RESEARCH ARTICLE Legume Research- An International Journal, Volume 48 Issue 8: 1274-1280 (August 2025)

Genetic Variability, Correlation and Path Coefficient Analysis in Advanced Matromorphic Generations of Garden Pea (*Pisum sativum* L.)

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10.18805/LR-5128

ABSTRACT

Background: Garden pea is an important leguminous vegetable crop but the lack of high yielding and stable varieties are the major constraint. There is a need to explore genetic variability for the crop improvement programs. Considering this, the current investigation was aimed to study the genetic variability and relationship among the yield and its contributing traits in advanced matromorphic progenies for effective production.

Methods: A two year experiment was carried out at SKUAST-Chatha, Jammu during the cropping season of 2020-21 and 2021-22 to find out the genetic variability parameters, path coefficient and correlation studies for thirteen yield contributing traits in twenty two garden pea genotypes (twelve advanced matromorphic progenies and ten parental lines).

Result: The results revealed high variability among the tested genotypes. The values of phenotypic coefficient of variation (PCV) were greater as compared to the genotypic coefficient of variation (GCV) for all the traits. High heritability along with GAM% (>20%) was observed for all the traits whereas pod length (PL) and shelling percentage (SP) were exceptions. Pod yield per plant (PYPP) had positive genotypic and phenotypic correlation with node at which first flower appears (NFFA), plant height (PH), internodal distance (ID), no. of pods per node (NPPN), pod length (PL), no. of seeds per pod (NSPP), no. of pods per plant (NPP), days to first picking (DFF), average pod weight (APW) and shelling percentage (SP). Positive direct effect on pod yield per plant (PYPP) was exhibited by traits *viz*., days to 50 per cent flowering (DFF), node at which first flower appears (NFFA), internodal distance (ID), no. of pods per node (NPPN), pod width (PW), no. of seeds per pod (NSPP), no. of pods per plant (NPPP), days to first picking (DFP) and average pod weight (APW) in path coefficient analysis.

Key words: Correlation, Genetic variability, Matromorph, Path analysis, Yield.

INTRODUCTION

Garden pea [*Pisum sativum* (L.) var. *hortense*], is the widely cultivated leguminous crop worldwide. It has been a valuable model crop for genetic research since the time of G.J. Mendel (Bar and Ori, 2015). The presence of genetic variability for the desirable traits in garden pea is considered crucial in the crop improvement programme for the development of commercial cultivars (Tiwari and Lavanya, 2012). Garden pea is highly self pollinated crop hence, the production and maintenance of homozygous lines constitute the raw material in pea improvement program. Matromorphy is a novel technique that facilitates in obtaining instant homozygous lines from heterozygous base population. In order to formulate an optimal breeding program targeted at harnessing the natural variability of the original population, variability indices such as GCV and PCV, heritability (h^2) and genetic advance (GA) are crucial (Raj *et al*., 2020). The phenotypic variability varies with environmental factors, whereas genetic variability remains constant and advantageous in breeding programme for selection or hybridization. Heritability (h^2), which represents the efficiency of genotype selection based on phenotypic performance has speculative aspect in crop breeding (Songsri *et al.,* 2008). The yield and quality traits can be selected to best possible extent with the available information about correlations between such traits followed by detailed knowledge of the association between the relevant characters obtained by

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How to cite this article: Sharma, S., Bhushan, A., Samnotra, R.K., Kumar, B., Wani, O.A., Naik, R. and Kumar, M. (2025). Genetic Variability, Correlation and Path Coefficient Analysis in Advanced Matromorphic Generations of Garden Pea (*Pisum sativum* L.). *Legume Research.* **48(8):** 1274-1280. doi: 10.18805/LR-5128.

Submitted: 04-03-2023 **Accepted:** 07-08-2023 **Online**: 23-08-2023

path coefficient analysis (Devi *et al.,* 2017). An appreciable yield enhancement in garden pea can be achieved by understanding the interactions between yield and contributing traits at genotypic and phenotypic levels and the selection of highly heritable traits. Therefore, the current investigation was undertaken with the aim of estimating genetic variability, heritability and correlation coefficients among different horticultural traits in garden pea to identify superior genotypes for their utilization in breeding programme with the aim to develop new varieties with higher yield.

MATERIALS AND METHODS

The present investigation involving 22 garden pea genotypes (12 matromorphic progenies ($Mat_{3/4}$) and 10 parental lines) was conducted at the Experimental Farm-I, Division of Vegetable Science and Floriculture, SKUAST-Jammu during *Rabi* season of 2020-21 and 2021-22. The plants were grown in 3 × 2.5 m^2 plot with 45 cm × 10 cm (R × P) with three replications in randomized complete block design (RCBD) following all recommendations (Anonymous, 2020). The data on various horticultural traits *viz*., days to 50% flowering (DFF), node at which first flower appears (NFFA), plant height (cm) (PH), number of primary branches per plant (NPB), internodal distance (cm) (ID), number of pods per node (NPPN), pod length (cm) (PL), pod width (cm) (PW), number of seeds per pod (NSPP), number of pods per plant (NPP), days to first picking (DFP), average pod weight (g) (PW), pod yield per plant (g) (PYPP) and shelling percentage (SP) was recorded on five plants of each genotype which were chosen randomly. The average mean for each trait over three replications was computed for each genotype and analysed statistically to determine analysis of variance (ANOVA) for all the traits as recommended by Goulden (1959). The phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) was estimated using Burton's approach (1952). Broad sense heritability (h^2bs) was assessed as per the procedure given by Lush (1949). Genetic advance (GA) and GA as percent of mean (GAM%) were calculated using the formula given by Johnson *et al.* (1955) and Genotypic (r_g) and phenotypic correlation coefficient (r_p) were computed using procedure recommended by Miller *et al.* (1983) and Johnson *et al.* (1955). Path coefficient analysis was done according to Dewey and Lu's method (1959).

RESULTS AND DISCUSSION

The ANOVA (Table 1) showed significant substantial differences between the tested genotypes for three traits *viz*., DFF, NFFA and PH under investigation. This variation in genotypes for all the traits may be a result of genotypic diversity, environmental effect and their interaction (G × E). Present results concur with the findings of Barcchiya *et al*., (2018); Singh *et al*., (2019); Thapa *et al*., 2020).

Table 1: Analysis of variance for 14 traits in garden pea.

Source of variation	d.f.	DFF	NFFA	PH	NPBP	ID	NPPN	PL	PW	NSPP	NPPP	DFP	APW	PYPP	SP
Replication	2	18.099	0.707	0.648	0.016	0.061	0.001	1.600	0.024	0.024	0.015	9.121	0.019	6.554	5.212
Treatment	21	6,115.944*	152.157*	17,702.099*	4.518	45.045	11.257	31.659	2.861	2.861	5,424.820	9,509.121	42.896	117,313.422	1,569.652
Error	42	166.924	13.821	133.078	0.149	1.072	0.055	6.857	0.512	0.512	38.710	213.879	0.248	466.040	654.121

Significance codes- *= 0.05; **= 0.01, d.f.- Degree of freedom, DFF- Days to 50% flowering, NFFA- Node at which first flower appears, PH- Plant height (cm), NPBP- No. of primary branches per plant, ID- Internodal distance (cm), NPPN- No. of pods per node, PL- Pod length (cm), PW- Pod width (cm), NSPP- No. of seeds per pod, NPPP- No. of pods per plant, DFP- Days to first picking, APW- Average pod weight (g), PYPP- Pod yield per plant (g), SP- Shelling percentage.

Genetic variability, heritability and genetic advance

For a successful selection programme of any crop, assessments of variability involving genetic characteristics such as genotypic variance, broad sense heritability (h^2) and genetic advance are essential (Thapa *et al.,* 2020). The higher PCV values with greater magnitude were recorded for all the studied traits as compared to GCV values indicating that the genetic material used was highly variable due to both genotypic effect and environmental influence (Table 2). However, there wasn't much of a difference between GCV and PCV values, suggesting that character expression was more influenced by genetic factors than environmental ones. As a result, the selection might be made based on phenotypic performance, which would allow for crop improvement. The different PCV and GCV values of the traits due to environmental effect was also recorded by Bijalwan *et al.* (2018) and Azam *et al.* (2020).

The maximum PCV and GCV value of >20 per cent were found for PYPP (37.84 and 37.72%), NPP (31.23 and 31.07%), NPPN (29.95 and 29.84%), PH (24.21 and 24.07%) and PW (20.92 and 20.83%), respectively. As has been observed in the present study maximum PCV and GCV values of these traits was also reported by various workers (Katoch *et al*., 2016; Singh *et al*., 2019 and Thapa *et al*., 2020).

Furthermore, it might be feasible to ascertain the extent to which a character is passed on from parent to progeny by assessing heritability (Hanson *et al*.,1956). In the present investigation, broad sense heritability ranged from 55.88 per cent (SP) to 99.41 per cent (PYPP) and high heritability (> 60%) was exhibited by thirteen traits except for shelling percentage. Kassaye (2006) reported that high broad sense heritability (h^2bs) along with GA would be a useful method for the selection of superior genotypes. High heritability (h^2) and GAM (>20%) was noticed for all the traits except PL and SP showing the preponderance of additive gene effect. The maximum value of GAM (77.48) was shown by PYPP followed by NPP (63.65), NSP (61.26), PH (49.31), APW (42.72), DFF (33.87), NFFA (30.51), ID (29.41), DFP (28.69), NSPP (26.28), NPBP (25.07), PW (24.52), PL (15.89) and SP (14.35) except NPBP which showed maximum heritability (95.20%) but low GA (0.53) (Table 2). Out of all the traits under study, five traits *viz*., PYPP, NPPN, PW, NPP and PH recorded maximum values for heritability (h^2bs), GCV and GAM% thus, depicting the effect of additive gene action on these traits and therefore, may be helpful for efficient selection. The findings of numerous studies are congruent with the current results (Georgieva *et al*., 2016; Singh *et al*., 2019; Thapa *et al*., 2020).

Correlation coefficients

The correlation coefficient, which offers a balanced assessment of the extent of relationship among two traits, aids in determining the type and amount of association between yield and its components (Singh *et al.,* 2018). The genotypic correlation coefficients between distinct traits were similar to the phenotypic correlation coefficients in the experiment in terms of sign and nature. However, genotypic correlations were larger than phenotypic correlations.

PYPP had highly significant and positive correlation with NFFA (r_g= 0.424, r_p= 0.399), PH (r_g= 0.523, r_p= 0.520), ID (r_g= 0.565, r_p= 0.549), NPPN (r_g= 0.439, r_p= 0.434), PL (r_g= 0.529, r_p= 0.445), NSPP (r_g= 0.662, r_p= 0.646), NPP (r_g= 0.968, r_p= 0.958), DFF (r_g= 0.468, r_p= 0.458), PW (r_g= 0.710, r_p= 0.706) and SP (r_g= 0.672, r_p= 0.495) both at genotypic and phenotypic levels (Table 3). DFF showed significant and positive correlation with NFFA, PH, NPBP, ID, PL and DFP. These traits were identified as most important component traits and were linked positively with PYPP

Table 2: Genetic parameters for various horticultural traits in garden pea genotypes.

Character	Range		Mean	PCV (%)	GCV (%)	h^2 (bs) (%)	GA	GAM (%)
	Maximum	Minimum						
DFF	75.00	44.00	58.32	17.12	16.78	96.02	19.75	33.87
NFFA	12.47	5.50	9.59	16.92	15.83	87.51	2.93	30.51
PH	90.00	24.27	69.50	24.21	24.07	98.88	34.27	49.31
NPBP	2.80	1.67	2.12	12.78	12.47	95.20	0.53	25.07
ID	7.10	3.41	5.78	14.79	14.53	96.52	1.70	29.41
NPPN	2.00	0.97	1.42	29.95	29.84	99.28	0.87	61.26
PL	8.34	5.47	7.42	10.52	9.01	73.30	1.18	15.89
PW	1.89	1.00	1.50	15.41	13.54	77.23	0.37	24.52
NSPP	7.83	4.30	5.97	13.37	13.06	95.44	1.59	26.28
NPPP	45.89	17.03	29.82	31.23	31.07	98.94	18.98	63.65
DFP	103.00	59.00	86.26	14.40	14.16	96.70	24.75	28.69
APW	6.40	3.33	0.13	20.92	20.83	99.14	1.69	42.72
PYPP	200.38	59.37	114.28	37.84	37.72	99.41	88.54	77.48
SP	58.33	39.00	47.64	12.47	9.32	55.88	6.84	14.35

GCV- Genotypic coefficient of variation, PCV- Phenotypic coefficient of variation, h^2(bs)- Broad sense heritability, GA- Genetic advance, GAM (%)- Genetic advance as per cent of mean.

Table 3: Genotypic and phenotypic correlation co-efficient for growth and yield components.

Characters	r	NFFA	PH	NPBP	ID	NPPN	PL	PW	NSPP	NPPP	DFP	APW	SP	PYPP
DFF	r_g	0.452**	0.394**	0.324**	0.425**	0.244*	0.585**	-0.055	0.294*	0.159	0.527**	0.019	0.175	0.106
	r_p	0.442**	0.385**	0.308*	0.410**	0.238	0.506**	-0.059	0.270*	0.155	0.511**	0.019	0.138	0.104
NFFA	r_g		0.751**	0.385**	0.785**	0.395**	0.695**	0.029	0.497**	0.417**	0.870**	0.187	0.423**	0.424**
	r_p		0.705**	0.339**	0.714**	0.369**	0.544**	-0.011	0.448**	0.380**	0.786**	0.185	0.280*	0.399**
PH	r_g			0.431**	0.966**	0.314*	0.719**	0.286*	0.653**	0.417**	0.641**	0.501**	0.432**	0.523**
	r_p			0.417**	0.940**	0.309*	0.599**	0.253*	0.636**	0.409**	0.624**	0.498**	0.340**	0.520**
NPBP	r_g				0.550**	0.136	0.304*	0.225	0.229	0.119	0.106	-0.059	0.183	0.077
	r_p				0.521**	0.133	0.242	0.163	0.226	0.121	0.110	-0.061	0.162	0.074
ID	r_g					0.368**	0.761**	0.312*	0.648**	0.494**	0.643**	0.429**	0.419**	0.565**
	r_p					0.362**	0.627**	0.273*	0.618**	0.486**	0.623**	0.423**	0.283*	0.549**
NPPN	r_g						0.420**	-0.203	0.446**	0.481**	0.201	0.094	0.397**	0.439**
	r_p						0.369**	-0.182	0.434**	0.480**	0.196	0.094	0.287*	0.434**
PL	r_g							0.134	0.826**	0.507**	0.658**	0.467**	0.277*	0.529**
	r_p							0.139	0.693**	0.431**	0.548**	0.399**	0.121	0.445**
PW	r_g								-0.085	-0.153	0.025	0.057	-0.279*	-0.009
	r_p								-0.084	-0.131	0.014	0.040	-0.134	-0.010
NSPP	r_g									0.646**	0.464**	0.615**	0.545**	0.662**
	r_p									0.627**	0.444**	0.597**	0.392**	0.646**
NPPP	r_g										0.447**	0.569**	0.581**	0.968**
	r_p										0.434**	0.563**	0.445**	0.958**
DFP	r_g											0.230	0.358**	0.468**
	r_p											0.223	0.257*	0.458**
APW	r_g												0.615**	0.710**
	r_p												0.450**	0.706**
SP	r_g													0.672**
	r_p													0.495**

Significance codes- *= 0.05; ** = 0.01.

Table 4: Partitioning of genotypic correlation (r_g) into direct and indirect effects for pod yield per plant.

Characters	DFPF	NFFA	PH	NPBP	ID	NPPN	PL	PW	NSPP	NPPP	DFP	APW	SP	PYPP	Correlation
DFPF	-	0.308	-0.712	-0.056	0.728	0.071	-1.080	-0.013	0.331	0.059	0.083	0.019	-0.114	**0.483**	0.106
NFFA	0.218	-	-1.356	-0.067	1.344	0.115	-1.283	0.007	0.558	0.154	0.137	0.192	-0.277	**0.682**	0.424**
PH	0.190	0.512	-	-0.075	1.654	0.092	-1.328	0.067	0.734	0.154	0.101	0.512	-0.283	**-1.807**	0.523**
NPBP	0.156	0.263	-0.779	-	0.942	0.040	-0.562	0.053	0.258	0.044	0.017	-0.060	-0.120	**-0.173**	0.077
ID	0.205	0.535	-1.745	-0.095	-	0.107	-1.405	0.073	0.728	0.182	0.101	0.439	-0.274	**1.713**	0.565**
NPPN	0.118	0.269	-0.568	-0.024	0.630	-	-0.776	-0.048	0.502	0.177	0.032	0.096	-0.260	**0.291**	0.439**
PL	0.282	0.474	-1.299	-0.053	1.302	0.123	-	0.031	0.928	0.187	0.104	0.478	-0.182	**-1.847**	0.529**
PW	-0.027	0.020	-0.517	-0.039	0.534	-0.059	-0.248	-	-0.095	-0.056	0.004	0.058	0.183	**0.234**	-0.009
NSPP	0.142	0.339	-1.180	-0.040	1.109	0.130	-1.526	-0.020	-	0.238	0.073	0.628	-0.357	**1.124**	0.662**
NPPP	0.077	0.285	-0.754	-0.021	0.846	0.140	-0.936	-0.036	0.726	-	0.070	0.582	-0.380	**0.368**	0.968**
DFP	0.254	0.594	-1.159	-0.018	1.102	0.059	-1.215	0.006	0.521	0.165	-	0.236	-0.234	**0.158**	0.468**
APW	0.009	0.128	-0.905	0.010	0.735	0.027	-0.863	0.013	0.691	0.210	0.036	-	-0.403	**1.022**	0.710**
SP	0.084	0.288	-0.781	-0.032	0.717	0.116	-0.512	-0.065	0.613	0.214	0.056	0.629	-	**-0.655**	0.672**

Significance codes- ** = 0.01; Residual effect= 0.041, Bold figures indicate the direct effect.

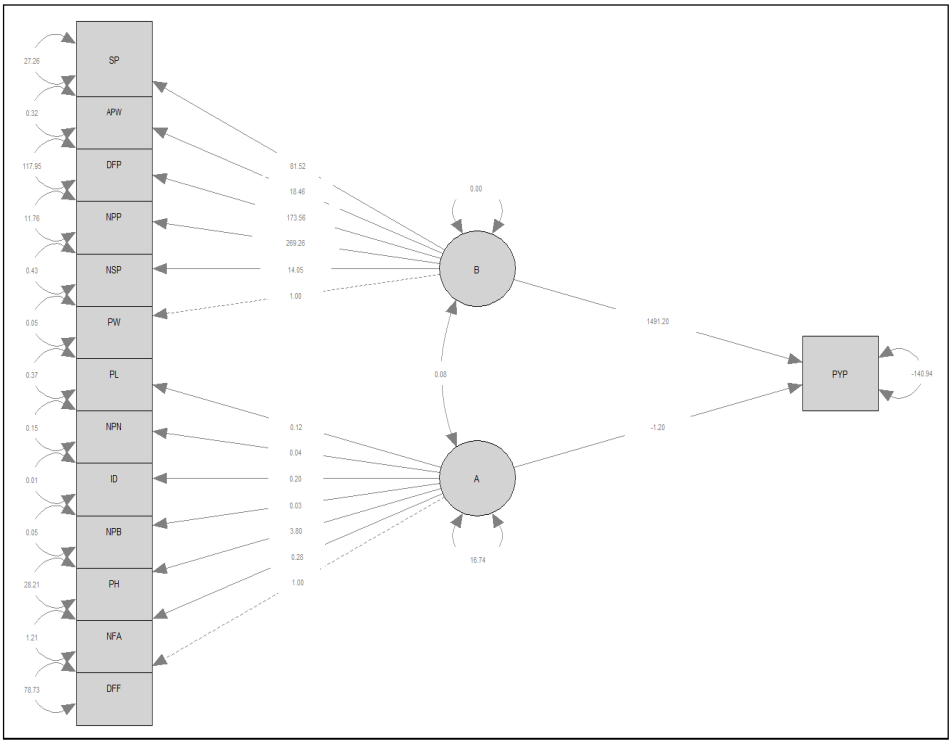

Fig 1: Genotypic path diagram of pod yield per plant and yield related traits.

implying that pod yield would increase by simultaneous selection for these traits. Earlier reports have also confirmed existence of strong positive correlation of PYPP with PH, NPPN, PL, NSPP and NPP (Kumar *et al*., 2019), days to first picking and shelling percentage (Rahman *et al.,* 2019), average pod weight (Tiwari *et al*., 2020).

Path co-efficient analysis

Path co-efficient analysis is an efficient approach to separate correlation coefficients into direct and indirect component effects since it assesses the direct impact of one variable on the other. This strategy is used to investigate the source and effect of a relationship between variables. Correlation studies give a greater understanding of the causes and effects of relationships between different pairs of component traits and the main trait when paired with path coefficient analysis (Verma *et al*., 2021). In the present study, PYPP was taken as a resultant (dependent) variable while 13 other traits were independent variables. The cause and effect relationship of PYPP and its related traits have been given in Table 4 (Fig 1). The results revealed that ID had maximum positive (1.713) and direct effect on PYPP followed by NSPP (1.124), APW (1.022), NFFA (0.682), DFF (0.483), NPPP (0.368), NPPN (0.291) and PW (0.234) suggesting that they are the major contributors to pod yield per plant and that if other characters remain constant, an increase or decrease in each of these characters will reflect in increase or decrease in pod yield. Positive and direct effect of NSPP, NPP, PW and DFF on PYPP was reported earlier also in field and garden pea (Tofiq *et al.,* 2015; Kumar *et al.,* 2019; Verma *et al.,* 2021). PH had highest indirect effect (1.654) via ID on PYPP. The residual effect was 0.041 which inferred that the character under study contributed 95.90% to the pod yield.

CONCLUSION

In the present study, it was reported that among all the traits studied, node at which first flower appears, internodal distance, number of pods per node, no. of seeds per pod, no. of pods per plant and days to first picking revealed significant positive correlation and had direct impact on pod yield per plant. This indicated that yield improvement is associated with these traits and selection would result in yield improvement in pea.

Conflict of interest

The authors declare no conflict of interest.

REFERENCES

Anonymous, (2020). In Package and Practices for Vegetable Crops. Directorate of Extension, SKUAST Jammu (J and K), India, pp: 82-83.

Azam, M.G., Iqbal, M.S., Hossain, M.A., Hossain, J., Hossain, M.F. (2020). Evaluation of Fieldpea (*Pisum sativum* L.) genotypes based on genetic variation and association among yield and yield related traits under high ganges river floodplain. *International Journal of Plant Biology and Research.* **8:** 1120.

Bar, M. and Ori, N. (2015). Compound leaf development in model plant species. *Current Opinion in Plant Biology.* **23:** 61-69.

Barcchiya, J., Naidu, A.K., Mehta, A.K., Upadhyay, A. (2018). Genetic variability, heritability and genetic advance for yield and yield components in pea (*Pisum sativum* L.). *International Journal of Chemical Studies*. **6:** 3324-3327.

Bijalwan, P., Raturi, A., Mishra, A.C. (2018). Genetic variability, heritability and genetic advance studies in pea (*Pisum sativum* L.) for yield and quality traits. *International Journal of Chemical Studies.* **6:** 3303-3305.

Burton, G.W. (1952). Quantitative inheritance in grasses. In: Proceedings of the Sixth International Grassland Congress. pp: 277-283.

Devi, S., Kumar, M., Thakur, K., Bharat, N.K., Dogra, R.K., Nagar, A. (2017). Variability, correlation and path analysis in pea (*Pisum sativum* L.) genotypes under Western Himalayan conditions. *Chemical Science Review and Letters.* **6:** 555-560.

Dewey, J.R. and Lu, K.H. (1959). Correlation and path coefficient analysis of components of crested wheat grass seed production. *Agronomy Journal.* **51:** 515-518.

Georgieva, N., Nikolova, I., Kosev, V. (2016). Evaluation of genetic divergence and heritability in pea (*Pisum sativum* L). *Journal of BioScience and Biotechnology.* **5:** 61-67.

Goulden, C.H. (1959). Method of Statistical Analysis. New York: John Wiley and Sons, Inc.

Hanson, C., Robinson, H., Comstock, R.E. (1956). Biometrical studies of yield in segregating populations of korean iespedeza. *Indian Journal of Agronomy*. **48:** 268-272.

Johnson, H.W., Robinson, H.F., Comstock, R.E. (1955). Estimates of genetic and environmental variability of soybean. *Agronomy Journal.* **47:** 314-318.

Kassaye, N. (2006). Studies on Genetic Divergence in Common Bean (*Phaseolus vulgaris* L.) Introduction of Ethiopia. MSc Thesis, Addis Ababa University of Life Science, Addis Ababa, Ethiopia.

Katoch, V., Singh, P., Mayanglambam, B.D., Sharma, A., Sharma, G.D., Sharma, J.K. (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 Research.* **39:** 163-169. doi: 10.18805/lr.v0iof.6775.

Kumar, T.N.V., Alloli, T.B., Hadimani, H.P., Ajjappalavar, P.S., Satish, D., Kareem, A., Hanchinamani, C.N. (2019). Studies on (*Pisum sativum* L.) varieties. *International Journal of Current Microbiology and Applied Sciences.* **8:** 3024-3031.

Lush, J.N. (1949). Animal Breeding Plans (3rd Edn). The Collegiate Press, Iowa.

Miller, J.D., Kang, M.S., Tai, P.Y.P. (1983). Genetic and phenotypic path analyses and heritability in sugarcane. *Crop Science.* **23:** 643-647.

Rahman, A.U., Katoch, V., Sharma, S. (2019). Studies on variability, correlation and path analysis in garden pea (*Pisum sativum* L.) for pod yield and its related traits under natural farming conditions. *Journal of Pharmacognosy and Phytochemistry.* **SPI:** 435-438.

Raj, J.V., Prasad, V.M., Bahadur, V., Srivastava, R., Singh, D. (2020). Genetic analysis for growth and yield traits of different genotypes of pea (*Pisum sativum* L.) under Prayagraj agro-climatic condition. *International Journal of Current Microbiology and Applied Sciences.* **9:** 797-805.

Singh, S., Verma, V., Singh, B., Sharma, V.R. Kumar, M. (2019). Genetic variability, heritability and genetic advance studies in pea (*Pisum sativum* L.) for quantitative characters. *Indian Journal of Agricultural Research.* **53:** 542-547.

Singh, S.K., Singh, V.P., Srivastava, S., Singh, A.K., Chaubey, B.K., Srivastava, R.K. (2018). Estimation of correlation coefficient among yield and attributing traits of field pea (*Pisum sativum* L.). *Legume Research.* **41:** 20-26. doi: 10.18805/LR-3449.

Songsri P., Jogloy, S., Kesmala, T. (2008). Heritability of drought resistance traits and correlation of drought resistance and agronomic traits in peanut. *Crop Science.* **48:** 2245-2253.

Thapa, U., Nandi, S., Gurung, D. (2020). Performance of garden pea (*Pisum sativum var hortense* L.) genotypes and their genetic variation, genetic advance, character association and path analysis for pod, seed and quality characters. *International Journal of Current Microbiology and Applied Sciences*. **9:** 3572-3586.

Tiwari, G. and Lavanya, G.R. (2012). Genetic variability, character association and component analysis in F_4 generation of field pea (*Pisum sativum var. arvense* L.). *Karnataka Journal of Agricultural Science.* **25:** 173-175.

Tiwari, S., Sharma, R.K., Kushwah, S.S., Pandey, B. (2020). Correlation analysis on different characters in garden pea (*Pisum sativum* var *hortense* L.). *International Journal of Chemical Studies*. **8:** 1180-1183.

Tofiq, S.E., Abdulkhaleq, D.A., Amin, T.N.H., Azez, O.K. (2015). Correlation and path coefficient analysis in seven field pea (*Pisum sativum* L.) genotypes created by half diallel analysis in sulaimani region for F2 generation. *International Journal of Plant Animal and Environmental Science.* **5:** 93-96.

Verma, A.K., Tiwari, P.K., Yadav, M.K., Lal, B., Prasad, D. (2021). Estimation of correlation and path coefficient for yield and yield attributing traits in vegetable pea [*Pisum sativum* (L.) var. *Hortense*]. *International Journal of Current Microbiology and Applied Sciences*. **10:** 336-344.