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CHARACTER ASSOCIATION AND GENETIC VARIABILITY ANALYSIS IN FIELD PEA GENOTYPES (PISUM SATIVUM L.)

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ABSTRACT

The present research program was conducted with thirty-two field pea varieties obtained from AICRP MULLaRP and sown in the research farm, TCA, Dholi, Muzaffarpur, Bihar during the *Rabi* season of 2020-21. The material was assessed using RBD (Randomized Block Design) with four replications. Twelve traits were selected for the study *viz.,* plant height (PH), days to 50 % flowering (DFF), number of primary branches per plant (PBPP), number of secondary branches per plant (SBPP), pods per plant (PPP), grains per pod (GPP), pod length (PL), 100 seeds weight (HSW), harvest index (HI), days to maturity (DM), growing degree days (GDD) and yield per plant (YPP). ANOVA exhibited significant Mean Sum of Square (MSS) values due to genotype for all traits, which is an indicative of the presence of ample amount of variability in field pea genotypes used for the study. The Phenotypic Coefficient of Variance (PCV) values were slightly greater than the Genotypic coefficient of Variance (GCV) values which was attributed for the meager effect of environment on the morphological appearance of the traits. In the study, high heritability coupled high genetic advance was observed for number of pods per plant, hundred seeds weight (gm), number of primary branches per plant, number of secondary branches per plant, harvest index, plant height and yield per plant, which indicated the preponderance of additive gene action. Therefore, response to early selection may be effective in improving these traits. Based on correlation and path analysis, number of pods per plant, harvest index, number of primary branches per plant and number of secondary branches per plant exhibited positive and significant correlation with yield per plant having their positive direct effect suggesting that during selection these traits may be considered as prime trait to improve yield of field pea. Based on diversity using Tocher's method, the thirty two genotypes were grouped into six different clusters. The inter-cluster distances were recorded higher than the intra-cluster distances further indicating a considerable amount of diversity in the genotypes involved. Highest inter-cluster distance was found between cluster I and VI. Among all the characters studied, plant height contributed maximum to the diversity. Further, genotypes HUPT 1810, TRCP 8 (cluster VI) and Pant P 449 (Cluster I) were selected as superior genotypes based on high inter cluster distance alongside mean performance for most of yield attributing traits suggesting that these genotypes may be used in crossing program to obtain heterotic recombinants as well as transgressive segregants.

KEYWORDS: Field pea (*Pisum sativum* L.) Genetic advance, Genetic variability, Heritability, Tocher's method.

INTRODUCTION

Field Pea (*Pisum sativum* L. *var. arvense*) is a well-known pulse crop that belongs to the Leguminosae family of the Vicieae tribe. It is having a diploid chromosome number of 2n = 2X = 14 (Lal *et al*., 2018). It is a grain crop cultivated in cool-season and can be produced in several kinds of soils ranging from light sandy loams to heavy clays (Kindie *et al*., 2019). It is a significant source of feeding material to humans and a good fodder material for livestock. It is a valuable and inexpensive source of protein, containing essential amino acids (23-25%) with good nutritional content (Ali *et al.,*

2021). In India, the average productivity of field pea is 1338 kilogram per hectare (Anonymous, 2019) which is even less than the Global Productivity, that is nearly 1718 kilogram per hectare (Anonymous, 2018). In Bihar field pea productivity is nearly 1036 kg per ha which is even less in compare to average productivity of the country (Anonymous, 2019). Primary reason for low productivity is scarcity of high yielding varieties.

Existent of genetic variation is prime requirement to get high yielding varieties. The level of variability within population is measured by using parameters such as

genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability, and genetic advance (Devi *et al.,* 2017). Yield being a complex character depends on several characters and available relation between economic desired trait and other traits can be assessed by using correlation coefficient. Further path analysis reveals interconnection among different traits and their indirect and direct impact on the yield components (Pal *et al.,* 2012). Therefore present study was done to determine the parameters of genetic variability and character association in field pea genotypes.

MATERIALS AND METHODS

The experiment was conducted using thirty two field pea genotypes including two checks *viz.,* Rachana and Aparna received from AICRP on MULLaRP running at TCA Dholi. Each genotype was placed under Randomized Block Design (RBD) with four replications at the farms of Tirhut College of Agriculture, Dholi, Muzaffarpur, Bihar during Rabi 2020-21. From each plot, 5 competitive individuals were picked at random to record observations and to evaluate all the quantitative characters under study except days to 50 percent flowering, growing degree days and days to maturity which were monitored on line basis. Recommended agronomic practices and plant protection operations were followed to raise good crop.

Statistical analysis

Variance Analysis (ANOVA):
As suggested by Panse and Sukhatme (1985), analysis of variance was done with the data collected on different quantitative traits:

$$Yij = \mu + gi + rj + eij$$

Coefficients of variability:
The formula proposed by Burton and De Vane (1953) was used for estimation of Coefficients of variability.
Phenotypic Coefficient of Variation (PCV)

$$PCV\ (\%) = \sqrt{\frac{Phenotypic\ variance\ (Vp)}{General\ mean\ of\ population(\mu)}} \times 100$$

Genotypic Coefficient of Variation (GCV)

$$GCV\ (\%) = \sqrt{\frac{Genotypic\ variance\ (Vg)}{General\ mean\ of\ population(\mu)}} \times 100$$

Heritability and genetic advance as percent of mean:

$$Heritability\ (\%) = \frac{Genotypic\ variance\ (Vg)}{Phenotypic\ variance\ (Vp)} \times 100$$

Genetic advance:
Allard (1960) gave the equation to calculate the expected genetic advance resulting from selection of 5 per cent superior individuals. The equation is as follows:

$$GA = K \times \sigma p \times H.$$

Genetic advance as percentage of mean {GA (%):

GA (%) = (GA/$\underline{X}$) ×100

Genetic advance and GAM was grouped into several categories by using technique that was given by Johnson *et al.* (1955).

Lesser to 10%	Low
10 to 20%	Moderate
Higher than 20%	Higher

Path coefficient analysis:
Dewey and Lu (1959)'s formula was utilized for calculating path coefficient. Lenka and Mishra (1973)'s classification was used to classify direct and indirect effects values.

<0.09	Considered negligible
0.10-0.19	Low
0.20-0.29	Moderate
0.30-0.99	high
More than 1.00	Very high

D² analysis (Genetic divergence):
The assessment of genetic diversity among the genotypes is done by calculating inter-se distance available among the genotypes. For this given purpose Mahalanobis (1928)'s method is most desirable, where generalized distance among genotypes is calculated.

RESULTS AND DISCUSSION

Results of variance and cluster analysis were depicted in table 1 and 2 respectively. The ANOVA revealed significant genotypic differences for all characters, meaning that the field pea genotypes used in the analysis had enough variation. In common, PCV values are higher than GCV values, indicating that the environment has an impact on the morphological features of the traits. Hundred seed weight (g), number of pods per plant, number of secondary branches per plant, plant height (cm), harvest index (%) and yield per plant (g) had high PCV and GCV values, indicating that these traits had a lot of variability compared to other traits. The higher PCV and GCV figures in these characteristics indicated that there is a better chance of improving these characteristics by selection.

Days to 50 % flowering (DFF)
Low level GCV and PCV of DFF was observed with the values 1.79, 3.18 respectively. Moderate level of broad sense heritability was expressed by DFF with value 32%. GAM was low level (2.08%) for DFF. DFF did not show any significant correlation with other studied attributes. Similar results were in trend with Pathak *et al.* (2019).

100 seed weight (g)
High level of GCV and PCV for HSW was 20.26, 20.88 respectively. Heritability (broad sense) was 94% (high level). GAM was found to be high level (40.51%). HSW was expressing significantly positive phenotypic

correlation with plant height (r_p=0.2435). Similar results were in trend with Basaiwala *et al.* (2013).

Days to maturity
Variability at low level was expressed by DM with GCV and PCV Values 1.42, 2.98 respectively. Low level of broad sense heritability was recorded for DM (23%). GAM values calculated were at low with values of 1.39%. DM exhibited significant and positive phenotypic correlation with growing degree days (r_p=0.6139), number of secondary branches per plant (r_p=0.2325) and significant negative correlation with harvest index (r_p=0.2194) and grains per pod (r_p=-0.1939). Similar results were in trend with Jeberson *et al.* (2016).

Grains per pod
Low level of GCV (9.83) and moderate level of PCV (14.63) were expressed by GPP. Moderate level of heritability (45%) and GAM (13.61%) was also exhibited by the attribute under study. The trait GPP exhibited significant positive correlation only with pod length (r_p=0.3504). Similar results were in trend with Barcchiya *et al.* (2018).

Growing degree days (◦c)
GDD expressed low level of variability with GCV and PCV values 1.33 and 2.18. Moderate heritability (broad sense) as 37% coupled with low GAM (1.66%) was estimated for the trait GDD. GDD exhibited positive significant phenotypic correlation with number of secondary branches per plant (r_p=0.1838). Similar results were in trend with Mahapatra *et al.* (2020).

Number of pod per plant
Phenotypic correlation revealed PPP was positively and significantly coupled with plant height (r_p=0.3694), number of primary branches per plant (r_p=0.3929), days to maturity (r_p=0.2280), number of secondary branches per plant (r_p=0.7507), harvest index (r_p=0.2823) and yield per plant (r_p=0.6925). Similar results were in trend with Siddika *et al.* (2013).

Number of primary branches per plant
GCV and PCV of the attribute PBPP was estimated from 13.99 and 16.98 which was classified as moderate level of variability. Estimated high level value of broad sense heritability (65%) and GAM (23.39%) were also recorded for the character PBPP. PBPP exhibited significant positive phenotypic correlation with harvest index (r_p=0.3506), and yield per plant (r_p=0.3182). Similar results were in trend with Kumar *et al.* (2019).

Number of secondary branches per plant
Estimated values of GCV and PCV for SBPP were 41.89, 43.30 respectively that was classified as high level of variability. Broad sense heritability value of 94% and GAM value of 83.50% were also estimated which was considered as high value level. SBPP exhibited significantly positive inter relation with harvest index

(r_p=0.3698) and yield per plant (r_p=0.7926). Similar results were in trend with khan *et al.* (2017).

Plant height (cm)
GCV and PCV for PH were 46.90 and 47.72 respectively. These values of variability were considered as high level. Heritability estimates have also showed high level of broad sense heritability (96.6%) for PH along with high level values of GAM 94.96%. PH was found to having positive and significant correlation with days to maturity (r_p=0.4689), hundred seed weight (r_p=0.2435) and secondary branches per plant (r_p=0.2480). PH exhibited significant phenotypic correlation negative correlation with primary branches per plant (r_p=-0.1987), harvest index (r_p=-0.5101). Similar results were in trend with Bahadur *et al.* (2021).

Pod length (cm)
For pod length GCV and PCV was found to be low level (7.97), moderate level (10.31) respectively. Moderate level (60.5%) of heritability and moderate level of GAM observed for PL (12.69%) were also estimated. PL expressed significant, positive phenotypic correlation with growing degree days (r_p=0.2215). Similar results were in trend with Devi *et al.* (2017).

Harvest index (%)
High level of variability for HI was noted as values for GCV and PCV were 27.60 and 28.74 respectively. High heritability (92%) with high GAM (54.57%) recorded for the trait HI. HI exhibited significant and positive relation with yield per plant (r_p=0.5986). Similar results were in trend with Lal *et al.* (2018).

Yield per plant (g)
GCV and PCV for YPP was 42.84 and 43.46 respectively that was classified as high level. High level of broad sense heritability (97%) with high level of GAM (86.98%) was observed for the attribute YPP. The trait YPP exhibited significant positive phenotypic correlation with pods per plant (r_p=0.6925), number of primary branches per plant (r_p=0.3182), number of secondary branches per plant (r_p=0.7926) and harvest index (r_p=0.5986). Similar results were in trend with Gautam *et al.* (2017).

Path coefficient analysis
Direct effect
Genotypic path coefficient analysis resulted very high positive direct effect of number of secondary branches per plant (1.0950) on yield per plant whereas high and significantly positive direct effect by harvest index (0.3055), pod length (0.3776), days to 50% flowering (0.4785) on yield per plant. Moderate negative direct effect was also exhibited by number of primary branches per plant (-0.2274), plant height (-0.1861) on YPP. Similar results were in trend with Mahapatra *et al.* (2020).

Phenotypic path analysis revealed high and positive direct effect of harvest index (0.3825), number of secondary branches per plant (0.5513) on YPP. Number of pods per plant (0.1330) had low positive direct effect on YPP. Similar results were in trend with Srivastava *et al.* (2018).

Indirect effect
Number of pod per plant (r_p=0.6925) was found to having positive significant correlation with YPP at phenotypic level. Significant positive correlation was found in between number of primary branches per plant (r_p=0.3182) and yield per plant because of its negligible positive direct effect and low level of positive indirect effect through harvest index (0.1341) on YPP. HI put high direct positive effect on YPP and moderate level positive indirect effect through number of secondary branches per plant (0.2039) on YPP. Similar results were in trend with Siddika *et al.* (2013).

Genetic diversity analysis
To determine available genetic divergence at sub species and inter-varietal level D^2 statistics followed by clustering the genotypes can be performed. (Nair *et al.*, 1960). Plant height, yield per plant, 100 seed weight and number of pods per plant contributed most of the diversity among all tested clusters. Inter cluster distances were higher than intra cluster distances that expressed availability of variability in genotypes. On the ground of mean yield per plant, harvest index, number of primary and secondary branches per plant and number of pod per plant, superior genotypes namely, FPT-19-6 and FPD-19-5 (cluster VI). These genotypes are diverse also as they expressed maximum inter cluster distance with most

of the other genotypes. Similar results were in trend with Parihar *et al.* (2014), Prasad *et al.* (2018), and Singh *et al.* (2019).

Heritability and Genetic advance
High heritability in relation with height genetic advance as percent of mean was expressed by 100 seed weight (94%, 40.51%), number of pods per plant(96.7%, 73.54%), number of primary branches per plant (65%, 23.39%), number of secondary branches per plant (94%, 83.50%), plant height (96.6%, 94.96%), harvest index (92%, 54.57%) and yield per plant (97%, 86.98%). As these characters showed high variability, so environment impact was less on their expression. Selection of genotypes on based of these traits may be rewarding.

Higher variability with high GAM was recorded for these traits which indicate the presence of additive gene action for controlling traits. So, selection can be performed by giving due considerations for these traits. Mahapatra *et al.* (2020) reported same findings for yield per plant, harvest index by Barcchiya *et al.* (2018), 100 seed weight by Mahapatra *et al.* (2020), number of primary and secondary branches per plant by Pathak *et al.* (2019), plant height by Kumar *et al.* (2019) and number of pods per plant by Basaiwala *et al.* (2013).
High heritability in relation with moderate GAM was recorded for grains per pod (45%, 13.61%). This indicates the presence of non-additive along with additive type gene. In earlier studies same result was reported by Devi *et al.* (2017). Pod length (60.5%, 12.69%) was found to express moderate heritability along with moderate GAM. Similar results were also observed by Bahadur *et al.* (2021).

Table 1: Estimates of variability parameters in twelve field pea genotypes.

	Range		CV%	GCV	PCV	h² (Broad sense)	5% GA as percent of mean
	Minimum	Maximum					
Days to 50 percent flowering	73.50	81.25	2.63	1.79	3.18	0.32	2.08
100 seed weight (g)	12.12	23.52	5.04	20.26	20.88	0.94	40.51
Days to maturity	117.75	128.50	2.62	1.42	2.98	0.23	1.39
Grains per pod	3.94	7.31	10.84	9.83	14.63	0.45	13.61
Growing degree days (∘c)	14.58	15.41	1.77	1.33	2.18	0.36	1.60
Number of pod per plant	13.00	47.80	6.71	36.30	36.92	0.97	73.54
Number of primary branches per plant	2.05	3.35	9.78	13.89	16.98	0.67	23.39
Number of secondary branches per plant	0.02	3.10	10.94	41.89	43.30	0.94	83.50
Plant height (cm)	43.70	151.55	8.80	46.90	47.72	0.97	94.96
Pod length (cm)	5.63	7.57	6.54	7.97	10.31	0.60	12.69
Harvest index (%)	17.10	54.11	8.06	27.60	28.74	0.92	54.57
Yield per plant (g)	5.37	25.92	7.36	42.84	43.46	0.97	86.98

Where, GCV- genotypic coefficient of variance, PCV - phenotypic coefficient of variance, h^2- broad sense heritability, G.A- genetic advance.

Table 2: Estimations of Phenotypic and Genotypic correlation coefficients for yield characters in field pea.

Traits		PPP	PH	DFF	DM	GPP	PL	GDD	PBPP	SBPP	HSW	HI
PH	P	0.3694**										
	G	0.3780										
DFF	P	-0.1095	-0.0199									
	G	-0.1486	-0.0273									
DM	P	0.2280**	0.4689**	-0.0696								
	G	0.4739	0.9662	0.1578								
GPP	P	-0.0032	-0.1569	0.0661	-0.1939 *							
	G	-0.0035	-0.2237	0.3438	0.0332							
PL	P	0.0219	-0.1042	0.1214	0.0606	0.3504 **						
	G	0.0436	-0.1270	0.1951	0.2377	0.7451						
GDD	P	0.0576	0.0675	0.0655	0.6139 **	0.0002	0.2215*					
	G	0.0775	0.1180	0.4272	0.6800	0.2294	0.4991					
PBPP	P	0.3929**	-0.1987*	-0.0268	-0.1425	0.0001	-0.0033	-0.0962				
	G	0.4847	-0.2338	-0.0306	-0.3156	-0.0996	-0.0911	-0.3131				
SBPP	P	0.7507**	0.2480 **	-0.1263	0.2325 **	0.1177	0.1210	0.1838 *	0.1519			
	G	0.7858	0.2645	-0.2080	0.5460	0.1403	0.1756	0.3503	0.2075			
HSW	P	0.1139	0.2435 **	0.1394	0.1364	-0.0445	-0.1716	0.0096	0.1024	-0.1552		
	G	-0.1164	0.2515	0.2410	0.2352	-0.0536	-0.2495	-0.0305	0.1467	-0.1536		
HI	P	0.2823**	-0.5101**	-0.1126	-0.2194 *	0.1445	0.0319	-0.0630	0.3506 **	0.3698 **	-0.1674	
	G	0.2910	-0.5444	-0.1740	-0.4800	0.1987	0.0388	-0.1227	0.4498	0.3987	-0.1837	
YPP	P	0.6925**	0.0574	-0.0742	0.0660	0.0893	0.0210	0.0161	0.3182**	0.7926**	-0.1114	0.5986**
	G	0.7171	0.0579	-0.1421	0.1169	0.1367	0.0368	0.0104	0.4059	0.8245	-0.1185	0.6274

Table 3: Path coefficients for Direct and Indirect effects on yield per plant.

Traits		PPP	PH	DFF	DM	GPP	PL	GDD	PBPP	SBPP	HSW	HI
PPP	P	0.1330	0.0491	-0.0146	0.0303	-0.0004	0.0029	0.0077	0.0523	0.0998	-0.0151	0.0375
	G	0.0283	0.0107	-0.0042	0.0134	-0.0001	0.0012	0.0022	0.0137	0.0222	-0.0033	0.0082
PH	P	0.0251	0.0679	-0.0014	0.0318	-0.0107	-0.0071	0.0046	-0.0135	0.0168	0.0165	-0.0346

	G	-0.0704	-0.1861	0.0051	-0.1798	0.0416	0.0236	-0.0220	0.0435	-0.0492	-0.0468	0.1013
DFF	P	-0.0072	-0.0013	0.0657	-0.0046	0.0043	0.0080	0.0043	-0.0018	-0.0083	0.0092	-0.0074
	G	-0.0711	-0.0131	0.4785	0.0755	0.1645	0.0933	0.2044	-0.0146	-0.0995	0.1153	-0.0833
DM	P	0.0039	0.0080	-0.0012	0.0171	-0.0033	0.0010	0.0105	-0.0024	0.0040	0.0023	-0.0038
	G	0.0428	0.0872	0.0142	0.0902	0.0030	0.0214	0.0614	-0.0285	0.0493	0.0212	-0.0433
GPP	P	0.0000	0.0009	-0.0004	0.0011	-0.0055	-0.0019	0.0000	0.0000	-0.0006	0.0002	-0.0008
	G	0.0014	0.0928	-0.1426	-0.0138	-0.4147	-0.3090	-0.0951	0.0413	-0.0582	0.0222	-0.0824
PL	P	-0.0009	0.0044	-0.0051	-0.0026	-0.0148	-0.0422	-0.0094	0.0001	-0.0051	0.0072	-0.0013
	G	0.0164	-0.0480	0.0737	0.0897	0.2813	0.3776	0.1885	-0.0344	0.0663	-0.0942	0.0147
GDD	P	-0.0042	-0.0050	-0.0048	-0.0451	0.0000	-0.0163	-0.0735	0.0071	-0.0135	-0.0007	0.0046
	G	-0.0576	-0.0877	-0.3174	-0.5053	-0.1704	-0.3709	-0.7430	0.2327	-0.2603	0.0226	0.0911
PBPP	P	0.0225	-0.0114	-0.0015	-0.0082	0.0000	-0.0002	-0.0055	0.0573	0.0087	0.0059	0.0201
	G	-0.1102	0.0532	0.0070	0.0718	0.0226	0.0207	0.0712	-0.2274	-0.0472	-0.0334	-0.1023
SBPP	P	0.4138	0.1367	-0.0696	0.1282	0.0649	0.0667	0.1013	0.0838	0.5513	-0.0856	0.2039
	G	0.8604	0.2896	-0.2277	0.5978	0.1537	0.1923	0.3836	0.2272	1.0950	-0.1682	0.4366
HSW	P	-0.0014	0.0037	0.0018	0.0017	-0.0006	-0.0022	0.0001	0.0013	-0.0020	0.0127	-0.0021
	G	-0.0119	0.0257	0.0246	0.0240	-0.0055	-0.0255	-0.0031	0.0150	-0.0157	0.1020	-0.0187
HI	P	0.1080	-0.1951	-0.0431	-0.0839	0.0553	0.0122	-0.0241	0.1341	0.1414	-0.0640	0.3825
	G	0.0889	-0.1663	-0.0532	-0.1466	0.0607	0.0119	-0.0375	0.1374	0.1218	-0.0561	0.3055
Correlation with YPP	P	0.6925**	0.0574	-0.0742	0.0660	0.0893	0.0210	0.0161	0.3182**	0.7926**	-0.1114	0.5986**
	G	0.7171	0.0579	-0.1421	0.1169	0.1367	0.0368	0.0104	0.4059	0.8245	-0.1185	0.6274

Clustering pattern of 32 field pea genotypes in accordance to D^2 analysis.

Cluster number	Genotypes numbers in cluster	Included genotypes
Cluster I	15	Pant P 455, IPFD 19-3, Pant P 250, HFP 715, HFP 1545, KPMR 890, Pant P 449, NDP 2018-3, HFP 1426, IPFD 19-1, Pant P 462, RACHNA, VL 68, IPF 18-20, Pant P 442
Cluster II	1	VL 42
Cluster III	8	Pant P 436, Pant P 476, RFPG 118, HUPT 1806, KPF 432, SKNP 04-09, IPF 18-17, HUDP 15
Cluster IV	5	KPF 14-29, IPFD 19-9, IPF 18-14, DDR-23, APARNA
Cluster V	1	RFPG 111
Cluster VI	2	TRCP 8, HUPT 1810

Average inters and intra-cluster distances in field pea genotypes.

S.N.		Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI
1.	Cluster I	4.87	6.35	7.84	7.48	8.84	15.74
2.	Cluster II		0.00	4.73	8.57	5.16	14.10
3.	Cluster III			5.10	9.76	7.34	14.94
4.	Cluster IV				6.38	10.38	12.59
5.	Cluster V					0.00	12.08
6.	Cluster VI						5.97

Cluster mean of field pea genotypes for 12 traits

S. N.	Characters	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI
1	Number of pod per plant	18.19	20.55	21.85	21.72	31.65	46.95
2	Plant height (cm)	63.57	132.30	136.95	49.77	151.55	123.88
3	Days to 50 percent flowering	77.27	77.00	77.34	77.25	78.00	76.13
4	Days to maturity	122.52	125.50	125.94	122.50	127.75	124.63
5	Grains per pod	5.53	4.44	5.45	5.60	5.38	5.56
6	Pod length (cm)	6.34	5.73	6.19	6.22	6.70	6.32
7	Growing degree days (°c)	15.09	15.27	15.12	15.09	15.41	14.99
8	Number of primary branches per plant	2.73	2.55	2.64	2.99	2.20	3.33
9	Number of secondary branches per plant	1.08	1.30	1.34	1.51	1.50	2.75
10	100 seed weight (g)	16.07	16.77	21.57	17.40	13.11	14.11
11	Harvest index (%)	36.34	24.43	27.13	45.51	26.19	52.05
12	Yield per plant (g)	8.09	10.07	8.72	15.10	9.97	22.12

CONCLUSION

In current experiment, the traits of number of pods per plant, hundred seeds weight (gm), number of primary branches per plant, number of secondary branches per plant, harvest index, plant height (cm) and yield per plant(g) were expressed high heritability coupled with high genetic advance so productive selection can be done by considering these traits. Based on correlation and path analysis, number of pods per plant, harvest index, number of primary branches per plant and number of secondary branches per plant exhibited positive and significant correlation with yield per plant having their positive direct effect suggesting that during selection these traits may be considered as prime trait to improve yield of field pea.

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