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Variability, character association and path analysis in garden pea (*Pisum sativum* L.)

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Abstract

The experimental material comprising of 41 genotypes was evaluated in randomized complete block design with three replications. Genotype DPPM-74 was the most promising with significantly highest number of pods per plant, total biomass, seed yield and protein content. The differences in performance of genotypes for seed yield per plant might be attributed to pods per plant, seeds per pod and 100-seed weight. Significant genetic variations were observed for seed yield and related traits. High PCV and moderate GCV were recorded for seed yield per plant. Moderate estimates of PCV and GCV were recorded for number of branches, internodal length, plant height, pod length, seeds per pod, harvest index, 100-seed weight, protein content, starch, pods per plant, total biomass and ascorbic acid. High heritability coupled with high genetic advance was observed for pods per plant, total biomass, seed yield per plant and harvest index. Seed yield per plant had positive association with internodal length, plant height, pod length, seeds per pod, pods per plant, total biomass, harvest index and 100-seed weight at phenotypic and genotypic levels. Total biomass and harvest index had maximum positive direct effects on seed yield/plant. Based on variability studies, it can be concluded that pods per plant, pod length, seeds/pod, total biomass and harvest index should be given due focus for the improvement of garden pea.

Key words: Garden pea, genotypes, PCV, GCV, heritability, correlation, path coefficient

Introduction

Pea (*Pisum sativum* L.) belonging to the family Leguminosae is one of the major vegetables grown in the world as well as in India. It is grown as a cool season vegetable crop and consumed widely as a rich source of protein, carbohydrates, vitamins and minerals. Pea protein is rich in lysine and other essential amino acids, but low in sulfur containing amino acids, cysteine and methionine (Ceyhan and Avci 2005). It is palatable and nutritious for human consumption and is eaten as fresh, canned, frozen or in dehydrated forms. Pea as a legume crop helps in fixing the atmospheric nitrogen and reduces the cost of production by providing the advantage of low input and sustainable organic farming (Sharma et al. 2020). It is a leading vegetable crop in the North-Western Himalaya region of India comprising the states of Himachal Pradesh, Jammu and Kashmir, and Uttarakhand (Sharma et al. 2010). Genetic variability in germplasm determines the level of success in the improvement of any crop through selection and an opportunity to improve the yield and quality through strategic breeding programme (Sekhon and Sharma 2019). Therefore, genetic restructuring of pea germplasm is the first step to identify the potential genotypes for use in breeding programme. Most of the desirable traits are quantitative in nature and their expression is influenced by the environment. The response of selection depends upon the relative proportion of the heritable component in the continuous variation which is due to genotype while the non-heritable portion is mainly due to the environmental factors.

It is also beneficial to make comparative study of a few characters to select the desirable ones in different genotypes. Study of association of characters is to identify the role of individual characters towards pod yield. As yield is a complex trait, indirect selection via correlated, less complex and easier measurable traits would be an advisable strategy to increase the yield. Efficiency of indirect selection depends upon the magnitude of association between yield and target yield components. Determination of correlation and path-coefficients between yield and yield components is

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important for the selection of desirable plant types for effective pea breeding programmes. The path analysis has been used to identify traits that are useful selection criteria to improve crop yield (Negi and Sharma 2019). Genetic variability, heritability, coefficient of variation and genetic advance are pre-requisite for improvement of any crop for selection of superior genotypes and improvement of any traits. Thus, investigation was done to estimate genetic variability for seed yield and related quantitative traits for selection of desirable genotypes vis-à-vis identification of suitable genotypes.

Materials and Methods

A field experiment was conducted at Department of Vegetable Science and Floriculture, College of Agriculture, CSKHPKV, Palampur during winters 2009-10 and 2010-11. The experimental material comprising of 41 genotypes of garden pea including four checks namely, Lincoln, Azad P-1, Palam Priya and Punjab-89 was evaluated in randomized complete block design with three replications to assess the nature of genetic variability, association of various traits with yield and their direct and indirect effects for effective selection, and to study the extent of genetic diversity among genotypes. Data were recorded on randomly taken ten plants of each genotype in each replication followed by computing their means for the various traits *viz.,* days to 50% flowering, number of branches, internodal length (cm), nodes per plant, plant height (cm), pod length (cm), seeds per pod, pods per plant, total biomass (g), seed yield per plant (g), harvest index (%), 100-seed weight (g), total soluble solids (^{o}brix), ascorbic acid (mg), protein content (%), total sugars (%) and starch content (%). Analysis of variance was performed for individual season and error variance was tested for homogeneity (Gomez and Gomez 1984). 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 the method of Burton and De Vane (1953). Genetic advance (GA) was calculated as per Burton and De Vane (1953) and Johnson et al. (1955). Coefficients of correlation were calculated as suggested by Al-Jibouri et al. (1958) while path coefficients of different traits with seed yield per plant were carried out as per Dewey and Lu (1959).

Results and Discussion

Significant variations were recorded in the performance of different genotypes for seed yield and related traits over the years (Table 1) indicating thereby role of environment in a particular season that determined the performance of particular genotype for different traits. Number of pods per plant has a direct bearing on the total productivity of garden pea crop. Among the top ten ranked genotypes, DPPM-74 had significantly the highest number of pods per plant and also showed high total biomass and seed yield along with protein content. Further, it was observed that Punjab-89 had significantly less total biomass than check Palam Priya but they had at par performance for seed yield per plant. Punjab-89 and DPPMR-09-2 outperformed all other genotypes for harvest index and 100-seed weight, respectively over all the genotypes and check varieties. The differences in performance of genotypes for seed yield per plant might be attributed to pods per plant, seeds per pod and 100-seed weight. Higher phenotypic coefficient of variation (PCV) than genotypic coefficient of variation (GCV) (Table 2) indicated that most of the yield attributes were under the influence of environment (Sekhon and Sharma 2019). Therefore, caution has to be applying in making selection for these characters on the basis of phenotype alone as environmental variation is unpredictable in nature. High PCV and moderate GCV were recorded for seed yield per plant in pooled over years indicating high potential of the traits for effective selection (Sharma and Swain 2018). The moderate estimates of PCV and GCV were recorded for number of branches, internodal length, plant height, pod length, seeds per pod, harvest index, 100-seed weight, protein content and starch content. The moderate estimates suggest that direct selection for these traits should be considered cautiously (Sharma et al. 2016).

Heritability in broad sense is of tremendous significance to the breeders as its magnitude indicates the reliability with which a genotype can be recognized by its phenotypic expression. High heritability estimates (>60%) were observed for internodal length, plant height, pod length, seeds per pod, pods per plant, total biomass and seed yield per plant. The high heritability estimates for these characters revealed the lesser influence of environment and greater role of genetic component of variation. For an effective selection programme, knowledge of estimates of heritability alone is not sufficient and it is therefore useful to study genetic advance along with heritability. Heritability alone could not be the sole guideline for improvement since high heritability does not mean high expected genetic advance. Hence, prediction on the basis of both the estimates could be more useful. High heritability coupled with high genetic advance was observed for pods per plant, total biomass, seed yield per plant and harvest index (Table 2). The results suggested the importance of additive gene action for the inheritance of these characters and improvement could be brought about by phenotypic selection. The earlier researchers have also reported high heritability and genetic advance for

Table 1: Mean performance of top 10 genotypes of garden pea for different traits in pooled over years

Genotypes/Traits	D5F	NB	IL	NPP	PH	PL	SPP	PPP	TB	SYPP	HI	TSS	AA	PC	TS	SC
DPPMFWR-12	93.17	1.66	4.45	19.67	54.67	8.07	6.18	13.79	37.00	10.23	27.70	16.93	12.74	13.89	6.86	22.05
DPPMFWR-30-1	93.83	1.67	5.65	18.90	60.36	8.01	5.76	13.30	31.83	10.07	32.25	17.77	13.83	12.58	7.56	22.80
DPPMFWR-30 -2	96.50	1.43	5.41	17.68	55.12	8.44	5.50	9.96	33.50	11.81	35.17	18.03	15.24	16.54	6.99	24.82
DPPM-1	96.00	1.70	5.92	18.10	68.22	9.76	6.92	10.69	31.67	11.23	35.24	17.67	15.34	14.15	7.07	22.27
DPPM-72	96.00	2.53	6.32	16.86	71.99	9.75	6.70	13.06	35.17	10.60	29.32	18.03	15.26	15.45	7.51	27.15
DPPM-73	95.17	1.60	5.87	16.20	72.84	9.84	7.09	10.38	35.50	12.33	34.99	18.50	12.93	16.04	7.22	27.80
DPPM-74	94.33	2.07	5.46	17.76	59.02	8.51	6.18	16.52	40.83	16.14	41.43	16.97	14.88	16.98	7.03	25.66
DPPM-07-4	92.67	2.10	4.89	17.73	71.59	9.96	6.61	11.00	32.33	14.14	44.32	18.47	13.08	14.41	6.50	24.83
DPPMR-09-2	98.67	1.57	5.46	16.73	60.20	8.81	5.01	6.81	32.67	11.40	34.28	17.67	15.12	14.27	6.39	20.88
VP-215	89.33	1.76	5.96	16.63	62.25	8.69	5.87	10.32	29.00	11.09	38.82	17.43	14.59	13.88	7.04	25.20
Lincoln	95.00	2.00	5.59	17.25	56.28	8.09	5.95	9.89	20.33	7.31	36.05	17.57	18.82	16.28	7.50	26.47
Azad P-1	94.17	1.77	5.57	17.57	65.89	8.38	6.17	10.80	30.00	9.84	31.96	17.00	18.38	14.54	6.35	25.87
Palam Priya	97.00	1.97	5.07	18.49	57.19	8.17	6.08	13.71	37.50	11.90	33.38	17.13	17.44	13.71	6.35	30.15
Punjab-89	88.67	2.13	5.79	15.70	59.28	10.40	8.04	10.80	26.50	12.95	49.02	17.18	18.70	16.51	6.70	25.27
Range	89-100	1.27-2.53	2.66-6.52	15.47-19.87	34.51-81.67	6.59-13.35	3.92-8.37	4.89-16.52	9.83-40.83	2.68-16.14	21.04-49.02	15.03-18.93	12.38-18.82	10.65-18.68	5.93-8.57	18.90-30.15
CD at P ≤ 0.05	2.96	0.31	0.35	1.06	3.50	0.52	0.47	1.44	2.54	1.15	2.99	0.96	0.96	1.28	0.38	2.04

Where, D5F: Days to 50% flowering; NB: Number of branches; IL: Internodal length (cm); NPP: Nodes per plant; PH: Plant height (cm); PL: Pod length (cm); SPP: Seeds per pod; PPP: Pods per plant; TB: Total biomass (g); SYPP: Seed yield per plant (g); HI: Harvest index (%); TSS: Total soluble solids (° brix); AA: Ascorbic acid (mg); PC: Protein content (%); TS: Total sugars (%); SC: Starch content (%)

Table 2: Estimates of different parameters of variability for different characters in garden pea pooled over years

Traits	Range	Population mean	GCV (%)	PCV (%)	h^2_{bs}	GA (%)
Days to 50% flowering	89-100	94.41±1.05	3.23	4.23	58.20	5.07
Number of branches	1.27-2.53	1.76±0.11	16.07	22.01	53.33	24.18
Internodal length	2.66-6.52	5.25±0.13	13.36	14.53	84.53	25.30
Nodes per plant	15.47-19.87	17.51±0.38	5.47	7.62	51.64	8.10
Plant height	34.51-81.67	61.43±1.25	14.26	15.11	89.16	27.75
Pod length	6.59-13.35	8.74±0.19	12.94	13.97	85.91	24.72
Seeds per pod	3.92-8.37	5.98±0.17	14.37	15.94	81.28	26.69
Pods per plant	4.89-16.52	9.77±0.51	24.92	28.06	78.85	45.58
Total biomass	9.83-40.83	27.76±0.90	21.65	23.07	88.05	41.85
Seed yield per plant	2.68-16.14	9.22±0.41	28.98	30.96	87.60	55.87
Harvest index	21.04-49.02	33.21±1.06	16.17	17.97	80.94	30.00
100-seed weight	12.83-25.33	17.98±0.52	13.91	15.59	79.64	25.57
Total soluble solids	15.03-18.93	17.58±0.34	3.57	5.95	35.98	4.41
Ascorbic acid	12.38-18.82	14.97±0.34	10.00	11.45	76.18	17.97
Protein content	10.65-18.68	14.70±0.45	10.87	13.25	67.31	18.37
Total sugars	5.93-8.57	6.97±0.14	7.48	8.86	71.18	13.00
Starch content	18.90-30.15	24.66±0.73	10.59	12.82	68.26	18.02

GCV and PCV genotypic and phenotypic coefficients of variations, respectively; h^2bs: Heritability in Broad sense; GA (%): Genetic advance (%) of mean

total biomass/biological yield, seed yield per plant (Sharma et al. 2003, Kumar 2008). High heritability along with moderate genetic advance was observed for pod length, seeds per pod, 100-seed weight, ascorbic acid, total sugars and starch content.

In general, the genotypic coefficients were higher than the phenotypic ones which suggested that there is a strong inherent association between various characters, though the phenotypic expression of the correlation gets reduced under the influence of environment. Seed yield per plant revealed positive association with internodal length, plant height, pod length, seeds per pod, pods per plant, total biomass, harvest index and 100-seed weight (Table 3). Plant height expressed positive correlation with pod length, harvest index, seeds per pod, total biomass and pods per plant at phenotypic and genotypic levels. The pod length was positively associated with seeds per pod, total biomass, harvest index, 100-seed weight, total soluble solids, protein content and total sugars at phenotypic and genotypic levels, along with ascorbic acid at genotypic level. Kumar et al. (2004) also reported positive association of pod length with seeds per pod and 100-seed weight. Similarly, seeds per pod revealed positive association with harvest index, total biomass, ascorbic acid, total sugars and protein content. A significant positive association of pods per plant with total biomass and harvest index, and total biomass with 100-seed weight was also noticed.

Path analysis revealed that total biomass and harvest index had maximum positive direct effects and also contributed indirectly to enhance the magnitude of

Table 3: Estimates of phenotypic (P) and genotypic (G) correlation coefficients for different pairs of horticultural traits in garden pea pooled over years

Trait		Days to 50% flowering	Number of branches	Internodal length	Nodes per plant	Plant height	Pod length	Seeds per pod	Pods per plant	Total biomass	Harvest index	100-seed weight	Total soluble solids	Ascorbic acid	Protein content	Total sugars	Starch content
Number of branches	P	-0.08															
	G	-0.14*															
Internodal length	P	-0.12	0.18*														
	G	-0.15*	0.28*														
Nodes per plant	P	0.15*	-0.11	0.07													
	G	0.38*	-0.31*	0.06													
Plant height	P	-0.03	0.28*	0.63*	0.28*												
	G	0.05	0.32*	0.76*	0.32*												
Pod length	P	-0.18*	0.13*	0.35*	-0.12	0.36*											
	G	-0.21*	0.25*	0.48*	-0.22*	0.46*											
Seeds per pod	P	-0.36*	0.12	0.36*	-0.09	0.27*	0.64*										
	G	-0.54*	0.23*	0.49*	-0.25*	0.39*	0.72*										
Pods per plant	P	-0.15*	0.28*	0.23*	0.08	0.22*	0.03	0.21*									
	G	-0.19*	0.46*	0.36*	0.30*	0.28*	0.06	0.35*									
Total biomass	P	-0.09	0.18*	0.32*	0.13*	0.29*	0.25*	0.29*	0.55*								
	G	-0.04	0.23*	0.42*	0.14*	0.39*	0.33*	0.35*	0.70*								
Harvest index	P	-0.11	0.14*	0.15*	-0.11	0.15*	0.37*	0.40*	0.27*	0.01							
	G	-0.28*	0.21*	0.37*	-0.09	0.25*	0.56*	0.70*	0.38*	0.36*							
100-seed weight	P	-0.02	0.08	0.11	-0.07	0.08	0.32*	0.06	0	0.34*	0.28*						
	G	-0.03	0.08	0.14*	-0.18*	0.04	0.41*	0.07	-0.04	0.45*	0.35*						
Total soluble solids	P	0.04	-0.01	0.05	-0.13*	0.01	0.18*	0.02	-0.05	0.01	0	0.02					
	G	0.12	-0.25*	0.1	-0.32*	-0.04	0.42*	0.1	-0.14*	-0.08	0.08	-0.02					
Ascorbic acid	P	0	0.12	0.27*	-0.1	0.07	0.12	0.27*	0.12	0.07	0.23*	0.16*	-0.04				
	G	-0.04	0.15*	0.35*	-0.16*	0.1	0.17*	0.38*	0.14*	0.05	0.42*	0.25*	-0.16*				
Protein content	P	-0.06	0.08	0.11	-0.07	0.04	0.20*	0.22*	-0.07	0.06	0.07	0.08	-0.14*	0.25*			
	G	-0.08	0.07	0.14*	-0.11	0.07	0.26*	0.22*	0.06	0.08	0.21*	0.13*	-0.36*	0.32*			
Total sugars	P	0.01	0.13*	0.16*	-0.06	0.12	0.24*	0.15*	-0.01	0.02	0.11	0.1	0.07	0.09	0.18*		
	G	-0.09	-0.02	0.35*	0.00	0.21*	0.50*	0.37*	0.13*	0.31*	0.17*	0.23*	0.40*	0.02	0.30*		
Starch content	P	0.01	-0.01	-0.09	-0.07	-0.15*	-0.05	-0.01	0.02	-0.04	0.09	-0.06	-0.07	0.06	-0.02	-0.1	
	G	0.01	0.17*	-0.21*	-0.29*	-0.31*	-0.13*	0.05	0.05	-0.13	0.15*	-0.05	-0.01	-0.01	-0.11	-0.09	
Seed yield per plant	P	-0.13*	0.23*	0.32*	0	0.30*	0.42*	0.46*	0.58*	0.75*	0.64*	0.44*	0.02	0.18*	0.11	0.07	0.05
	G	-0.16*	0.27*	0.45*	0.02	0.37*	0.53*	0.59*	0.65*	0.86*	0.78*	0.49*	-0.01	0.22*	0.19*	0.27*	0.02

*Significant at P d ≥ 0.05

Table 4: Estimates of direct and indirect effects of different traits on seed yield/plant at phenotypic (P) and genotypic (G) levels in garden pea in pooled over years

Trait		Days to 50% flowering	Number of branches	Internodal length	Nodes per plant	Plant height	Pod length	Seeds per pod	Pods per plant	Total biomass	Harvest index	100-seed weight	Total soluble solids	Ascorbic acid	Protein content	Total sugars	Starch content	R
Days to 50% flowering	P	**-0.006**	0.000	0.003	-0.003	-0.001	0.002	0.004	0.002	-0.065	-0.066	0.000	0.001	0.000	-0.002	0.000	0.000	-0.13*
	G	**0.129**	0.008	0.000	-0.016	-0.003	-0.048	-0.045	-0.106	-0.030	-0.154	-0.002	0.010	-0.001	-0.003	0.006	0.000	-0.16*
Number of branches	P	0.001	**-0.003**	-0.004	0.003	0.006	-0.001	-0.001	-0.003	0.129	0.086	0.001	0.000	-0.002	0.002	-0.003	0.000	0.23*
	G	-0.018	**-0.059**	0.001	0.013	-0.020	0.057	0.019	0.251	0.176	0.118	0.006	-0.021	0.004	0.003	0.001	-0.007	0.27*
Internodal length	P	0.001	-0.001	**-0.025**	-0.002	0.013	-0.004	-0.004	-0.003	0.235	0.091	0.001	0.001	-0.005	0.003	-0.003	-0.002	0.32*
	G	-0.019	-0.016	**0.002**	-0.003	-0.047	0.109	0.041	0.198	0.315	0.207	0.010	0.008	0.009	0.005	-0.024	0.009	0.45*
Nodes per plant	P	-0.001	0.000	-0.002	**-0.023**	0.006	0.001	0.001	-0.001	0.096	-0.067	-0.001	-0.002	0.002	-0.002	0.001	-0.001	0.00
	G	0.049	0.018	0.000	**-0.041**	-0.020	-0.052	-0.021	0.163	0.106	-0.049	-0.013	-0.026	-0.004	-0.004	0.000	0.012	0.02
Plant height	P	0.000	-0.001	-0.016	-0.007	**0.021**	-0.004	-0.003	-0.003	0.209	0.094	0.001	0.000	-0.001	0.001	-0.002	-0.003	0.30*
	G	0.006	-0.019	0.002	-0.013	**-0.063**	0.105	0.032	0.157	0.290	0.141	0.003	-0.003	0.003	0.003	-0.014	0.013	0.37*
Pod length	P	0.001	0.000	-0.009	0.003	0.007	**-0.010**	-0.007	0.000	0.184	0.226	0.003	0.002	-0.002	0.006	-0.005	-0.001	0.42*
	G	-0.027	-0.015	0.001	0.009	-0.029	**0.230**	0.060	0.035	0.246	0.311	0.030	0.034	0.004	0.010	-0.034	0.005	0.53*
Seeds per pod	P	0.002	0.000	-0.009	0.002	0.006	-0.007	**-0.011**	-0.003	0.212	0.249	0.001	0.000	-0.005	0.006	-0.003	0.000	0.46*
	G	-0.070	-0.013	0.001	0.010	-0.024	0.167	**0.083**	0.191	0.264	0.385	0.005	0.008	0.010	0.009	-0.026	-0.002	0.59*
Pods per plant	P	0.001	-0.001	-0.006	-0.002	0.005	0.000	-0.002	**-0.012**	0.395	0.165	0.000	-0.001	-0.002	-0.002	0.000	0.000	0.58*
	G	-0.025	-0.027	0.001	-0.012	-0.018	0.014	0.029	**0.552**	0.528	0.209	-0.003	-0.012	0.004	-0.002	-0.009	-0.002	0.65*
Total biomass	P	0.001	-0.001	-0.008	-0.003	0.006	-0.003	-0.003	-0.007	**0.724**	0.005	0.003	0.000	-0.001	0.002	0.000	-0.001	0.75*
	G	-0.005	-0.014	0.001	-0.006	-0.024	0.075	0.029	0.389	**0.751**	0.199	0.032	-0.007	0.001	0.003	-0.021	0.005	0.86*
Harvest index	P	0.001	0.000	-0.004	0.003	0.003	-0.004	-0.004	-0.003	0.005	**0.618**	0.003	0.000	-0.005	0.002	-0.002	0.002	0.64*
	G	-0.036	-0.013	0.001	0.004	-0.016	0.129	0.057	0.209	0.270	**0.553**	0.025	0.007	0.011	0.008	-0.012	-0.006	0.78*
100-seed weight	P	0.000	0.000	-0.003	0.002	0.002	-0.003	-0.001	0.000	0.244	0.171	**0.010**	0.000	-0.003	0.002	-0.002	-0.001	0.44*
	G	-0.004	-0.005	0.000	0.008	-0.003	0.094	0.006	-0.025	0.334	0.192	**0.072**	-0.002	0.006	0.005	-0.161	0.002	0.49*
Total soluble solids	P	0.000	0.000	-0.001	0.003	0.000	-0.002	0.000	0.001	0.009	0.001	0.000	**0.013**	0.001	-0.004	-0.001	-0.001	0.02
	G	0.016	0.015	0.000	0.013	0.022	0.097	0.008	-0.080	-0.063	0.044	-0.002	**0.019**	-0.004	-0.014	-0.028	0.001	-0.01
Ascorbic acid	P	0.000	0.000	-0.007	0.002	0.001	-0.001	-0.003	-0.002	0.047	0.140	0.002	-0.001	**-0.020**	0.007	-0.002	0.001	0.18*
	G	-0.006	-0.009	0.001	0.007	-0.006	0.039	0.031	0.076	0.038	0.231	0.018	-0.013	**0.025**	0.012	-0.002	0.000	0.22*
Protein content	P	0.000	0.000	-0.003	0.002	0.001	-0.002	-0.002	0.001	0.047	0.044	0.001	-0.002	-0.005	**0.029**	0.004	0.000	0.11
	G	-0.011	-0.004	0.000	0.005	-0.004	0.060	0.018	-0.035	0.059	0.114	0.009	-0.029	0.008	**0.038**	-0.021	0.005	0.19*
Total sugars	P	0.000	0.000	-0.004	0.002	0.002	-0.003	-0.002	0.000	0.013	0.068	0.001	0.001	-0.002	0.005	**-0.021**	-0.002	0.07
	G	-0.011	0.001	0.001	0.000	-0.013	0.114	0.031	0.070	0.232	0.097	0.017	0.033	0.001	0.011	**-0.069**	0.004	0.27*
Starch content	P	0.000	0.000	0.002	0.002	-0.003	0.001	0.000	0.000	-0.026	0.054	-0.001	-0.001	-0.001	-0.001	0.002	**0.020**	0.05
	G	0.001	-0.010	-0.001	0.012	0.019	-0.029	0.004	0.029	-0.099	0.083	-0.004	-0.001	0.000	-0.004	0.007	**-0.041**	0.02

*Significant at P d ≥ 0.05

correlation of different traits with seed yield per plant, suggesting their importance in selection programme for improving yield. Togay et al. (2008) has also indicated the importance of direct effects of biological yield and harvest index on the seed yield. In addition, pods per plant had also contributed indirectly to total biomass, harvest index, plant height, ascorbic acid and internodal length at genotypic level to increase the magnitude of total association with seed yield per plant (Table 4). Indirect contribution of plant height, branches per plant, seeds per pod, pod length and harvest index on seed yield per plant had also been observed by Singh and Singh (2005) and that of biological yield and harvest index by Usmani and Dubey (2007). It can be concluded that the genotypes DPPM-74, DPPM-73, DPPM-72, DPPMFWR-30-2 and DPPM-07-4 appeared to be promising on the basis of seed yield characters and yield. DPPMFWR-30-2 had fasciation plant type. High heritability coupled with high genetic advance was observed for pods per plant, total biomass, seed yield per plant and harvest index revealing the importance of additive gene action. For garden pea improvement, emphasis should be given to pods per plant, pod length, seeds per pod, total biomass and harvest index.

सारांश

सब्जी मटर की 41 प्रभेदों का मूल्यांकन तीन प्रतिकृति वाले रैंडमाइज्ड कम्पलीट ब्लॉक डिजाइन में गिया गया। प्रभेद डीपीपीएम–74 से सर्थक रूप में अधिकतम फलियों की कुल संख्या, कुल जैव भार, बीज उपज एवं प्रोटीन की मात्रा पायी गयी। प्रति पौध बीज की उपज की प्राप्ति सम्भवतः प्रति पौध फलियों की संख्या, बीजों की संख्या प्रति फली एवं 100 बीज भार के कारण हो सकता है। बीज उपज व संबंधित लक्षणों के लिए महत्वपूर्ण आनुवंशिक विविधता देखी गयी। उच्च पीसीवी और मध्यम जीसीवी के प्रति पौध बीज उपज के लिए पाया गया। शाखाओं की संख्या, पार्श्व गांठ की लम्बाई, पौधे की ऊँचाई, फली की लंबाई, प्रति फली बीजों की संख्या, फसल तुड़ाई सूचकांक, 100 बीज वजन, प्रोटीन की मात्रा, स्टार्च, प्रति पौध फलियों की संख्या, कुल जैव–भार और एस्कार्बिक एसिड के लिए मध्यम पीसीवी और जीसीवी दर्ज किया गया। उच्च वंशागतित्व के साथ उच्च आनुवांशिक योज्य प्रति पौध फलियों की संख्या, कुल जैव भार, बीज की उपज प्रति पौध और फसल तुड़ाई सूचकांक के लिए दर्ज किया गया। प्रति पौध बीज उपज पार्श्व गांठ लंबाई, पौध ऊँचाई, फली की लंबाई, प्रति फली बीजों की संख्या, फली प्रति पौध, कुल जैव भार और फसल तुड़ाई सूचकांक और बाह्यदृश्य प्रारूप और अनुवांशिक स्तरों पर 100 बीज वजन के साथ सकारात्मक सहयोग पाया गया। कुल जैव भार और फसल सूचकांक का प्रति पौध बीज उपज पर अधिकतम सीधा सकारात्मक एवं महत्वपूर्ण प्रभाव पाया गया। सहसंबंध और पथ गुणांक विश्लेषण के अधार पर यह निष्कर्ष निकला कि उच्च उपज वाले प्रभेदों को विकसित करने के लिए प्रति पौध फलियों की संख्या, फली की लम्बाई, बीज/फली कुल जैव भार एवं फसल तुड़ाई सूचकांक को चयन मापदंडों के रूप में प्रयोग किया जा सकता है।

References

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

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

Ceyhan E and Avci MA (2005) Combining ability and heterosis for grain yield and some yield components in pea (*Pisum sativum* L.). Pakistan J Biol Sci 8: 1447-1452.

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

Gomez KA and Gomez AA (1984) Statistical procedures for agricultural research. 2nd Ed. John Wiley and Sons, New York, 680p.

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

Kumar B (2008) Variability, heritability and genetic advance in pea (*Pisum sativum* L.). Int J Plant Sci 3: 211-212.

Kumar P, Partap PS and Rana MK (2004) Correlation studies in garden pea (*Pisum sativum* L.). Haryana J Hortic Sci 33: 243-245.

Negi P and Sharma A (2019) Determination of selection parameters for genetic improvement by evaluating F_7 progenies of green chilli. Veg Sci 46 (1&2): 102-106

Sekhon BS and Sharma A (2019) Genetic studies based on selected morpho–physiological parameters in garden pea (*Pisum sativum* L.). Indian J Plant Genet Resour 32(1): 59-65.

Sharma A and Swain D (2018) Estimation of genetic variability in advance breeding lines derived from inter-varietal crosses in chilli. Indian J Hortic 75:440.

Sharma A, Devi J and Katoch V (2016) Genetic variability and genotypic × environment interaction for seed yield and related traits in French bean germplasm. Indian J Plant Genet Resour 29(2): 39-45.

Sharma A, Plaha P, Rathour R, Katoch V, Singh Y and Khalsa GS (2010) Induced mutagenesis for improvement of garden pea. Int J Veg Sci 16: 60-72.

Sharma A, Sekhon BS, Sharma S and Kumar R (2020) Newly isolated intervarietal garden pea (*Pisum sativum* L.) progenies (F_7) under north western Himalayan conditions of India. Exp Agric 56: 76-87

Sharma AK, Singh SP and Sarma MK (2003) Genetic variability, heritability and character association in pea (*Pisum sativum* L.). Crop Res 26: 135-139.

Singh JD and Singh IP (2005) Studies on correlation and path coefficient analysis in field pea (*Pisum sativum* L.). National J Plant Improv 7: 59-60.

Togay N, Togay Y, Yildirim B and Dogan Y (2008) Relationships between yield and some yield components in Pea (*Pisum sativum* ssp. *arvense* L.) genotypes by using correlation and path analysis. African J Biotech 7: 4285-4287.

Usmani MG and Dubey RK (2007) Association and path coefficient analysis in field pea (*Pisum sativum* var. *arvense*). Adv Plant Sci 20: 603-607.