

Original Research Article

<https://doi.org/10.20546/ijcmas.2023.1210.025>

## Studies on Genetic Variability, Heritability and Genetic Advance in Field Pea (*Pisum sativum* L)

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### ABSTRACT

Study on association analysis for seed yield and its yield contributing traits in field pea genotypes for characters to identify genotypes to be used in future breeding programme. The result showed high GCV and PCV was recorded for the characters number of primary branches per plant (GCV= 25.12; PCV= 26.87) followed by seed yield per plant(23.70 ; 26.17), harvest index(%) (23.49; 25.00) and number of pods per plant(19.40 ; 21.19). If the value of PCV is higher than the GCV, suggested that the apparent variation is not only due to genotypic but also due to the influence of environment. High heritability coupled with high genetic advance as percentage of mean reported in harvest index (88.28%), number of primary branches per plant (87.41%), number of pod per plant (83.88%), seed yield per plant(82.04%), pod length (80.01%) and number of seed per pod (78.69%). This indicated substantial of additive genetic variance in expression of these characters and can be useful in hybridization and selection for higher pod yield.

#### Keywords

Assessment, genetic variability, heritability, genetic advance, pea (*Pisum sativum* L.)

#### Article Info

##### Received:

05 August 2023

##### Accepted:

28 September 2023

##### Available Online:

10 October 2023

### Introduction

The field pea (*Pisum sativum* L.) is a self-pollinated crop with chromosomal number  $2n=14$  that belongs to the Papilionaceae sub family of the Leguminosae family and commercially grown worldwide, is generally used as vegetable as well as pulse crop (Dhar *et al.*, 2001). Vavilov (1926) cited a number of different pea origins based on genetic diversity the area including Central Asia, the Near East, Abyssinia, and the Mediterranean is the centre of origin. Field pea world's third most significant grain

legume after beans and chickpea. The crop is grown for its soft and immature pods, which can be used as a vegetable and mature dry pods, which can be used as a pulse. Field pea are strong in digestible protein (22.5%), carbohydrate (62.1%), fat (1.8%), moisture (11%), vitamin- C (9 mg), phosphorus (139 mg), calcium (64 mg/100g) and iron (4.8 mg/100g) (Gueguen and Barbot, 1988).

Soups with tender seeds canned, frozen, and dehydrated peas are frequently used during the off-season. Because of its soil enriching and

conditioning capabilities, pea is an important part of sustainable agriculture.

Heritability used in the fields of breeding and genetics that estimates the degree of variation in a phenotypic trait in a population that is due to genetic variation between individuals in that population.

The value of heritability is determined by all of the components of variance and any change in one of them will impact the estimations. It's vital to remember that heritability estimates vary depending on the population under investigation and the environmental conditions to which the individuals are exposed.

### **Materials and Methods**

The present experiment was conducted Instructional cum Research Farm of S.G. College of Agriculture and Research Station, Kumhrawand, Jagdalpur during *rabi season* 2017-18.

The experimental materials consisted of 10 F<sub>1</sub>s from a 5x5 half diallel cross involving five parents of field pea which were cultivated in three replications with a Randomized Complete Block Design (RBD). The crop was successfully raised by following recommended agronomic practices during period of crop growth.

Five plants selected at random per variety per replication avoiding border plants were tagged, which constituted the sample for observations. Observations were recorded on 11 different traits. Phenotypic and genotypic co-efficient of variation, heritability and genetic advance were estimated.

### **Results and Discussion**

Analysis of variances recorded that mean sum square due to genotypes was highly significant for all the characters (Table.1). The extent of genetic variability, phenotypic and genotypic co-efficient of variation, heritability and genetic advance for different traits (Table.2) showed wide range of

variability for all the traits. High (>20%) GCV and PCV were observed for number of primary branches per plant (25.12) and (26.87) followed by seed yield per plant (g) (23.70; 26.17), harvest index (%) (23.49; 25.00), one characters the high PCV and moderate GCV was recorded of pods per plant (21.19; 19.40). Moderate (10-20%) GCV and PCV was recorded for number of secondary branches per plant (16.36; 18.64), plant height (cm) (14.91; 17.17), pod length (cm) (11.53; 12.89), number of seeds per pod (10.10; 11.38) respectively. Similar phenotypic and genotypic coefficient of variation result reported by Tiwari and Lavanya (2012) and Afreen *et al.*, (2017). The nature and extent of genetic variability is one of the most important criteria in formulating an efficient breeding programme and knowledge of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) is much helpful in predicting the amount of variation present in a given genetic stock.

In present investigation the high heritability(>70%) was recorded for the character harvest index (88.28%) followed by number of primary branches per plant (87.41%), number of pods per plant (83.88%), seed yield per plant (82.04%), pod length(80.01%), number of seeds per pod (78.69%), number of secondary branches per plant (77.04%) and plant height (75.41%).

The Genetic advances as percent of mean was observed high(>20%) for character number of primary branches per plant (48.39%), followed by harvest index(45.47%), seed yield per plant (44.22%) number of pods per plant (36.61%), number of secondary branches per plant (29.58%) plant height (26.66%) and pod length(21.24%). High heritability coupled with high genetic advance as percent of mean are controlled by additive gene action and high heritability values indicated that the characters under study were less influenced by environment in their expression. Similar result of found by Bijalwan *et al.*, (2018) and Kumar *et al.*, (2019).

**Table.1** Analysis of variance for parent, hybrids and check in field pea

Sourced of variation	df	DFF	PH(cm)	DM	NPB/P	NSB/P	PL(cm)	P/P	NS/Pod	TW (g)	HI(%)	SY/P(g)
<b>REP</b>	2	5.15	22.00	16.90	0.03	8.27	0.02	4.78	0.21	1.33	13.80	10.28
<b>Genotypes</b>	15	18.65**	474.37**	43.42**	0.97**	11.15**	1.39**	32.02**	0.95**	3.92**	59.05**	26.55**
<b>EROR</b>	30	3.68	46.51	8.50	0.04	1.01	0.11	1.93	0.08	0.75	2.50	1.81
<b>C.D. at 5%</b>		3.214	11.428	4.884	0.17	1.703	0.551	2.329	0.47	1.455	2.578	2.252
<b>C.V. (%)</b>		3.264	8.513	3.119	9.436	9.18	5.848	8.656	5.254	5.512	8.457	11.297
<b>Total</b>	47	8.52	182.02	20.00	0.34	4.55	0.51	11.65	0.36	1.79	21.03	10.06

\*, \*\* significant at 5% and 1% level of significance. DFF= Days to 50 percent flowering, DM= Days to maturity, PH= Plant height, NPBPP=Number of primary branches per plant, NSBPP =Number of secondary branches per plant, NPPP= Number of pods per plant, PL= Pod length, NSPP= Number of seeds per pod, SYPP= Seed yield per plant, HI= Harvest index, TW (g) = 100 seed weight.

**Table.2** Genetic parameters of variation for seed yield and its component traits in field pea

S. No.	Characters	Mean	Min	Max	GCV (%)	PCV (%)	Heritability(bs) (%)	GA% mean
<b>1</b>	Days of 50% flowering	58.77	54.33	65.33	3.80	5.01	57.57	<b>5.94</b>
<b>2</b>	Plant height	80.12	52.17	92.67	14.91	17.17	75.41	<b>26.66</b>
<b>3</b>	Days of maturity	93.46	88.33	105.33	3.65	4.80	57.81	<b>5.72</b>
<b>4</b>	No. of primary branches/plant	2.21	1.60	3.60	25.12	26.87	87.41	<b>48.39</b>
<b>5</b>	No. of secondary branches/plant	11.24	7.70	15.23	16.36	18.64	77.04	<b>29.58</b>
<b>6</b>	Pod length	5.67	4.57	6.70	11.53	12.89	80.01	<b>21.24</b>
<b>7</b>	Pod/plant	16.32	12.49	25.72	19.40	21.19	83.88	<b>36.61</b>
<b>8</b>	Number of Seed /pod	5.34	4.20	6.37	10.10	11.38	78.69	<b>18.45</b>
<b>9</b>	100 seed weight(g)	15.76	13.47	18.03	6.52	8.54	58.33	<b>10.26</b>
<b>10</b>	Harvest index(%)	18.48	12.03	31.29	23.49	25.00	88.28	<b>45.47</b>
<b>11</b>	<b>Seed yield /plant(g)</b>	<b>12.12</b>	<b>8.02</b>	<b>20.86</b>	<b>23.70</b>	<b>26.17</b>	<b>82.04</b>	<b>44.22</b>

From the present study, it could be concluded that PCV and GCV were high for number of primary branches per plant, seed yield per plant (g) and harvest index, where high heritability coupled with high genetic advance as percentage of mean reported in harvest index, number of primary branches per plant, number of pod per plant which indicated that high degree of variability in these characters and suggested that possibility of yield improvement through selection of this trait.

## References

- Afreen, S., Singh, A. K., Moharana, D. P., Singh, V., Singh, P. and Singh, B. (2017). Genetic evaluation for yield and yield attributes in garden pea (*Pisum sativum* var. *hortense* L.) under North Indian gangetic plain conditions. *Int. J. Curr. Microbiol. App. Sci*, 6(2): 1399- 1404.
- Bijalwan, P., Raturi, A. and Mehra, A. C. (2018). Genetic variability, heritability and genetic advance studies in pea (*Pisum sativum* L.) for yield and quality traits. *J Chem. Stud*. 6(5): 3303- 3307.
- Dhar, S. S., G. Singh., A. Yadav., V. Mittal., D. V. Singh and B. Singh. 2001. Seasonal incidence of the pod borers, *Etiella zinckenella* (Treitschke) and *Helicoverpa armigera* (Hubner) on vegetable pea in Meerut. *Annals of Horticulture*, 4(1): 89-94.
- Gueguen, J. and Barbot, J. 1988. Quantitative and qualitative variability of pea (*Pisum sativum* L.) protein composition. *Journal of the Science of Food and Agriculture*.42: 209-224.
- Kumar, N., Mishra, S., Pandey, S., Mishra, D. P. and Pandey, V. P. (2019). Studies on phenotypic and genotypic coefficient of variation (PCV and GCV) between different characters in Pea (*Pisum sativum* L.) genotypes in sodic condition. *J Pharmacogn Phytochem*. 8(1): 349-351.
- Tiwari, G. and Lavanya, G. R. (2012). Genetic variability, character association and component analysis in F<sub>4</sub> generation of field pea (*Pisum sativum* var. *arvense* L.). *Karnataka Journal of Agricultural Science*, 25(2): 173-175.
- Vavilov, N. I. Origin and Geography of Cultivated Plants. Ed. V. F. Dorofeyev, Trans. Doris Loeve. Cambridge: Cambridge University Press, 1992.

### How to cite this article:

Lokesh, P., R. R. Kanwar, Sonali Kar, A. Sao, A. K. Gupta, Ravi R. Saxena and Mandavi, J. S. 2023. Studies on Genetic Variability, Heritability and Genetic Advance in Field Pea (*Pisum sativum* L.). *Int.J.Curr.Microbiol.App.Sci*. 12(10): 229-232. doi: <https://doi.org/10.20546/ijcmas.2023.1210.025>