Website : www.asthafoundation.in
Frontiers in Crop Improvement
Vol 12 (1) : 1-6 (January-2024) Print ISSN : 2393-8234 Online ISSN : 2454-6011
Astha Foundation, Meerut (U.P.) India

Analysis of Genetic Variability and Association of Polygenic Traits among Elite Cultivars of Pea (*Pisum sativum* L.)

Ajay Yadav[1], P.N. Singh[1], S.C. Gaur[1], Tarkeshwar[2]*, Kamlesh Kumar[1] and S.P. Singh[3]
[1]*Department of Genetics and Plant Breeding, BRD (PG) College, Deoria-274001 U.P.*
[2]*Department of Genetics and Plant Breeding, ANDUAT, Kumarganj, Ayodhya-224229 U.P.*
[3]*CSAUAT–Agriculture Research Station, Kalai, Aligarh, U.P.*
**Corresponding Author Email : tarkeshwar.barhaj2014@gmail.com*

Abstract

The present investigation was carried out at Agricultural Research Farm of B.R.D.P.G. College, (Main Campus) Deoria to assess the genetic variability and character association among eleven biometric traits of fourteen elite cultivars of field pea. The experiment was sown during the rabi 2021-22 in Randomized Block Design with replications. Analysis of variance for seed yield per plant and its contributing traits showed significant mean sum of square due to genotypes. This indicates that there was considerable variability for these traits in the present material. High heritability with high genetic advance as % of mean was recorded for biological yield per plant, plant height, pod Length, seed Yield Per plant, primary branches, seed per pod, harvesting index, 100 Seed weight, which indicated that such traits could be improved by simple selection methods. The high heritability with high genetic advance as per cent of mean observed for these traits might be due to additive gene effects. Hence, selection in the segregating generation would be fairly effective for them. Harvesting index and biological yield per plant emerged as major contributors towards seed yield per plant. These characters show very high direct effect on seed yield. Further these traits were significantly and positively correlated with seed yield per plant. Selection based on these traits would leads to increase yield.

Key words : *Field pea, Pisum sativum, genetic variability, heritability, correlation coefficient and path coefficient.*

Introduction

Amidst the verdant landscape of the plant kingdom, the field pea (*Pisum sativum* (L.) emerges as a prominent contender. Belonging to the illustrious Leguminosae family, subfamily Papilionaceae, and the discernible class of dicotyledons, it exudes nutritional prowess. As a self-pollinating gem, it boasts a diploid chromosome count of 2n=2x=14. In the realm of linguistics, it is referred to as "Matar,". Geographically, its tendrils reach across the terrains of India, gracing the plains of the north during winter and the elevated domains during summer. Tender seeds, both consumed fresh and preserved via freezing or canning, constitute its gastronomic contribution. This verdant treasure finds a dual purpose, catering to the fresh market and the ever-thriving food processing industry on a global scale. The germination process thrives in the embrace of temperatures around 22°C, while growth unfolds in the amiable warmth of 13-18°C (1).

From 2013-2014 to 2021-22, the total acreage under pulses has almost slightly (+) being showed, however, the maximum growth rate in area and production was recorded with 18% & 42% during 2016-17 over previous year (2015-16). This trend is continuously maintained with highest area (31.24 Mha) and production (27.75 mt) with a productivity of 888 kg per ha. was also recorded during 2021-22 and it was ever highest recorded both in area and production in last 08 years. (Source: Department of agriculture and farmer welfare, Directorate of pulse development 2021-22-3rd Adv. Estimates).

Thus, pulses as a group, has tremendous scope for expansion in space and time. Recently developed early maturing varieties of pulses can fit well in various cropping systems thus increasing not only the area under pulses but also sustaining the cereal-based cropping systems in the long run.

Among various grain legumes, garden pea (*Pisum sativum* L.) is one of the ancient domesticated popular pulse crops of India and has versatile uses in both food and feed. The dry seed contains 19-27 per cent (22.5 g) protein and 62.1 g carbohydrate and having relatively less anti-nutritional substances.

There is an urgent need to evolve high yielding varieties having high protein content and resistance to biotic and abiotic stresses coupled with suitability for different agro-climatic conditions and cropping system. Despite of inherent high productivity potential of pea, the production has been on decline and average productivity is miserably low due to non-availability of input responsive multiple disease resistant high yielding varieties having resistance to high temperature at reproductive phase. With the increase in irrigated area, pulses are further being pushed to marginal and sub-marginal levels

Received : January-2024; Revised : January-2024; Accepted : January-2024

because of their ability to survive under adverse conditions. They face tough competition with commercial crops, which have also greater stability in production.

Materials and Methods

The present experiment was carried out during Rabi season 2021-22 at Baba Raghav Das P.G. College Deoria, (U.P.) at Agricultural Research Farm situated at 26°51´ North latitude and 83°77´ East longitude and at an altitude of 68m (223 feet) above the mean sea level (Source : Wikipedia). The climate of district Deoria has a humid subtropical, dry winter climate (Classification : CWA) with hot summer and cold winter nearly 80% of total rain fall is received during monsoon with a few showers in the winter, average annual precipitation is 864.38mm (Wikipedia). The soil of the experimental plot was fertile, alluvial loam and well characterized as soil of Deoria.

The experimental materials of studies comprise of 14 pea genotypes from exotic and indigenous these germplasms were procured from genetic stock available in garden pea. The experiment was sown in randomized block design with three replications during rabi 2021-22. After eliminating the border plants, observations were recorded on five randomly selected plants from each plot in each replication. Each plot was tagged with name of genotype and no. of replication. The observations were taken on following eleven quantitative traits as Days to germination, Plant height (cm), Number of primary branches per plant, Days to 50% flowering, Days to maturity, Pod length (cm), Number of Seeds per pod, 100 seed weight (g), Seed yield per plant (g), Biological yield per plant (g) and Harvesting index (%).

The various statistical analyses were done using the formulae given as Analysis of variance for Randomized Block Design (2), Coefficient of variation (3), Heritability in broad sense (4), Genetic advance (5), Correlation coefficient (6) and Path coefficient (7).

Results and Discussion

Genetic variability and heritability : Analysis of variance for seed yield per plant and its contributing traits is presented in Table-1. All eleven traits studied *viz*., days to 50% germination, days to 50% flowering, days to maturity, plant height, number of primary branches per plant, pod length (cm), number of seed per pod, 100 seed weight (g) and seed yield per plant (g), biological yield per plant, harvesting index showed significant mean sum of square due to genotypes. This indicates that there was considerable variability for these traits in the present material.

Mean performance revealed that genotypes, VL-42 was earlier in term of days to germination , DMR-7 was earliest in term of days to 50% flowering, VL-1 was earliest to maturity, HUP-2 showed shortest stature in plant height, HPF-8909 significant higher in number of primary branch per plant, VL-42 showed the largest pod length, IPF5-19 significantly showed in higher number of seeds per pod, KPF-103 had higher 100-seed weight, biological yield per plant, HUP-2 showed highest harvesting index, VL-42 significantly shows highest seed yield per plant. Earlier, (8,9,10,11) also observed high mean performance for some of the genotypes.

Data presented in table-2 showed that estimated phenotypic variance was higher than genotypic variance for all traits studied. The lowest phenotypic and genotypic variance was recorded for number of primary branches (0.1492) and seed per pod (0.4151). Respectively among all the quantitative traits, while the highest phenotypic and genotypic variance was recorded for plant height among the quantitative traits studied. This showed that the phenotypic variance was highly contributed by genetic makeup and little by environment for most of the trait under study. Genotypic variance was observed highest for plant height (418.0244) followed by days to maturity (55.8236), biological yield per plant (26.1661), harvesting index (12.7311), days to 50% flowering (12.7049), seed yield per plant (1.5254), test weight (1.2807), days to 50% germination (1.0952), pod length (0.8348), seed per pod (0.4151), primary branch (0.1492). Similarly, phenotypic variance also observed for all eleven quantitative traits in pea, where plant height has highest phenotypic variance (422.1618), followed by days to maturity (56.4895), biological yield per plant (26.5512), harvesting index (13.1676), days to50% flowering (123.9445), seed yield per plant (1.6343), test weight (1.6124), days to 50% germination (1.2765), pod length (0.9240), seed per pod (0.4980), primary branch (0.1625). Similar results were reported by (12,13,14,15,16).

Estimated phenotypic coefficient of variance was higher than genotypic coefficient of variance for all the traits studied which has been presented in table-2. Phenotypic coefficient of variance was recorded highest for biological yield per plant (21.07) followed by plant height (20.31), seed yield per plant (16.44), pod length (15.75), primary branch (14.58), seed per pod (14.47), harvesting index (11.13), days to germination (9.07), test weight (6.79), days to maturity (6.46) and lowest is days of 50% flowering (4.84). Genotypic coefficient of variation (GCV) estimated for all traits under study revealed to be highest for biological yield per plant (20.92), followed by primary branch (13.97), seed per pod (13.21), harvesting index (10.94), days to germination (8.40), days to maturity (6.42), test weight (6.05) and lowest is days to 50% flowering.

Table-1 : Analysis of variance for eleven yield traits in garden pea (*P. sativum* L.).

Character	Mean sum of square		
	Replication d.f.=2	Genotype d.f.=13	Error d.f.=26
Days to germination	0.30	3.46**	0.18
Days to 50% flowering	0.77	38.35**	0.24
Days to maturity	0.58	168.13**	0.66
Plant height	1.50	1258.2**	4.14
Primary branch	0.03	0.46**	0.01
Pod length	0.06	2.59**	0.08
Seed per pod	0.01	1.32**	0.08
Test weight	0.31	4.17**	0.33
Biological yield per plant	0.81	78.88**	0.38
Harvesting index	0.20	38.63**	0.43
Seed yield per plant	0.02	4.68**	0.10

**Significant at 5% level of significance.

Table-2 : Estimates of mean, range, variance, coefficient of variation, heritability and genetic advance in 14 genotypes of pea.

S. No.	Traits	General mean	Range		Variance		Coefficient of variation		H^2(BS)	Genetic advance	
			Max.	Min.	Genotypic variance	Phenotypic variance	GCV	PCV		GA	GAM
1.	Days to 50% germination	12.45	15	11	1.09	1.27	8.4	9.17	0.85	1.99	16.03
2.	Days to 50% flowering	74.26	82.6	66.8	12.7	12.94	4.79	4.84	0.98	7.27	9.79
3.	Days to maturity	116.22	134	104.6	55.82	56.48	6.42	6.46	0.98	15.3	13.16
4.	Plant height	101.15	138.4	71.8	418.02	422.16	20.21	20.31	0.99	41.91	41.43
5.	Primary branch per plant	2.76	3.4	2	0.14	0.16	13.97	14.58	0.91	0.76	27.58
6.	Pod length	6.1	7.74	4.15	0.83	0.92	14.97	15.75	0.9	1.78	29.32
7.	Seed per pod	4.87	6.2	3.5	0.41	0.49	13.21	14.47	0.83	1.21	24.86
8.	Test weight	18.69	21.7	16.12	1.28	1.61	6.05	6.79	0.79	2.07	11.11
9.	Biological yield per plant	24.44	31.65	15.18	26.16	26.55	20.92	21.07	0.98	10.46	42.79
10.	Harvesting index	32.59	40.96	28.59	12.73	13.16	10.94	11.13	0.96	7.22	22.17
11.	Seed yield per plant	7.77	10.43	6.02	1.52	1.63	15.88	16.44	0.93	2.45	31.62

Table-3 : Phenotypic correlation coefficient among different traits in pea.

Traits	DF	DM	PH	PB	PL	SPP	TW	BYPP	HI	SYPP
DG	0.74**	0.77**	0.25	-0.16	0.08	0.17	0.35*	0.22	-0.14	0.24
DF		0.94**	0.2	-0.22	0.01	-0.01	0.30*	0.13	0.25	0.36*
DM			0.15	-0.18	-0.01	-0.15	0.23	0.18	0.24	0.41**
PH				-0.80**	0.35*	0.17	-0.35*	0.70**	-0.67**	0.46**
PB					-0.22	-0.08	0.39**	-.56**	0.32*	-0.46**
PL						0.34*	0.13	0.38**	-0.39*	0.32*
SPP							0.17	-0.11	-0.21	-0.24
TW								-0.07	0.09	0.01
BYPP									-0.61**	0.84 **
HI										-0.18

Where, DM=days to germination, DF=days to 50% germination, DM=days to maturity, PH=plant height, PB=primary branch, PL=pod length, SPP= seed per pod, TW= test weight, SYPP=seed yield per plant, *,**Significant at 5% and 1% level of probability.

The data pertaining to heritability and genetic advance of all the traits under consideration have been presented in table-2. Result revealed high heritability for plant height (0.99), followed by days to maturity (0.98), biological yield per plant (0.98), days to 50% flowering (0.98), harvesting index (0.96), primary branch (0.91), days to germination (0.85), seed yield per pod (0.83) and lowest heritability for test weight (0.79). Thus, heritability values coupled with genetic advance would be more reliable and useful in formulating selection criteria (8,9,15).

High heritability with high genetic advance as % of mean was recorded for biological yield per plant, plant height, pod Length, seed Yield Per plant, primary branches, seed per pod, harvesting index, 100 Seed weight, which indicated that such traits could be improved by simple selection methods. The high heritability with

Table-4 : Genotypic correlation coefficient among different traits in pea.

Traits	DF	DM	PH	PB	PL	SPP	TW	BYPP	HI	SYPP
DG	0.79**	0.84**	0.28	-0.18	0.06	0.16	0.36	0.25	-0.14	0.28
DF		0.95**	0.2	-0.25	0.02	-0.01	0.36	0.14	0.26	0.37
DM			0.15	-0.19	-0.01	-0.17	0.26	0.19	0.24	0.42
PH				-0.84**	0.37	0.18	-0.38	0.71**	-0.69**	0.48
PB					-0.25	-0.09	0.44	-0.58 *	0.34	-0.48
PL						0.31	0.17	0.40	-0.42	0.36
SPP							0.23	-0.12	-0.20	-0.26
TW								-0.06	0.13	0.01
BYPP									-0.62*	0.88**
HI										-0.20

Where, DM=days to germination, DF=days to 50% germination, DM=days to maturity, PH=plant height, PB=primary branch, PL=pod length, SPP= seed per pod, TW= test weight, SYPP=seed yield per plant, *,**Significant at 5% and 1% level of probability.

Table-5 : Phenotypic direct and indirect effect of ten component traits of yield on seed yield per plant in pea.

Traits	DG	DF	DM	PH	PB	PL	SPP	TW	BYPP	HI
DG	-0.054	0.005	0.109	0.007	-0.013	0.009	-0.002	-0.002	0.25	-0.07
DF	-0.040	0.007	0.133	0.005	-0.019	0.002	0.001	-0.002	0.15	0.12
DM	-0.041	0.007	0.141	0.004	-0.015	-0.002	0.002	-0.002	0.20	0.11
PH	-0.014	0.001	0.022	0.028	-0.068	0.040	-0.002	0.003	0.79	-0.33
PB	0.008	-0.001	-0.026	-0.023	0.084	-0.026	0.001	-0.003	-0.63	0.15
PL	-0.004	0.001	-0.002	0.010	-0.019	0.115	-0.005	-0.001	0.42	-0.19
SPP	-0.009	-0.001	-0.022	0.005	-0.007	0.039	-0.016	-0.001	-0.13	-0.10
TW	-0.017	0.002	0.033	-0.010	0.033	0.015	-0.002	-0.008	-0.08	0.04
BYPP	-0.012	0.001	0.026	0.020	-0.047	0.044	0.001	0.001	1.11	-0.30
HI	0.007	0.001	0.034	-0.019	0.027	-0.045	0.003	-0.001	-0.68	0.48
SYPP	0.176	0.023	0.448	0.027	-0.044	0.191	-0.019	-0.016	1.41	-0.14

Where, DM=days to germination, DF=days to 50% germination, DM=days to maturity, PH=plant height, PB=primary branch, PL=pod length, SPP= seed per pod, TW= test weight, SYPP=seed yield per plant.

Table-6 : Genotypic direct and indirect effect of ten component traits of yield on seed yield per plant in pea.

Traits	DG	DF	DM	PH	PB	PL	SPP	TW	BYPP	HI
DG	-0.91	0.35	0.78	-0.29	0.02	0.01	0.05	-0.13	0.33	0.06
DF	-0.72	0.45	0.88	-0.21	0.03	0.01	-0.01	-0.13	0.18	-0.11
DM	-0.77	0.43	0.92	-0.16	0.02	0.01	-0.06	-0.09	0.24	-0.10
PH	-0.26	0.09	0.14	-1.03	0.11	0.01	0.06	0.13	0.92	0.29
PB	0.16	-0.11	-0.17	0.87	-0.13	-0.01	-0.03	-0.16	-0.75	-0.14
PL	-0.05	0.01	-0.01	-0.38	0.03	0.01	0.11	-0.06	0.52	0.17
SPP	-0.14	-0.01	-0.15	-0.19	0.01	0.01	0.37	-0.08	-0.16	0.08
TW	-0.33	0.16	0.24	0.39	-0.05	0.01	0.08	-0.36	-0.08	-0.05
BYPP	-0.23	0.06	0.17	-0.74	0.07	0.01	-0.04	0.02	1.28	0.26
HI	0.13	0.12	0.22	0.72	-0.04	-0.01	-0.07	-0.04	-0.81	-0.42
SYPP	-3.12	1.58	3.05	1.03	0.08	0.02	0.48	0.91	1.68	0.04

Where, DM=days to germination, DF=days to 50% germination, DM=days to maturity, PH=plant height, PB=primary branch, PL=pod length, SPP= seed per pod, TW= test weight, SYPP=seed yield per plant.

high genetic advance as per cent of mean observed for these traits might be due to additive gene effects. Hence, selection in the segregating generation would be effective for them. Similar results were obtained by (17,18). High heritability with low genetic advance was recorded for primary branches, that indicated these traits were governed by nonadditive genes hence hybridization breeding would be recommended for these traits' improvement.

Correlation and Path coefficient analysis : Estimates of genotypic and phenotypic correlation coefficients are very essential for evaluating the possibility of simultaneous improvement of multiple traits as it affects the selection for one trait on the other related traits. Phenotypic and Genotypic correlation coefficients were worked out among different quantitative trait under study and the results have been presented in Table-3 and Table-4, respectively. In general, it was observed that the magnitude of genotypic correlation coefficient was lower than the respective phenotypic correlation coefficient. The phenotypic correlation for seed yield per plant were significantly and positively correlated with biological yield per plant (0.84) followed by plant height (0.46), days to maturity (0.41), days to flowering (0.36), pod length (0.32), days to germination (0.24) while significant negatively correlated with primary branch (-0.46), harvesting index (-0.18). These results agree with the reports noted by (19,20).

Day to germination significant and positively correlated with days to maturity (0.77), followed by days to flowering (0.74), while negatively correlated with primary branch (-0.16), and harvesting index (-0.14). Days to 50% flowering were significant and positively correlated with days to maturity (0.94), test weight (0.31), while negatively correlated with primary branch (0.22). days to maturity was highly positive correlated with seed yield per plant (0.41), while negatively correlated with primary branch (-0.18). plant height was significantly positive correlated with biological yield per plant (0.70), followed by seed yield per plant (0.46), while negative significantly correlated with primary branch (-0.8), followed by harvesting index (-0.67), primary branch was significantly positive correlated with test weight (0.39), while negatively correlated with biological yield per plant (-0.56). pod length was positively correlated with biological yield per plant (0.38) followed by seed yield per plant (0.32) and negatively correlated with harvesting index (-0.39). seed per pod was positively correlated with test weight (0.17) while negatively correlated with seed yield per plant (-0.24). test weight low positively correlated with harvesting index while negatively correlated with biological yield per plant (-0.07), biological yield per plant significant positive correlated with seed yield per plant (0.84) while significant negatively correlated with harvesting index (-0.61). Harvesting index negatively correlated with seed yield per plant (-0.18). (21,23) also noted similar reports for most of the traits in their study.

Correlation coefficients, which measure the association between any two traits, may not give a true or comprehensive picture of a rather complex situation. Path coefficient analysis provides an efficient means of measuring the direct and indirect effects of one variable through the other variables on the end product. The path coefficient analysis was carried out at both phenotypic and genotypic levels, taking harvest index as dependent variable (Table-5 and 6).

At phenotypic direct (diagonal) and indirect effect of various traits on seed yield revealed that the trait; days to 50% flowering, days to maturity, plant height, primary branches per plant, pod length, biological yield per plant and harvesting index, exhibited high positive direct effect for seed yield while days to germination seed per pods and test weight, exhibited negative direct effect on seed yield, as presented in Table 6. Days to 50% germination exhibit indirect positive effect on seed yield via primary branch and harvesting index. Days to 50% flowering recorded positive indirect effect on seed yield via plant height, number of pods per plant. Day to maturity possessed positive indirect effect on seed yield via, days to 50% flowering, days to germination, days to maturity, plant height, weight of 100 seed and biological yield per plant. Harvesting index possess positive indirect effect on seed yield via days to 50% flowering, days to maturity, primary branches and test weight. The Residual effect value was found high thus it indicates that other characters which have not been studied here, need to include in this analysis to account fully for the variation on seed yield. (16) revealed that number of pods per plant and pod length have highest positive direct effect on yield in garden pea. (19) studied the path coefficient analysis for seed yield and its components in pea and reported that protein content had the negligible positive direct effect on seed yield. (22) conducted path coefficient analysis in pea and reported that, number of pods per plant had the maximum positive direct effect on pod yield per plant followed by the number of seeds per pod, number of branches per plant, internode length and dry matter content.

Conclusions

High heritability with high genetic advance as % of mean was recorded for biological yield per plant, plant height, pod Length, seed Yield Per plant, primary branches, seed per pod, harvesting index, 100 Seed weight, which indicated that such traits could be improved by simple selection methods. The high heritability with high genetic advance as per cent of mean observed for these traits might be due to additive gene effects. Hence, selection in the segregating generation would be fairly effective for them. Harvesting index and biological yield per plant emerged as major contributors towards seed yield per plant. These characters show very high direct effect on seed yield. Further these traits were significantly and positively correlated with seed yield per plant. Selection based on these traits would leads to increase yield.

References

1. Kalpana Dahatonde, A.V. Kshirsagar and N.N. Dahatonde (2023). Changes in chemical composition of bottle gourd (*Lagenaria siceraria* Mol. Standl.) fruits cv. smrat during maturation. *Progressive Research : An International Journal,*18(1): 84-86.
2. Panse V.G. and Shukhatme P.V. (1967) Statistical methods for agricultural workers, 2nd Ed., ICAR, New Delhi.
3. Burton G.W. and Devane E.H. (19530. Estimating

heritability in tall Fescue (*Festuca arundinaceia*) from replicated clonal material. *Agronomy Journal*, 45: 478-481.

3. Bradford M.M. (1976). Analytical Biochemistry 72: 248-254.
4. Hanson W.D. (1963). Heritability. Statistical genetics and plant breeding NAS, NRC, Washington, Publ., 125-140.
5. Johnson H.W., Robinson H.F. and Comstock R.R. (19550. Estimates of genetic and environmental variability in soybeans. *Agronomy Journal,* 47: 314-318.
6. Searle S.R. (1961). Phenotypic, genotypic and environment correlation. *Biometrics*, 17: 474-775.
7. Dewey J.R. and Lu K.H. (19590. A correlation and path analysis of components of crested wheat grass seed production. *Journal of Agronomy*, 51: 515-518.
8. Singh M., Malik S., Kumar M., Singh K.V., Kumar S., Dev P. and Kumar V. (2012). Studies of variability, heritability and genetic advance in field pea (*Pisum sativum* L.). *Progressive Agriculture,* 12(1): 219-222.
9. Habtamu S. and Million F. (2013). Multivariate analysis of some Ethiopian field pea (*Pisum sativum* L.) genotypes. *International Journal of Genetics and Molecular Biology*, 5(6): 78-87.
10. Gupta A.J., Singh Y.V. and Verma T.S. (2006). Genetic variability and heritability in garden pea (*Pisum sativum* L.). *Indian Journal Horticulture,* 63(3): 332-334.
11. Yadav R, Kumar R, & Kumar U. (2023). Technological advancements driving agricultural trans-formation. *Agrisustain-an International Journal*, 01(02), 05–11.
12. Tiwari S.K., Kumar R., Singh H.L. and Katiyar R.P. (2001). Genetic diversity analysis in pea (*Pisum sativum* L.). *Indian Journal of Agricultural Research*, 38(1): 60-64.
13. Sharma A., Sood M., Rana A. and Singh Y. (2007). Genetic variability and association studies for green pod yield and component horticultural traits in garden pea under high hill dry temperate conditions. *Indian Journal of Horticulture,* 64(4): 410-414.
14. Choudhary H., Verma M.K. and Sofi A.A. (2010). Genetic variability, heritability and genetic advance for yield components in garden pea. *Pantnagar Journal of Research*, 8(2): 195-197.
15. Lal G.M., Meena M.L., Chandra K. and Singh C.M. (2011). Assessment of genetic variability and interrelation between yield and its contributing components in field pea (*Pisum sativum* L.). *Environment Ecology*, 29(3): 1235-1239.
16. Katoch V., Singh P., Devi M.B., Sharma A., Sharma G.D. and 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* L. var. *hortense*) under mid-hill conditions of Himachal Pradesh, India. *Legume Research*, 39(2): 163-169.
17. Sharma V.K. and Bora L. (2013). Studies on genetic variability and heterosis in vegetable pea (*Pisum sativum* L.) under high hills condition of Uttarakhand, India. *African Journal of Agricultural Research*, 8(18): 1891-1895.
18. Tambolkar B.B., Chavan N.H. and Vidhate S.B. (2016). Variability studies in pea (*Pisum sativum* L.) with respect to growth yield and yield attributes parameters. *National Academy of Agricultural Sciences,* 34(6): 1765-1769.
19. Topo H., Sharma R.N. and Thakur A. (2017). Path analysis for quality traits in field pea (*Pisum sativum* L.). *Agricultural Science Digest,* 37(4): 324-326.
20. Bhuvaneswari S., Sharma S.K., Punitha P., Shashidhar K.S., Naveenkumar K.L. and Prakash N. (20170. Evaluation of morphological diversity of field pea (*Pisum sativum* L. ssp. *arvense*) germplasm under sub-tropical climate of Manipur. *Legume Research,* 40(2): 215-223.
21. Devi J., Sanwal S.K., Koley T., Dubey R.K., Singh P.M. and Singh B. (20180. Variability and character association studies for horticultural and quality traits in garden pea (*Pisum sativum* L. var. *hortense*). *Vegetable Science,* 45(2): 161-165.
22. Singh A.K., Pant S.C. and Paliwal A. (2019). Assessment of genetic divergence and association of horticultural traits with yields in garden pea on Shivalik hills of Uttarakhand. *International Journal of Agricultural Sciences,* 15(1): 184-189.