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Genetic variability and character association studies for yield and its contributing traits in Field pea (*Pisum sativum* L.)

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Abstract
Genetic variability and correlation coefficient were estimated in 60 genotypes of field pea grown in an Randomized Block Design during *Rabi* 2020-21. Analysis of variance showed significant differences among the genotypes for all the traits studied. The high percentage of PCV and GCV were observed for number of clusters per plant, plant height, seed yield per plant, biological yield per plant, number of primary branches per plant and number of pods per plant. The high estimates of heritability and genetic advance as percentage of mean were found for plant height, number of clusters per plant, number of pods per plant, biological yield per plant, 100-seed weight, protein content and seed yield per plant. Correlation studies revealed that seed yield per plant exhibited highly significant positive correlation with biological yield per plant, 100-seed weight, pod length, number of seeds per pod, number of pods per plant, harvest index and number of cluster per plant at both genotypic and phenotypic levels.

Keywords: Genetic variability, correlation, seed yield and Field pea

Introduction
Pulse crops play an important role in Indian agriculture besides being a valuable staple food for both rural and urban people. It has the capability to improve the soil fertility by adding atmospheric nitrogen to the soil through a symbiotic relationship developed between root nodules and nitrogen fixing bacteria of *Rhizobium* species. Pea (*Pisum sativum* L.) as the major pulse crop contributes to soil improvement either as green manuring crop or as cover crop to reduce soil erosion. It also utilizes as a common forage legume for animal feeds.

Field pea (*Pisum sativum* L.) is one of the oldest cultivated crops and was grown in farming villages of the China as early as 8000 B.C but origin of field pea is near the Mediterranean. This plant is a common forage legume in the semiarid regions of the Anatolia and Mediterranean area (rain fall 350-550mm). It performs best on fertile, well- drained soils with high moisture holding capacity. Optimum growth is obtained on loam, silt loam, or well texture soils with a pH 6.0-7.5.

Pisum sativum L. (2n=2x=14) is an annual self-pollinated diploid, temperate legume, belongs to family Leguminoseae or Fabaceae, subfamily Papillionaceae, and tribe Vicieae. It comprises two species, *Pisumfulvum Sibth* and Sm. and *Pisum sativum* L. (Smykal *et al*. 2012).

There are two type of cultivated pea i.e., garden pea and field pea. Field pea (P. sativum var. *arvense*) is identical to garden pea in most of its characters except leaves, flowers and pods.In India, pea is grown in an area of about 0.60 M hectare production of 0.86 metric tonnes and productivity of about 1441 kg/ha (Anonymous 2019-20) [1]. In Rajasthan, field pea is grown in an area of 13000 hectares which accounts about 1.18% of the India's total acreage with the estimated production of 26000 tones and productivity of 2000 kg/ha during 2018-19 (Anonymous, 2019) [1].

Yield enhancement is the major breeding objective in field pea breeding programmes. In self-pollinated crops like fieldpea (*Pisum sativum* L.), it is important to select the divergent parents for hybridization to obtain desirable segregants for selection in advanced breeding generations. Progenies of a cross between genetically diverse parents are often expected to exhibit a broad spectrum of variability. Varieties from distinct geographical regions are usually selected for hybridization programme presuming presence of considerable genetic diversity among them.

Hence, in the present study, attempt was made to measure the genetic diversity among the genotypes of field pea (*Pisum sativum*) and to identify diverse genotypes for their further use in breeding programme.

Material and Methods
The present study was carried out with 60 genotypes of field pea during *Rabi*, 2020-21 at experimental field, Agricultural Research Station, Ummedganj, Agriculture University, Kota (Raj.) The experiment was laid out in an Randomized Block Design in three rows of 4 meter long, 30 cm apart. The observations were recorded for thirteen quantitative characters *viz.*, days to 50 percent flowering, days to maturity, plant height (cm), number of primary branches per plant, pod length, number of clusters per plant, number of pods per plant, number of seeds per pod, 100-seed weight (g), biological yield per plant (g), harvest index (%), protein content (%) and seed yield per plant (g). The data were subjected to analysis of variance adopting standard statistical methods (Panse and Sukhatme, 1985 and Singh and Choudhary, 1979) [15, 23]. The genotypic and phenotypic correlation coefficients were calculated using the formula given by Johnson *et al*., (1955) [5].

Results and Discussion
The analysis of variance (Table 1) revealed that the difference among the genotypes for all the traits were highly significant indicating sufficient magnitude of variability present in the material. A wide range of variability for various traits has been observed earlier by Parihar *et al*. (2014) [16], Saxesena *et al*. (2014) [18], Devi *et al*. (2017) [3], Sharma *et al*. (2017) [19], Singh *et al*. (2019) [21] and Kanwar *et al*. (2020).

Genotypic and Phenotypic coefficient of variation
The estimate of genotypic and phenotypic coefficient of variation in present study indicated that the values of phenotypic coefficient of variation were higher than that of genotypic coefficient of variation in most of the cases, indicating influence of environmental factors in the expression of the traits (Table 2). High magnitude of GCV (more than 20%) was recorded for number of clusters per plant, plant height, seed yield per plant, biological yield per plant and number of pods per plant indicating a good deal of genetic variability for the characters under study to allow further improvement by selection of the individual traits. Similar results were also reported by Kumar *et al*.(2013) [9], Ahmad *et al*. (2014) [2], Kumar *et al*.(2018) [12] and Yimam *et al*. (2020) [25]. Number of primary branches per plant, 100-seed weight and harvest index had moderate genotypic coefficient of variation (10-20%), While pod length, number of seeds per pod, protein content and days to maturity exhibited low GCV (Less than 10%). High magnitude for seed yield per plant was also reported by Ahmad *et al*. (2014) [2], Kumar *et al*.(2018) [12] and Yimam *et al*. (2020) [25].
The relative magnitude of difference between phenotypic and genotypic coefficient of variation was low for days to maturity, days to 50% flowering, plant height, number of clusters per plant, seed yield per plant, biological yield per plant, pod length and protein content, indicating that these characters were less influenced by the environment. Similar results were also supported by Kumar *et al*. (2013) [9], Parihar *et al*. (2014) [16], Kosev (2015) [8] and Devi *et al*. (2017) [3]. These findings suggested that selection can be effective on the basis of phenotype along with equal consideration of genotypic values.

Heritability and Genetic advance as percent of mean
The estimates of heritability (broad sense) for all the traits under study are presented in Table 2. High heritability (more than 80%) was observed for protein content, number of pods per plant, biological yield per plant, plant height, 100-seed weight, seed yield per plant, number of clusters per plant. High heritability for these traits that are controlled by polygenes might be useful to the plant breeders for making effective selection. Similar results were reported earlier by Ketoch *et al*. (2016), Lal *et al*. (2018a) [14], Kumar *et al*. (2018) [12] and Kumar *et al*. (2019) [11]. Heritability estimate was moderate for number of primary branches per plant and harvest index. Whereas, it was low for days to 50% flowering followed by pod length, days to maturity and number of seeds per pod. Similar results were also reported by Habtamu *et al*. (2013) [4], Ahmad *et al*.(2014) [2] and Kumar *et al*. (2019) [11].
In the present study, the high estimates of genetic advance as per cent of mean was observed for number of clusters per plant followed by plant height, seed yield per plant, number of pods per plant, biological yield per plant, number of primary branches per plant, 100-seed weight, harvest index and protein content. Similar results were also reported by Ahmad *et al*.(2014) [2], Devi *et al*. (2017) [3], Lal *et al*. (2018a) [14] and Kumar *et al*. (2018) [12]. The values were moderate for pod length and number of seeds per pod. Low estimates were observed for days to 50% flowering and days to maturity. Habtamu *et al*. (2013) [4], Ahmad *et al*.(2014) [2], Ketoch *et al*. (2016), Lal *et al*. (2018a) [14] and Kumar *et al*. (2018) also reported low estimates were observed for days to 50% flowering and days to maturity.
The heritability estimate along with genetic advance is more useful than the heritability alone in predicting the resultant effect of selection, therefore, both the parameters should be considered together in designing breeding programme (Johnson *et al*. (1955) [5]. The characters showing high heritability coupled with high genetic advance generally indicates that heritability is more due to the additive gene effect and advocates the exploitation of high heritability estimates along with high magnitude of genetic advance for genetic improvement in any trait through selection. High heritability coupled with high genetic advance as per cent of mean was observed for plant height, number of clusters per plant, number of pods per plant, biological yield per plant, 100-seed weight, protein content and seed yield per plant.

Correlation
The correlation coefficients between seed yield per plant and its component characters as well as among themselves were estimated at genotypic and phenotypic levels (Table 3). Correlation coefficient analysis revealed that there was a close agreement between phenotypic and genotypic correlation coefficients. In general the value of genotypic correlation coefficient were higher them their corresponding phenotypic correlation coefficients. Seed yield per plant had significant positive correlation with biological yield per plant, 100-seed weight, pod length, number of seeds per pod, number of pods per plant, harvest index and number of cluster per plant at both genotypic and phenotypic levels. This suggests that simultaneous selection for these traits will have a better efficiency for improving the seed yield per plant in field pea.

Similar results were also earlier reported by Saeed *et al.* (2013) [17], Siddika *et al.* (2013) [20], Kumar *et al.* (2014) and Singh *et al.* (2019) [21]. Plant height and number of primary branches per plant did not show any significant correlation with seed yield per plant, But these characters revealed significant positive correlation with number of clusters per plant and number of pods per plant, which were positively correlated with seed yield per plant. This indicate that taller plant with more number of primaries may increase seed yield per plant. Similar results were also earlier reported by Singh and Lavanya (2014) [22], Khan *et al.*(2017) [7] and Kumawat *et al.*(2018) [13]. Days to 50% flowering did not show significant correlation with seed yield per plant indicating its less influence on seed yield per plant. Saeed *et al.* (2013) [17], Siddika *et al.* (2013) [20] and Singh *et al.* (2019) [21] also earlier reported days to 50% flowering did not show significant correlation with seed yield per plant indicating its less influence on seed yield per plant.

Table 1: Analysis of variance for yield and its contributing traits in field pea genotypes

Source of variation	d.f	Mean sum of square												
		DTF	DTM	PH(cm)	NPBPP	PL(cm)	NCPP	NPPP	NSPP	BYPP(g)	HI(%)	TW(g)	PC(%)	SYPP(g)
Replication	2	0.57	0.81	206.28	0.01	0.19	1.52	4.56	0.48	7.53	40.21	0.92	0.36	0.03
Genotypes	59	6.23**	3.07**	3626.78**	0.27**	0.99**	15.24**	38.78**	0.60**	59.82**	112.04**	16.11**	10.00**	9.83**
Error	118	1.88	1.35	210.80	0.05	0.41	1.11	1.62	0.28	3.10	26.37	0.99	0.15	0.68

*,** = Significant at 5 and 1 per cent,respectively

Table 2: Genetic variability parameters for yield and its contributing characters in field pea genotypes

Sr. No.	Characters	Range		Mean	GCV	PCV	Heritability (bs) %	Genetic Advance as % of mean
		Lowest	Highest					
1.	Days to 50% flowering	58.67	64.67	62.15	1.94	2.94	43.39	3.37
2.	Days to maturity	112.67	117.33	114.80	0.66	1.21	29.79	0.95
3.	Plant height (cm)	58.73	192.80	126.46	26.68	29.04	84.38	64.71
4.	Number of primary branches per plant	1.00	2.50	1.38	19.50	26.29	55.01	38.18
5.	Pod length (cm)	4.86	7.20	6.12	7.13	12.76	31.24	10.52
6.	Number of clusters per plant	4.46	17.73	7.85	27.65	30.74	80.89	65.65
7.	Number of pods per plant	9.93	28.26	15.65	22.48	23.91	88.39	55.8
8.	Number of seeds per pod	3.44	5.46	4.31	7.55	14.41	27.48	10.46
9.	Biological yield per plant (g)	8.00	31.96	19.11	22.75	24.55	85.89	55.67
10.	100-seed weight (g)	9.19	19.59	14.27	15.72	17.2	83.57	37.95
11.	Harvest index (%)	21.73	50.30	37.61	14.21	19.71	51.99	27.04
12.	Protein content (%)	16.06	22.90	19.60	9.24	9.46	95.41	23.83
13.	Seed yield per plant (g)	3.75	10.90	7.09	24.62	27.24	81.66	58.73

Table 3: Correlation coefficients between different characters in field pea at genotypic level

Characters	DTF	DTM	PH (cm)	NPBPP	PL (cm)	NCPP	NPPP	NSPP	TW (g)	BYPP(g)	HI (%)	PC (%)	SYPP (g)
DTF	1.00	-0.091	-0.222**	0.051	-0.048	0.088	-0.039	0.401**	-0.102	-0.065	-0.048	-0.165*	-0.102
DTM		1.00	0.300**	-0.254**	0.032	-0.042	-0.012	-0.108	0.089	-0.008	0.14	-0.124	0.088
PH (cm)			1.00	-0.088	-0.317**	0.275**	0.271**	-0.306**	0.1	0.294**	-0.328**	-0.01	0.113
NPBPP				1.00	-0.407**	0.313**	0.452**	0.314**	-0.413**	0.131	-0.226**	0.032	0.024
PL (cm)					1.00	-0.264**	-0.343**	0.046	0.810**	0.176*	0.599**	-0.014	0.528**
NCPP						1.00	0.948**	0.439**	-0.243**	0.597**	-0.346**	-0.02	0.365**
NPPP							1.00	0.409**	-0.258**	0.595**	-0.335**	0.05	0.367**
NSPP								1.00	-0.092	0.353**	0.271**	-0.009	0.471**
TW (g)									1.00	0.360**	0.448**	0.01	0.617**
BYPP(g)										1.00	-0.236**	0.035	0.808**
HI (%)											1.00	0.024	0.365**
PC (%)												1.00	0.056
SYPP(g)													1.00

*, ** significant at 5% and 1% levels respectively

Table 4: Correlation coefficients between different characters in field pea at phenotypic level

Characters	DTF	DTM	PH (cm)	NPBPP	PL (cm)	NCPP	NPPP	NSPP	TW (g)	BYPP(g)	HI (%)	PC (%)	SYPP (g)
DTF	1.00	0.147*	-0.114	0.016	0.092	0.004	-0.017	0.073	-0.022	-0.037	-0.028	-0.097	-0.049
DTM		1.00	0.14	-0.063	-0.042	-0.069	-0.011	-0.002	-0.001	0.029	0.043	-0.094	0.077
PH (cm)			1.00	-0.118	-0.119	0.247**	0.260**	-0.115	0.105	0.266**	-0.206**	0.004	0.113
NPBPP				1.00	-0.242**	0.198**	0.368**	0.178*	-0.339**	0.102	-0.124	0.012	0.03
PL (cm)					1.00	-0.164*	-0.178*	0.152*	0.550**	0.173*	0.319**	-0.028	0.398**
NCPP						1.00	0.825**	0.258**	-0.215**	0.507**	-0.245**	-0.013	0.288**
NPPP							1.00	0.255**	-0.240**	0.540**	-0.222**	0.045	0.336**
NSPP								1.00	-0.092	0.256**	0.174*	-0.012	0.335**
TW (g)									1.00	0.323**	0.286**	-0.001	0.531**
BYPP(g)										1.00	-0.261**	0.025	0.733**

HI (%)												1.00	0.001	0.436**
PC (%)													1.00	0.032
SYPP(g)														1.00

*, ** significant at 5% and 1% levels respectively

References

1. Anonymous. PC Report (Rabi crop). AICRP MULLaRP, IIPR, Kanpur, 2019-20.
2. Ahmad BH, Rauf S, Rafiq MC, Mohsin UA, Iqbal A. Estimation of genetic variability in pea (*Pisum sativum* L.). J Glob. Agric. Soc. Sci. 2014;2(2):62-64.
3. Devi S, Kumar M, Thakur K, Bharat KN, Dogra KR, Nagar A Variability, correlation and path analysis in pea (*Pisum sativum* L.) genotypes under western himalayan conditions. Chemical Science Review and Letters. 2017;6(21):555-560.
4. Habtamu S, Million F. Multivariate analysis of some ethiopian field pea (*Pisum sativum* L.) genotypes. International Journal of Genetic and Molecular Biology. 2013;5(6):78-87.
5. Johnson HW, Robinson HF, Comstock RE. Estimates of genetic and environmental variability in soybean. Agronomy Journal. 1955;47:314-318.
6. Katoch V, Singh P, Devi MB, Sharma A, Sharma GD, Sharma JK. Study of genetic variability, character association, path analysis and selection parameters for heterotic recombinant inbred lines of garden peas (*Pisum sativum* L.) under mid-hill conditions of Himachal Pradesh, India. Legume Research. 2016;39(2):163-169.
7. Khan MRA, Mahmud F, Reza MA, Mahbub MM, Shirazy BJ, Rahman MM. Genetic diversity, correlation and path analysis for yield and yield components of pea (*Pisum sativum* L.). World Journal of Agricultural Sciences. 2017;13(1):11-16.
8. Kosev LV. Multivariate analysis of spring field pea genotypes. Banat's Journal of biotechnology. 2015;6(11):23.
9. Kumar B, Kumar A, Singh KA, Lavanya RG. Selection strategy for seed yield and maturity in field pea (*Pisum sativum* L. arvense). Global Journal of Crop, Soil Science and Plnat Breeding. 2013;1(1):129-133.
10. Kumar C, Singh AK, Kumar H, Vani VM, Rajkumar BV. Interrelationship between different characters in pea (*Pisum sativum* L.) using correlation and path coefficient analysis. Annals of Agri Bio Research, 2014;19(3):474-478.
11. Kumar M, Jeberson MS, Singh NB, Sharma R, Dahiphale AV, Singh V. Genetic diversity and trait association analysis in field pea (*Pisum sativum* L.) Journal of Pharmacognosy and Phytochemistry. 2019a;8(2):2186-2193.
12. Kumar V, Singh J, Srivastava PC, Lal C. Genetic variability, heritability and genetic advance for seed yield and related traits in diverse genotypes of pea (*Pisum sativum* L.). International Journal of Chemical Studies. 2018;6(5):1174-1178.
13. Kumawat PK, Singh P, Singh D, Mukherjee S, Kumawat M. Study of correlation and path analysis for green pod yield and its contributing traits in vegetable pea (*Pisum sativum* L.) International Journal of Current Microbiology and Applied Sciences. 2018;7:3497-3502.
14. Lal K, Kumar R, Shrivastav SP, Kumar A, Singh Y. Genetic variability, character association and path analysis of seed yield and its contributing traits in field pea (*Pisum sativum* L. var. arvense). International Journal of Current Microbiology and Applied Sciences. 2018a;7(6):1815-1820.
15. Panse VG, Sukhatme PV. Statistical methods for agricultural workers. Indian Council of Agricultural Research, New Delhi. 1954, pp. 361.
16. Parihar AK, Dixit GP, Pathak V, Singh D. Genetic diversity and trait inter-relationship studies in a diverse set of field pea (*Pisum sativum* L.) genotypes. Journal of Food Legumes. 2014;27(4):297-301.
17. Saeed MA, Khan AJA, Saeed AAN. Character association and path analysis in pea (*Pisum sativum* L.). International Journal of Biology and Biotechnology. 2013;10(5):213-215.
18. Saxesena RR, Vidyakar V, Vishwakarma KM, Yadav SP, Meena LM, Lal MG. Genetic variability and heritability analysis for some quantitative traits in field pea (*Pisum sativum* L.). An International Quarterly Journal of Life Sciences. 2014;9(2):895-898.
19. Sharma PP, Vyas M, Meghawal RD. Estimation of genetic variability and correlation analysis in field pea (*Pisum sativum* L.) genotypes. Journal of Plant Development Sciences. 2017;9(1):53-56.
20. Siddika A, Islam AKM, Aminul R, Golam M, Mian M, Abdul K, Jalal UA. Genetic variability in advanced generations of vegetable pea (*Pisum sativum* L.). International Journal of Plant Breeding. 2013;7:124-128.
21. Singh S, Singh B, Sharma VR, Verma V, Kumar M. Character association and path analysis in diverse genotypes of pea (*Pisum sativum* L.).International Journal of Current Microbiology and Applied Sciences. 2019;8:706-71.
22. Singh A, Lavanya GR. Character association studies in field pea (*Pisum sativum* L.). National Journal of Plant Improvement. 2014;1(1):51-53.
23. Singh RK, Chaudhary BD. Biometrical methods in quantitative genetic analysis. Kalyani publishers, New Delhi & Ludhiana, 1979.
24. Smykal P, Aubert G, Burstin J, Coyne CJ, Ellis NTH, Flavell AJ, *et al*. Pea (*Pisum sativum* L.) in the Genomic Era. Agronomy. 2012;2(2):74-115.
25. Yimam K, Robsa A, Yilma G, Abo T. Evaluation of field pea (*Pisum sativum* L.) genotypes for yield and yield attributing traits at high land of arsi, South east Ethiopia. Science Journal of Applied Mathematics and Statistics. 2020;8(6):73-80.