

Genetic Variability, Heritability and Genetic Advance Estimates for Various Quantitative Traits in Fieldpea (*Pisum sativum* L. var. *arvense*)

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ABSTRACT

The present investigation was carried out to estimate the extent of genetic variability, heritability and genetic advance for various quantitative traits among one hundred twenty genotypes and four check varieties of Fieldpea. Analysis of variance (ANOVA) revealed significant differences among all the genotypes for majority of the traits except number of primary branches per plant. Moderate to high level of genotypic coefficient of variance (GCV) and phenotypic coefficient of variance (PCV) were exhibited by the genotypes under study. In general, phenotypic coefficient of variance was found to be higher than their genotypic coefficient of variance but difference was quite meager, indicating negligible environmental influence on the expression of the characters. Higher estimate of GCV (30.414) was recorded for number of seeds per pod followed by seed yield per plant (28.874). Moderate to high level of heritability and genetic advance were reported for various quantitative traits under study. Maximum heritability in broad sense, were reported for seed yield per plant (99.78), seeds per pod (99.69), pod length (99.43), biological yield per plant (98.78) and harvest index (98.68). Maximum genetic advance in percent of mean was reported for seeds per pod (62.55), seed yield per plant (59.41), plant height (47.63), pod length (46.66) and harvest index (35.85). The characters such as seeds per pod, seed yield per plant, pod length and harvest index, showed high GCV, heritability and genetic advance would be more helpful in formulation of selection strategy for prediction of the gain under selection.

Keywords: Genetic variability, GCV and PCV, Heritability, Genetic advance and Fieldpea (*Pisum sativum* L. var. *arvense*).

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INTRODUCTION

Pea is a member of Fabaceae family which belongs to the genus *Pisum* and species *sativum*. Pea can be further divides in two cultivated varieties, hortense and arvensis. The Fieldpea, *Pisum sativum* L. $2n=2x=14$) comes under the variety hortense (Ambrose, 1995; Zohary & Hopf, 2000). It is an annual herbaceous crop of the family Fabaceae. According to Blixt (1970), the primary centre of diversity for pea is Mediterranean and secondary centre of diversity for pea is Ethiopia. Peas are starchy but, high in fiber, protein, vitamins (vitamin A, C, K and B complex vitamins such as folic acid, pantothenic acid, niacin, thiamine and pyridoxine), minerals (iron, magnesium, phosphorus and zinc) and lutein (a yellow carotenoid pigment that benefits vision). The dry pea seeds are rich source of proteins (about 19-27%) and are free of anti-nutritional substances (Pettersson et al., 1997). Since our country's population is increasing day by day therefore it becomes essential to identify such genotypes that are able to provide maximum yield under various ecological conditions. To fulfill such type of requirements, calculation of genetic variability in the existing genotypes is much more essential because genetic variability is a prerequisite for any breeding programme. Heritability estimates are useful in predicting the transmission of characters from the parents to their offspring that enabled us to select elite genotypes from the mixed parental population or segregating populations, while estimation of genetic advance help in understanding the type of gene action involved in the expression of various polygenic characters, thus for the development of an intensive breeding and improvement program needs thorough knowledge of the existence of genetic variability, the mode of inheritance of economic characters, heritability, the kind of gene action and the relative magnitude of additive, dominance and total genotypic and phenotypic variance of the population. Taking a lot of such type of problems in consideration, the present investigation carried out with the aim to estimate genetic variability, heritability

and genetic advance of different yield contributing traits in Fieldpea genotypes.

MATERIALS AND METHODS

The present investigation was carried out at the Genetics and Plant Breeding Research Farm of Narendra Deva University of Agriculture and Technology, Narendra Nagar, Kumarganj, Ayodhya (U.P.). Geographically this place is located in between 26.470N latitude, 82.120E longitude and at an altitude of 113 meters above from mean sea level. This area falls in sub-tropical zone (Indo-gangatic plain) and the soil texture is characterized by silty loam in nature having 0.40% organic carbon, 9.2 pH, 2.21dSm^{-1} EC and 45 ESP. The climate of district Ayodhya is semi-arid with hot summer and cold winter.

One hundred twenty Fieldpea genotypes with four check varieties viz., Ambika, Rachna, HUDP 15 and HFP 8909 were evaluated in Augmented block design during *Rabi* 2015-16 at the Genetics and Plant Breeding Research Farm of Narendra Deva University of Agriculture and Technology, Narendra Nagar, Kumarganj, Ayodhya (U.P.). The seeds of different genotypes were available with the Pulses Section of the university. The entire experimental field was divided into 12 blocks of equal size and each block had 14 plots. Out of 14 plots in a block, 10 plots were used for accommodating the unreplicated test genotypes while 4 were allocated to the four check varieties. The four checks were randomly allocated along with the test genotypes in a block. Each plot consisted of a single row of 4 m length, following inter and intra row spacing 30 cm and 10 cm, respectively. Recommended cultural practices were practiced to raise a good crop.

The observations were recorded on randomly selected five competitive plants from each genotypes for nine characters viz., plant height (cm), number of primary branches per plant, number of pods per plant, pod length (cm), number of seeds per pod, 100-seed weight, biological yield per plant, harvest index and seed yield per plant (g), while two characters viz., days to 50 percent flowering,

days to maturity were recorded on the plot basis. Analysis of variance for augmented block design was done as per Federer (1956), GCV and PCV as per Burton & de Vane (1953), heritability in broad sense as per Hanson et al. (1963) and genetic advance as percent of mean was estimated using formula

suggested by Johnson et al. (1955). The ANOVA for different traits is given in table 1, estimates of GCV and PCV in table 2 and Estimates of heritability and genetic advance for 11 characters in Fieldpea are given in table 3.

Table 1: Analysis of variance for Augmented Block Design for 11 characters in Fieldpea genotypes

S.V.	df	Days of 50% flowering	Days to maturity	Plant height (cm)	Number of Pods/plant	Pod length (cm)	Number of Primary branches/plant	Number of Seeds/Pod	100-Seed weight (g)	Biological yield/plant (g)	Seed yield (g)	Harvest index (%)
Block (ignoring Treatments)	11	38.383 **	33.383 **	3339.912 **	16.654 **	4.035**	0.747**	5.076**	11.367**	53.927**	25.134**	86.862**
Checks	3	40.076 **	51.028 **	11884.360 **	9.629 **	0.449**	0.180	0.541**	11.369**	7.847**	1.604**	40.878**
ERROR	33	2.864	4.088	248.028	0.087	0.008	0.067	0.005	0.074	0.188	0.024	0.773

*,** Significant at 5% and 1% probability level respectively

Table-2: Range, mean, coefficient of variation and least significant differences for 11 characters of Fieldpea genotypes

Characters	Range (Min-Max)	Mean Value	Coefficient of variation (%)			Range of parameters			
			PCV (%)	GCV (%)	Coefficient of variation (%)	LSD ₁	LSD ₂	LSD ₃	LSD ₄
						5%	5%	5%	5%
Days to 50% flowering	61.188-77.938	71.458	5.524	4.989	6.377	1.406	4.870	5.444	4.007
Days to maturity	111.875-130.375	122.415	3.169	2.703	3.768	1.679	5.818	6.504	4.787
Plant height (cm)	12.700-139.650	74.659	35.597	28.690	38.197	13.081	45.313	50.662	37.286
Number of primary branches plant ⁻¹	0.718-2.697	1.433	28.317	21.789	29.253	0.215	0.746	0.834	0.614
Number of pods plant ⁻¹	10.885-26.060	15.282	14.571	14.442	16.863	0.245	0.850	0.950	0.699
Number of seeds pod ⁻¹	1.738-8.411	4.261	30.460	30.414	34.181	0.060	0.207	0.231	0.170
Pod length (cm)	3.005-9.018	5.293	22.786	22.720	25.659	0.076	0.263	0.294	0.216
100-seed weight (g)	10.872-27.432	18.348	14.463	14.386	16.163	0.226	0.783	0.875	0.644
Biological yield plant ⁻¹ (g)	15.999-38.913	26.101	15.047	14.955	17.107	0.360	1.247	1.394	1.026
Harvest index (%)	23.039-61.684	43.405	17.639	17.522	19.795	0.730	2.530	2.828	2.082

LSD₁ = difference between adjusted yield of two genotype in the same block.

LSD₂ = difference between two check means.

LSD₃ = difference between adjusted mean of two genotypes in the different block.

LSD₄ = difference between adjusted yield of genotype and check mean.

PCV = phenotypic coefficient of variance.

GCV = genotypic coefficient of variance.

Table 3: Estimates of heritability and genetic advance for 11 characters in Fieldpea

S.N.	Traits	$h^2(b)$	Genetic Advancement	Genetic advance as percent of mean
1	Days to 50 per cent flowering	81.56	6.62	9.28
2	Days to maturity	72.78	5.81	4.75
3	Plant height (cm)	64.96	35.59	47.63
4	Number of primary branches /plant	59.21	0.49	34.53
5	Number of pods/ plant	98.24	4.50	29.48
6	Number of seeds/ pod	99.69	2.65	62.55
7	Pod length (cm)	99.43	2.47	46.66
8	100-seed weight (g)	98.95	5.40	29.47
9	Biological yield/plant(g)	98.78	7.98	30.61
10	Harvest index (%)	98.68	15.54	35.85
11	Seed yield/plant(g)	99.78	6.84	59.41

RESULT AND DISCUSSION

The effectiveness of selection for any characters depends not only on the amount of variability for a character present in the population but also type of inheritance from parent to their off-springs. The heritable variation can be obtained through heritability and genetic advance of different characters.

From breeding point of view, only heritable component of the total variation is great importance for crop improvement. This revealed the imperative need of partitioning the overall variability into heritable and non heritable component with the help of heritability and genetic advance estimates. The heritability estimates along with genetic advance gives more reliable information than the heritability alone. Heritability estimate does not provide ample evidence regarding the amount of genetic progress, which could be possible through selection. If heritability is mainly due to non-additive gene effect, the value of genetic gain would be low but if heritability is mainly due to additive gene

effect the value of genetic gain would be high. In the present investigation sufficient variability was observed among all the genotypes for almost all the characters under study except number of primary branches per plant. This indicated that there were much more chances of selection according to our interest. Khan et al. (2017), Gudadinni et al. (2017), Pal and Singh (2012), Kumar (2008) and Ranjan et al. (2006) also found that the genotypes differed significantly for all the traits except the number of branches per plant. The estimates of genotype coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were observed and are given in Table 2. The genotypes showed moderate to high level of genotypic coefficients of variance (GCV) and phenotypic coefficients of variance (PCV). In general, phenotypic coefficient of variance was found to be higher than their genotypic coefficient of variance but difference was quite meager, indicating negligible environmental influence on the expression of the characters. Bashir et al.

(2017) and Meena et al. (2017) also reported that relative magnitude of phenotypic coefficients of variation was higher than genotypic coefficients of variation for all the characters under study. Higher estimate of PCV was recorded for plant height (35.597 %) followed by seeds per pod (30.460 %). While higher estimate of (GCV) was recorded for number of seeds per pod (30.414 %) and seed yield per plant (28.874 %). The characters which exhibited moderate estimates (between 14 to 22 %) of PCV and GCV were 100-seed weight, number of pods per plant, biological yield per plant, harvest index, pod length. While days to maturity exhibited lowest estimate of PCV (3.169) and GCV (2.703).

Heritability provides information about the transmissibility of characters from parents to their offspring; hence it is much more essential to know the magnitude of heritability of a trait for efficient selection strategy. Knowledge of heritability of a character is important as it indicates the possibility and extent to which improvement is possible through selection Robinson et al. (1949). In the present investigation it was found that almost all the characters under study were showed high heritability in broad sense. The higher value of broad sense heritability was reported for seed yield per plant (99.78%) followed by seeds per pod (99.69%), pod length, (99.43%), 100 seed weight (98.95%), biological yield per plant (98.78%), harvest index (98.68%), pods per plant (98.24), days to 50% flowering (81.56%), days to maturity (72.78%), plant height (64.96%) and primary branches per plant (59.21%). The higher value of genetic advance as percent of mean was reported for seeds per pod (62.55%), seed yield per plant (59.41%), plant height (47.63%), pod length (46.66%), harvest index (35.85%), primary branches per plant (34.53), biological yield per plant (30.61), pods per plant (29.48%), 100 seed weight (29.47%), days to 50% flowering (9.28%) and days to maturity (4.75%). The characters such as seeds per pod, seed yield per plant, pod length and harvest index, showed high GCV, heritability and genetic

advance would be more helpful in formulation of selection strategy for prediction of the gain under selection. Meena et al. (2017) also reported that high heritability with high genetic advance as per cent of F1 mean for plant height clusters per plant, pod bearing length, pods per plant and seed yield per plant. This finding is also in the agreement of Barcchiya et al. (2018), Gupta et al. (2018), Gudadinni et al. (2017), Singh, J.D., & Singh, I.P. (2006).

CONCLUSION

The characters such as seeds per pod, seed yield per plant, pod length and harvest index, showed high GCV, heritability and genetic advance indicated that these traits were least influenced by the environmental interactions. Thus, selection for these traits would be quite effective in enhancing grain yield per plant and also simultaneously its relative attributes. Therefore, emphasis should be paid on the above-mentioned traits for improving the productivity during selection.

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