) which emphasized special focus on these traits. Pod yield/plant had revealed negative association with first flower node (-0.194), days to flowering (-0.317) and days to first picking (-0.248) during both the years and pooled years suggesting to adopt cautious approach while selecting for early genotypes. Negative association of pod yield/plant with total soluble solids (-0.151) and ascorbic acid (-0.153) was also observed during 2015–16 and pooled years. Earlier reports of many research workers have also indicated negative correlation for pod yield/plant with days to flowering and days to first picking (Rathi and Dhaka, 2007).

Correlation analysis indicates the association pattern of component traits with yield and simply represents the overall influence of a particular trait on yield rather than providing cause and effect relationship. Path coefficient analysis measures the direct influence of one variable upon the other, and permits separation of correlation coefficients into components of direct and indirect effects. Therefore, for assessing the cause–effect relationship as well as effective selection, path coefficient analysis is used. Pods/plant and average pod weight had maximum positive direct effect on fresh pod yield/plant during both the years and pooled years suggesting the importance of these traits in selection programme for improving yield (Table 4). Selvi *et al.* (2016) have also reported

Table 4. Estimates of path analysis at phenotypic level (P) for different pairs of horticultural traits in garden pea in 2014-15 (I), 2015-16 (II) and pooled years (III).

Trait		First flower node	Days to flowering	Days to first picking	Number of branches	Internodal length (cm)	Nodes /plant	Plant height (cm)	Pod length (cm)	Seeds / pod	Shelling (%)	Pods / plant	Average pod weight (g)	Total soluble solids (º brix)	Ascorbic acid (mg)	Pod yield /plant (g)
First flower node	I	0.046	-0.018	-0.010	0.004	0.000	-0.001	-0.002	0.000	-0.004	-0.013	-0.197	-0.033	-0.001	0.001	-0.228**
	II	-0.010	-0.003	0.009	0.002	0.000	-0.005	0.000	-0.001	-0.010	-0.002	-0.206	0.003	0.000	-0.001	-0.224**
	III	0.016	-0.003	-0.005	0.000	0.002	0.000	-0.001	-0.001	-0.009	-0.005	-0.170	-0.017	-0.001	0.000	-0.194**
Days to flowering	I	0.033	-0.026	-0.012	0.003	0.000	-0.001	-0.002	0.001	-0.006	-0.015	-0.268	-0.027	0.000	0.002	-0.316**
	II	-0.004	-0.008	0.012	0.001	0.000	-0.002	0.001	-0.003	-0.004	-0.001	-0.322	0.003	0.000	0.000	-0.325**
	III	0.008	-0.006	-0.006	0.000	0.003	0.000	0.001	-0.003	-0.007	-0.005	-0.297	-0.009	0.001	0.001	-0.317**
Days to first picking	I	0.019	-0.012	-0.024	0.002	0.000	-0.001	-0.002	0.001	-0.006	-0.015	-0.292	0.030	0.001	0.002	-0.298**
	II	-0.005	-0.005	0.019	0.002	0.000	-0.002	0.001	-0.004	-0.001	-0.003	-0.311	0.012	0.000	0.001	-0.297**
	III	0.007	-0.003	-0.012	0.000	0.002	0.000	0.000	-0.004	-0.008	-0.007	-0.248	0.021	0.001	0.001	-0.248**
Number of branches	I	0.007	-0.003	-0.002	0.027	0.000	-0.006	0.001	0.001	0.001	-0.008	0.041	0.044	0.001	0.002	0.105
	II	0.002	0.001	-0.003	-0.010	0.000	0.010	-0.001	0.001	0.003	-0.001	0.231	-0.005	0.000	0.000	0.228**
	III	0.000	0.000	0.000	-0.004	-0.001	0.007	-0.001	0.000	0.002	-0.003	0.166	0.017	0.000	0.001	0.185**
Internodal length (cm)	I	-0.013	0.007	0.003	-0.001	0.001	0.000	-0.007	0.002	0.004	0.010	0.223	0.127	0.001	-0.003	0.351**
	II	0.000	0.002	-0.004	-0.003	0.000	0.000	-0.003	0.001	0.003	0.004	0.132	0.089	0.000	-0.001	0.219**
	III	-0.003	0.001	0.002	0.000	-0.013	0.000	-0.006	-0.002	0.006	0.006	0.142	0.104	0.001	-0.002	0.235**
Nodes/plant	I	0.005	-0.002	-0.001	0.013	0.000	-0.014	0.002	0.001	0.002	-0.003	0.160	-0.040	0.002	0.000	0.123
	II	0.002	0.001	-0.002	-0.004	0.000	0.023	0.000	0.001	0.007	-0.002	0.276	-0.054	0.000	0.000	0.248**
	III	0.000	0.000	0.000	-0.002	0.000	0.017	0.001	0.000	0.005	-0.002	0.206	-0.044	0.002	0.000	0.183**
Plant height (cm)	I	0.005	-0.003	-0.003	-0.001	0.000	0.002	-0.016	0.001	-0.001	0.000	-0.047	0.099	0.000	-0.002	0.037
	II	0.000	0.002	-0.003	-0.003	0.000	0.001	-0.005	0.001	0.000	0.001	0.168	0.034	0.000	-0.001	0.195*
	III	0.001	0.001	0.000	0.000	-0.006	-0.001	-0.012	-0.001	-0.001	0.001	0.085	0.065	0.000	-0.001	0.129*
Pod length (cm)	I	0.003	-0.004	-0.004	0.003	0.000	-0.001	-0.003	0.007	0.002	-0.003	0.021	0.237	0.002	0.005	0.264**
	II	-0.001	-0.002	0.009	0.001	0.000	-0.002	0.000	-0.009	0.007	-0.002	-0.092	0.210	0.000	0.001	0.119
	III	0.002	-0.001	-0.003	0.000	-0.002	0.000	-0.001	-0.014	0.005	-0.003	-0.048	0.213	0.003	0.003	0.154**
Seeds/pod	I	-0.012	0.010	0.009	0.002	0.000	-0.002	0.001	0.001	0.015	0.022	0.431	0.072	0.001	-0.003	0.546**
	II	0.003	0.001	0.000	-0.001	0.000	0.005	0.000	-0.002	0.034	0.003	0.364	0.031	0.000	-0.001	0.436**
	III	-0.004	0.001	0.003	0.000	-0.002	0.003	0.000	-0.002	0.033	0.009	0.352	0.049	0.002	-0.002	0.441**
Shelling (%)	I	-0.011	0.007	0.006	-0.004	0.000	0.001	0.000	0.000	0.006	0.056	0.268	0.056	0.000	-0.005	0.379**
	II	0.002	0.001	-0.005	0.001	0.000	-0.003	-0.001	0.001	0.009	0.013	0.215	0.076	0.000	0.000	0.308**
	III	-0.003	0.001	0.003	0.000	-0.003	-0.001	-0.001	0.001	0.011	0.026	0.209	0.063	0.001	-0.002	0.306**
Pods/plant	I	-0.011	0.008	0.009	0.001	0.000	-0.003	0.001	0.000	0.008	0.019	0.814	0.016	0.001	0.000	0.863**
	II	0.002	0.003	-0.006	-0.002	0.000	0.007	-0.001	0.001	0.013	0.003	0.936	-0.061	0.000	-0.004	0.890**
	III	-0.003	0.002	0.003	-0.001	-0.002	0.004	-0.001	0.001	0.013	0.006	0.900	-0.035	0.002	-0.004	0.885**
Average pod weight (g)	I	-0.003	0.002	-0.002	0.003	0.000	0.001	-0.003	0.004	0.002	0.007	0.030	0.452	0.000	0.000	0.492**
	II	0.000	0.000	0.001	0.000	0.000	-0.003	0.000	-0.004	0.002	0.002	-0.128	0.448	0.000	0.000	0.317**
	III	-0.001	0.000	-0.001	0.000	-0.003	-0.002	-0.002	-0.007	0.004	0.004	-0.073	0.430	0.001	0.000	0.349**
Total soluble solids (º brix)	I	0.006	-0.001	0.002	-0.002	0.000	0.003	0.000	-0.002	-0.001	0.001	-0.043	0.004	-0.009	0.000	-0.044
	II	0.002	0.003	-0.003	0.000	0.000	-0.001	0.000	0.002	-0.008	-0.003	-0.223	-0.073	0.001	0.003	-0.302**
	III	0.001	0.001	0.001	0.000	0.001	-0.003	0.000	0.003	-0.005	-0.002	-0.113	-0.022	-0.014	0.001	-0.151**
Ascorbic acid (mg)	I	0.002	-0.002	-0.002	0.002	0.000	0.000	0.001	0.001	-0.002	-0.011	-0.013	0.001	0.000	0.026	0.003
	II	0.001	0.000	0.002	0.000	0.000	0.000	0.000	-0.001	-0.003	0.000	-0.250	0.006	0.000	0.014	-0.232**
	III	0.000	0.000	-0.001	0.000	0.001	0.000	0.001	-0.002	-0.004	-0.003	-0.167	0.003	-0.001	0.019	-0.153**

*P < .05, **P < .01; Unexplained variation (P) I: 0.0374 (P) II: 0.0084 (P) III: 0.0349

direct effect of these traits in different studies in different environments. The positive and significant association of different traits with pod yield/plant was mainly due to indirect effects via pods/plant and average pod weight over the years. Therefore, these traits provide an important criterion of selection procedures for achieving enhanced performance of genotypes for higher pod yield. Patel *et al.* (2006) and Katoch *et al.* (2016) also suggested pods/plant as most reliable component in breeding programme in pea for increased yield potential. The low magnitude of residual effects indicated that the traits included in the present investigation accounted for most of the variation present in the dependent variable. A more detailed study of the relationships obtained by path analysis revealed that relationship between yield and component traits are somewhat different from that of simple correlation. In correlation studies, internodal length was the main trait related to yield increase while its manifestation was secondary as depicted from path analysis. The apparent divergence is due to the analytical approach since correlation simply identifies the mutual associations among the parameters while path analysis allows determination of the relative magnitude of each effect (Okuyama *et al.*, 2004). This indicates that path coefficient analysis is a more efficient method than the correlation analysis (Dewey and Lu, 1959) when the objective is to establish relationships among the variables that affect yield. Thus, it can be concluded that pods/plant and average pod weight should be considered as selection criteria for yield improvement of garden pea.

Conclusion

On the basis of parameters of variability, it can be concluded that for pods/plant and pod yield/plant selection in early generations would be effective. Significant correlation of pod yield/plant was recorded with internodal length, seeds/pod, shelling (%), pods/plant and average pod weight. The positive association of these traits with pod yield/plant was mainly due to direct and indirect effects via pods/plant and average pod weight. Therefore, these traits provide an important criterion of selection procedures for achieving enhanced performance of genotypes for higher pod yield.

References

Ajmal SU, N Zakir and MY Mujahid (2009) Estimation of genetic parameters and character association in wheat. *Agric. Biol. Sci.* **1**: 15–18.

Al–Jibouri HA, PA Miller and HF Robinson (1958) Genotypic and environmental variance and co–variance in upland cotton crops of inter–specific origin. *Agron. J.* **50**: 633–636.

Alkuddsi Y, SS Patil, SM Manjula and BC Patil (2013) Correlation Studies on Yield and its Components in Inter Specific Cotton Hybrids (*G. hirsutum* × *G. barbadense*) for Developing Heterotic Box. *Mol. Plant. Breed.* **4**: 228-237 doi: 10.5376/mpb.2013.04.0028

Ashok Jat, Prasad SV Sai, Ambati Divya, Singh J, Gautam Amit, Dubey VG (2018) Genetic Variability, Heritability and Diversity for Yield Contributing Traits in Reference Varieties of Wheat. *Indian J. Plant Genet. Res.* **31**(1): 11-16.

Bagati S, AK Singh, RK Salgotra, R Bhardwaj, M Sharma, SK Rai and A Bhat (2016) Genetic variability, heritability and correlation coefficients of yield and its component traits in basmati rice (*Oryza sativa* L.). *SABRAO J. Breed. Genet.* **48**: 445–452.

Bhargava A, S Shukla, RS Katiyar and D Ohri (2003) Selection parameters for genetic improvement in Chenopodium grain on sodic soil. *J. Appl. Hort.* **5**: 45–48.

Bozokalfa MK, D Eşiyok, H Ilbi and TA Kaygisiz (2010) Estimates of genetic variability and association studies in quantitative plant traits of *Eruca* spp. landraces. *Genetika* **42**: 501–512.

Burton GW and EH DeVane (1953) Estimating heritability in tall fescue (*Festuca arundinacea*) from replicated clonal material. *Agron. J.* **54**: 478–481.

Dar SA, A Ishfaq, G Ali, FA Pir and A Manzar (2013) Studies on genetic variability, heritability and genetic advance in pea (*Pisum sativum* L.). *Ann. Horti.* **6**: 161–163.

Dewey DR and KH Lu (1959) A correlation and path analysis of components of crested wheat–grass seed production. *Agron. J.* **51**: 515–518.

Falconer DS (1981) Introduction to Quantitative Genetics, 2nd Edition, Longman Group Limited, Longman House, Harrow, England pp 350.

Gomez KA and AA Gomez (1983) Statistical procedures for agricultural research. 2nd Ed. John Wiley and Sons, New York, 357–427.

Habtamu S and F Million (2013) Multivariate analysis of some Ethiopian field pea (*Pisum sativum* L.) genotypes. *Int. J. Genet. Mol. Biol.* **5**: 78–87.

Jalal A and Ahmad H (2012) Genetic Variation, Heritability, Phenotypic and Genotypic Correlation Studies for Yield and Yield Components in Promising Barley Genotypes. *J. Agric. Sci.* **4**: 193–210.

Johnson HW, HF Robinson and RE Comstock (1955) Estimates of genetic and environmental variability in soybeans. *Agron. J.* **47**: 314–318.

Katoch V, P Singh, MB Devi, A Sharma, GD Sharma and JK Sharma (2016) Study of genetic variability, character association, path analysis and selection parameters for heterotic recombinant inbred lines of garden peas (*Pisum sativum* var. *hortense* L.) under mid–hill conditions of Himachal Pradesh, India. *Legume Res.* **39**: 163–169.

Kumar R, M Kumar, RK Dogra and NK Bharat (2015) Variability and character association studies in garden pea (*Pisum sativum* var. *hortense* L.) during winter season at mid hills of Himachal Pradesh. *Legume Res.* **38**: 164–168.

Okuyama LA, LC Federizzi and JFB Neto (2004) Correlation and path analysis of yield and its components and plant traits in wheat. Cienc. Rural. 34(6): 1701–1708 http://dx.doi.org/10.1590/S0103–84782004000600006.

Patel PJ, NH Patel, BH Prajapati, SBS Tikka and PT Patel (2006) Correlation and path analysis in field pea. *Indian J. Pulses Res.* **19**: 109–110.

Ranganna S (1979) Manual of analysis of fruits and vegetables products. Tata McGraw Hill Book Company, New Delhi

Ranjan S, M Kumar and SS Pandey (2006) Genetic variability in pea (*Pisum sativum* L.). *Legume Res.* **29**: 311–312.

Rathi RS and RPS Dhaka (2007) Genetic variability, correlation and path analysis in pea (*Pisum sativum* L.). *J. Plant Genet. Res.* **20**: 126–129.

Saxesena RR, V Vidyakar, MK Vishwakarma, PS Yadav, ML Meena and GM Lal (2014) Genetic variability and heritability analysis for some quantitative traits in field pea (*Pisum sativum* L.). *The Bioscan* **9**: 895–898.

Selvi SB, J Rajangam, J Suresh and R Muthuselvi (2016) Character association and path analysis studies for yield and its components in pea (*Pisum sativum* L.). *Elect. J. Plant Breed.* **7**: 750–757.

Sharma A and RP Sharma (2016) Effects of Boron and Lime on Productivity of Garden Pea under Acidic Soils in Northwestern Himalayas. *Commun. Soil Sci. Plant Anal.* **47**: 291–297. doi: 10.1080/00103624.2015.1122798.

Sharma A, A Bhardwaj, V Katoch and J Sharma (2013) Assessment of genetic diversity of garden pea (*Pisum sativum*) as perspective to isolate horticulturally desirable transgressive segregants. *Indian J. Agr. Sci.* **83**: 1334–39.

Sharma A, D Jyoti and V Katoch (2016) Genetic Variability and Genotypic × Environment Interaction for Seed Yield and Related Traits in French Bean Germplasm. *Indian J. Plant Genet. Res.* **29**(2): 156-162.

Sharma A, R Rathour, P Plaha, V Katoch, GS Khalsa, V Patial, Y Singh and NK Pathania (2010) Induction of Fusarium wilt (*Fusarium oxysporum* f. sp. *pisi*) resistance in garden pea using induced mutagenesis and *in vitro* selection techniques. *Euphytica* 173: 345–356. doi 10.1007/s10681–009–0099–x

Sharma MK, A Chandel and UK Kohli (2009) Genetic evaluation, correlations and path analysis in garden pea (*Pisum sativum* var. *hortense* L.). *Ann. hort.* **2**: 33–38.

Shrimali J, AS Shekhawat and S Kumari (2017) Genetic variation and heritability studies for yield and yield components in barley genotypes under normal and limited moisture conditions. *J Pharmacognasy Phytochem.* **6**(4): 233–235.

Shukla S, A Bhargava, A Chatterjee and SP Singh (2004) Estimates of genetic parameters to determine variability for foliage yield and its different quantitative and qualitative traits in vegetable amaranth (*A. tricolor*). *J. Genet. Breed.* **58**: 169–176.

Singh SK, CM Singh and GM Lal (2011) Assessment of genetic variability for yield and its component characters in rice (*Oryza sativa* L.). *Res. Plant Biol.* **1**: 73–76.

Tyagi MK and CP Srivastava (2002) Genetic variability and correlation among yield and yield characters over two environments in pea. *Indian J. Agr. Res.* **36**: 53–56.

Unche PB, MB Misal, SB Borgaonkar, GV Godhawale, BD Chavan and DR Sawant (2008) Genetic variability studies in sweet sorghum (*Sorghum bicolor* L. Moench). *Int. J. Plant Sci.* **3**: 16–18.

Wright S (1921) Correlation and causation. *J. Agric. Res.* **20**: 557–585.