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ESTIMATION OF GENETIC VARIABILITY, HERITABILITY AND GENETIC ADVANCE FOR YIELD AND YIELD-CONTRIBUTING TRAITS IN FIELD PEA (*Pisum sativum* L.)

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ABSTRACT

Pea (*Pisum sativum* L.) is a grain legume crop grown globally for human consumption and good source of protein. An experiment was conducted in augmented randomised complete block design to estimation of genetic variability, heritability and genetic advance in field pea among fifty-four genotypes with twelve traits. The ANOVA results indicated substantial variations among the genotypes for all traits, demonstrating a broad spectrum of variability among them. The result shows that found were highly significant for the trait Days to 50% flowering, Number of pods per plant, Number of seeds per pod, 100 seed weight (gm) and Yield per plant (gm) Days to Maturity, Plant Height (cm) and moderately significant in the characters Number of Primary branches per plant, Pod length (cm). These traits which are superior and used to select cultivars for yield augmentation showed the highest values of genetic variability (PV 27.01, 25.74) and genetic coefficient of variation (GCV 5.89, 5.56) among harvested traits; while the lowest heritability (15.38%) and Genetic advance as a percentage of mean was classified as high genetic advance (>20%), medium genetic advance (10%-20%) and low genetic advance (<10%) 2025The highest percent of mean genetic advance was recorded for biological weight (50.60 %), days to maturity (27.86 %) and plant height (17.91 %) low genetic advance values was observed for the number of seeds per plant (5.48%), harvest index (5.07%), number of seeds per pod (5.06%), days to 50% flowering (4.85%), seed yield per plant (4.34%), 100-seed weight (2.18%).

Keywords : Heritability, Genetic advance, Variability, Characters

Introduction

Field Pea is an important legume cultivated worldwide for human consumption. It is an excellent source of protein while its root nodules improve fertility of the soil. (Singh *et al.*, 2025). The pea having a chromosome number $2n = 14$, belongs to the leguminosae family (Fabaceae) and ranks among the most important annual herbaceous legume crops in India. It is valued for its role as a fresh vegetable and in processed, canned or dehydrated form, while its dry seeds are eaten as pulses. Peas are grown plants with branched taproot structure where seeds lack endosperm and have thick cotyledons. (Risipail *et al.*, 2024). The field pea comes from the Mediterranean region, extending from southern Europe to western Asia. It probably originates from an area that comprises Italy,

southwestern Asia and stretches eastward to the Himalayas, encompassing portions of northern India. (Anchal Thakur *et al.*, 2024). Pea possess a considerable amount of protein in seed and tender pods which is the primary nutrient, accounting for 15–30% of their dry weight. The levels of protein vary between 20% and 25%. (Deka *et al.*, 2021) One of the main goals of pea breeding programs is still to generate genotypes with high genetic potential for fodder and seed yield. To achieve the greatest genetic potential and boost productivity, it is crucial to identify and produce high-yielding cultivars that are specifically suited to target environments, as genotypes frequently show differential performance across agroecological regions. Therefore, in order to find superior genotypes that can be used in future breeding programs, it is essential to explore and characterize various pea

germplasm. Any successful crop improvement program is built on genetic variability since the degree of variety in the breeding material determines how effective selection is. There are more options for choosing suitable genotypes with enhanced agronomic performance when the genetic basis is larger.

However, the degree of genetic diversity is not sufficiently reflected by the absolute variability found in many phenotypes alone. Therefore, in order to evaluate the degree of variability and differentiate genetic impacts from environmental factors, it is required to estimate phenotypic and genotypic coefficients of variation. Heritability is a good predictor of the response to selection combined with genetic advancement. High heritability and high genetic advancement indicate more potential for genetic improvement and the prevalence of additive gene action. Therefore, determining suitable breeding materials and creating better pea cultivars depend on the evaluation of genetic variability, heritability, and genetic advance for economically significant features. Taking these factors into consideration the current study was conducted to estimate the degree of genetic variability, heritability, and genetic advancement among pea genotypes.

Materials and Method

The experiment was conducted in the rabi season (2024-2026) at crop research centre-I, Sithouli Campus, ITM University, Gwalior, located in the gird agroclimatic zone of Madhya Pradesh. Total fifty genotypes along with four checks of field pea were assessed for fourteen economically significant traits during the rabi season-I (2024-2025) and season-II (2025-2026). The experimental location was positioned at 26°08'22.6" N latitude, 78°11'42.9" E longitude with an elevation of 211.5 m. The experiment was organised into five blocks, featuring a total of 70 plots. The size of each plot was 2.5x2.5 m (6.25 m²) spaced 30x15 cm apart between rows and plants. The total area used for the experiment was 577.5m² and the net experimental area used was 437.5 m². The experiment was designed in Augmented Randomised Complete Block Design (ARCBd) with four checks. The mean values of different genotypes for all the characters were subjected to analysis of variance to determine the significance of differences among genotypes as per procedure given by Panse and Sukhatme (1967) and

method suggested by Fisher (1954). The PCV and GCV have been calculated and categorized as low (below 10%), medium (10–20%) and high (beyond 20%) as described by Deshmukh *et al.* (1986). Heritability (h²) Broad sense heritability represents the proportion of genotypic variance. The heritability estimates (BS) for all traits were classified as very high (over 90%), high (70 to 90%), medium (50-70%), and low (under 50%). Genetic advance as a percentage of mean was classified as high genetic advance (>20%), medium genetic advance (10%-20%) and low genetic advance (<10%) as described by Johansson *et al.* (1955).

Results and Discussion

The Analysis of Variance (ANOVA) of Rabi season 2024-2025, 2025-2026 indicated that the mean sum of squares for fifty four genotypes of field pea were found highly significant for the traits like Days to 50% flowering, Number of pods per plant, Number of seeds per pod, 100 seed weight (gm) and Yield per plant (gm) Days to Maturity, Plant Height (cm) and moderately significant for the traits like Number of Primary branches per plant, Pod length (cm).

Kumar *et al.* 2022 showed high level of significance for all the characters studied in the advanced breeding lines of field pea which indicates that useful variability was present amongst the genotypes. The differences noted between the various plants are quite large for the four green plant parameters (plant height, number of branches per plant, number of pods per plant, number of seeds per pod) and for seed yield. Varma *et al.*, 2023 found seed yield as highly significant for different varieties and also observed the highly significant difference for plant height, number of pods per plant and other yield attributes in field pea. The ANNOVA results showed the significant differences in genotype implying that selection should be able to be used to further enhance their productivity. Parth *et al.*, 2024 found substantial significant ANOVA results in field pea for plant height, branches per plant, pods per plant, seed yield, and test weight. A notable genetic variation exhibited moderate to high heritability and genetic improvement for the majority of traits, indicating that additive gene action played a crucial role in trait expression, thereby enhancing the effectiveness of direct selection for yield enhancement.

Table 1: Analysis of Variance Among Fifty four Field Pea Genotypes for Twelve Trait.

S. No	Source		D.F	DF	PH	DM	NPB	PL	PPP	SPP	SPPL	100SW	BW	HI	YPP
1.	Blocks	E-1	4	4.23**	503.78**	256.76**	1.17*	36.24**	16.55	4.69	46.16	2.63	2387.77	29.85	9.01
		E-2	4	163.08	322.68	591.31	0.53	1.15	4.75	0.64	11.81	11.81	177.94	6.61	12.06
		POOLED	4	38.88	267.83	241.59	0.20	4.58	69.99	1.83	2.68	2.21	197.22	2.93	3.68

2.	Treatment	E-1	53	6.78**	333.79**	78.52**	0.84**	9.84*	14.77	0.99	40.20	5.29	456.01	7.23	7.43
		E-2	53	46.06	379.12	379.41	0.54	1.36	15.14	0.68	7.73	7.73	303.51	5.34	3.4
		POOLED	53	15.53	242.83	147.50	0.86	7.16	31.71	0.46	6.74	2.02	446.60	5.77	3.45
3.	Treatment Check	E-1	3	10.58**	851.82**	162.80**	2.11**	1.60	65.65	0.06	201.78	22.79	201.64	30.02	31.21
		E-2	3	12.23	877.45	1256.18	0.66	1.13	33.80	0.86	1.73	1.73	390.66	2.65	2.57
		POOLED	3	1.27	858.78	548.98	2.87	5.25	29.22	0.26	11.75	3.58	1878.54	23.06	2.85
4.	Treatment: Test vs. Check	E-1	50	6.55**	302.71**	73.46**	0.76**	10.34*	11.72	1.05	30.50	4.24	471.27	5.87	6.00
		E-2	50	48.09	349.22	326.80	0.53	1.37	14.02	0.67	8.09	8.09	298.28	5.51	3.4
		POOLED	50	16.39	205.87	123.41	0.74	7.28	31.86	0.47	6.44	1.92	360.68	4.73	3.48
5.	Residuals	E-1	12	0.75	0.86	6.22	0.22	3.58	4.15	0.70	3.32	1.51	7.17	0.68	0.94
		E-2	12	2.43	16.23	2.39	0.15	0.17	7.47	0.55	4.62	4.62	16.63	0.76	0.99
		POOLED	12	0.93	4.90	2.53	0.16	0.17	2.65	0.36	3.75	0.86	11.32	0.35	0.69
6.	Std. error	E-1	-	1.06	1.13	3.05	0.58	2.32	2.49	1.02	2.23	1.51	3.28	1.01	1.19
		E-2	-	1.91	4.93	1.89	0.48	0.50	3.35	0.90	2.63	2.63	4.99	1.07	1.22
		POOLED	-	1.18	2.71	1.95	0.48	0.50	2.00	0.73	2.37	1.14	4.12	0.72	1.02
7.	CD 5%	E-1	-	2.31	2.47	6.65	1.27	5.05	5.44	2.23	4.87	3.28	7.15	2.19	2.59
		E-2	-	4.16	10.75	4.13	1.04	1.09	7.29	1.97	5.73	5.73	10.88	2.32	2.66
		POOLED	-	2.58	5.91	4.24	1.05	1.10	4.35	1.59	5.16	2.48	8.98	1.58	2.22

The phenotypic variation coefficient, genotypic variation coefficient for heritability, and genetic advance for the years 2025 and 2026.

The PCV and GCV have been calculated and categorized as low (below 10%), medium (10–20%) and high (beyond 20%) as described by Deshmukh *et al.* (1986). In the Year 2025 Harvest index (27.01%), number of pods per plant (22.47%) and number of seeds per plant (13.86%) showed high PCV and moderate PCV was observed for biological weight (17.60%), number of primary branches per plant (18.31%), 100-seed weight (11.02%), plant height (7.94%), days to maturity (8.48%), days to 50% flowering (5.89%) and number of seeds per pod (5.06%). Seed yield per plant (25.74%), number of seeds per pod (25.74%), harvest index (19.14%), number of pods per plant (18.65%) and 100-seed weight (17.49%) had showed high genotypic coefficient of variance (GCV) and number of seeds per plant, biological weight, days to 50% flowering, pod length and number of primary branches per plant exhibited moderate GCV (22.83%, 16.70%, 11.84%, 11.84% and 11.69%, respectively). Days to maturity (8.29%) and plant height (4.17%) have shown lowest GCV.

In the year 2026, Harvest index, number of seeds per plant and number of pods per plant showed a high phenotypic coefficient of variation (PCV) (22.91%, 21.93% and 15.46% respectively). Moderate PCV was observed for days to 50% flowering (16.90%), biological weight (14.06%), number of primary branches per plant (12.98%), number of seeds per pod (17.55%), 100-seed weight (17.06%) and plant height (12.38%). Harvest index (25.30%) number of seeds per pod (21.35%) and plant yield (21.35%) showed the highest genotypic coefficient of variation (GCV) while

days to 50% flowering (20.27%) had the lowest GCV. Moderate GCV was observed for pod length (20.27%), biological weight (14.05%), 100-seed weight (13.66%), number of pods per plant (13.24%), plant height (12.23%), number of seeds per plant (11.86%), and days to maturity (11.86%). The smallest GCV occurred with number of primary branches/plant (5.09%). Heritability (Broad Sense) components were used to estimate the relative contribution of genetic and environmental factors to the expression of all characters and the heritability (BS) was calculated. Heritability estimates were classified as very high (>90%), high (70–90%), moderate (50–70%), and low (<50%) In the Year 2025 Days to maturity (95.84%), number of pods per plant (92.53%), pod length (92.88%) and days to 50% flowering (90.80%) had very high heritability. The heritability was high for number of seed per plant (89.19%). There was moderate heritability for 100 seed weight. The other traits had less heritability estimates, suggesting that environmental factors have more influence on their expression.

In the year 2026 The heritability of number of seeds per plant was very high (96.10%), days to maturity was also very high (94.35%), number of pods per plant was very high (94.87%) and pod length was very high (99.22%). High heritability was observed for days to 50% flowering (86.84%). Heritability for 100-seed weight was moderate, and the other traits had lower levels of heritability, indicating that the environment has a greater effect on the expression of these traits. The genetic advance that estimates the selection intensity (k) was 5% which gave the estimated genetic advance under selection (g) at 2.06. There was a great deal of variation in genetic advance as percent of mean between traits suggesting

differential responses to selection and the effect of the environment on the expression of the traits. In the year 2025 The highest percent of mean genetic advance was recorded for biological weight (50.60 %), days to maturity (27.86 %) and plant height (17.91 %). The average genetic advance was moderate for pod length (10.69%). However, low genetic advance values was observed for the number of seeds per plant (5.48%), harvest index (5.07%), number of seeds per pod

(5.06%), days to 50% flowering (4.85%), seed yield per plant (4.34%), 100-seed weight (2.18%), number of primary branches per plant (1.91%), and number of pods per plant (1.21%). In 2026, plant height (35.85%), days to maturity (34.80%), and biological weight (33.41%) exhibited the highest genetic advance as a percentage of the mean. A moderate genetic improvement of 15.65% was observed for Days to 50% Flowering

Table 2 : Genotypic coefficient of variation (GCV %), Genotypic coefficient of variation (PCV %), Heritability Broad sense and genetic advance (GA) for different characters.

Trait	PCV			GCV			Heritability			Genetic Advance		
	E1	E2	Polled	E1	E2	Polled	E1	E2	Polled	E1	E2	Polled
Days of Flowering	5.89	16.97	9.69	5.56	16.63	9.46	89.19	96.1	95.3	4.85	15.65	8.77
Days to maturity	19.19	25.97	15.91	19.14	25.3	15.59	92.53	94.87	96	27.86	34.8	21.93
Plant height	7.94	12.38	8.76	7.66	12.33	8.68	92.88	99.22	93.04	17.91	35.85	22.94
Number of pods per plant	22.47	15.46	20.5	18.65	13.24	17.38	68.88	73.36	71.86	1.21	1.14	1.1
Number of seeds per plant	13.86	21.93	49.4	11.84	20.27	48.86	72.98	85.41	97.81	5.48	1.89	5.61
Number of seeds per pod	5.06	17.55	8.43	4.17	12.23	8.12	68.03	48.55	92.72	5.06	3.82	11.55
Number of Primary branches per plant	18.31	12.98	11.59	11.69	5.09	6.08	40.76	15.38	27.53	1.91	1.25	3.4
Pod Length	24.07	17.06	11.74	22.83	11.86	7.81	89.97	48.32	44.26	10.69	2.98	2.37
100seed weight	11.02	17.06	10.24	8.29	11.86	7.82	56.62	48.32	58.34	2.18	2.98	1.73
Biological Weight	17.6	14.06	15.27	17.49	13.66	15.04	95.84	94.35	96.91	50.64	33.41	38.28
Harvest index	27.01	22.91	19.07	25.74	21.35	18.31	90.8	86.84	92.21	5.07	4.3	4.03
Seed yield per plant	18.15	16.15	13.76	16.7	14.05	12.34	84.7	75.68	80.36	4.34	3.15	3.11

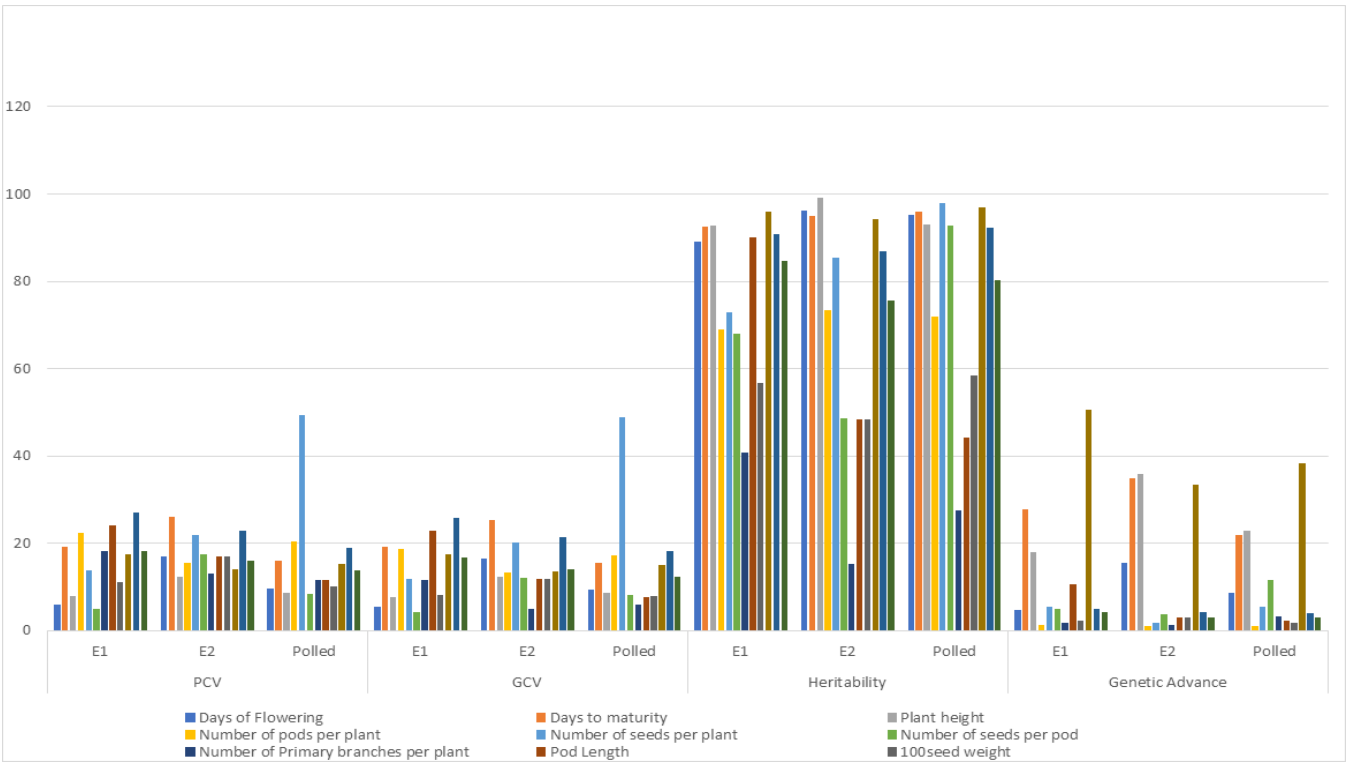


Fig. 1 : Graphical View of Variability Parameters

Meena *et al.*, 2017 found PCV values were higher than the corresponding GCV values for all the traits, which showed the effect of the environmental factors on the expression of the traits studied. Further, reported

that higher PCV than GCV over all yield and yield contributing traits of field pea indicated environmental modification of the phenotypic expression. Singh *et al.*, 2013 found the small difference in days to flowering

and days to maturity between PCV and GCV showed that the environment had little influence and that genetic factors have more influence on the control of these traits. In a similar study, have inferred that traits having similar PCV and GCV are less responsive to environmental changes and hence selection can be effective.

Jaiswal *et al.* (2015) there is a significant genetic variability among the genotypes as revealed by high PCV and GCV values obtained for number of pods per plant, seed yield per plant and harvest index recorded higher GCV and PCV for plant height and seed yield per plant and number of seeds per pod for plant pea in the field.

Saxena *et al.* (2014) The high heritability estimates obtained for days to maturity, plant height, biological weight and seed yield per plant indicate that these characters are mainly genetic in nature and less influenced by environment. The same results in field pea for plant height and flowering characteristics.

Meena *et al.* (2017) High heritability coupled with high genetic advance for biological weight, plant height and days to maturity indicates the predominance of additive gene action and greater effectiveness of direct selection.

Conclusion

In this study, a total of Fifty four genotypes were assessed using an Augmented Randomised Complete Block Design, involving twelve traits. The experimental design replicated the test genotypes across five blocks alongside four checks. The results indicated that traits such as Days to 50% flowering, Number of pods per plant, Number of seeds per pod, 100 seed weight (grams), and Yield per plant (grams) exhibited highly significant differences. Additionally, Days to Maturity, Plant Height (cm) showed moderately significant results in the variability parameters. Among these, the Harvest Index (PCV 27.01, GCV 25.74) and Seeds per plant (PCV 49.40) demonstrated the greatest genetic variability, while Days to Flowering (PCV 5.89, GCV 5.56) showed the least. heritability, Biological Weight (GA 38.28, heritability 96.91%) and Plant Height (GA 35.85, heritability 99.22%) displayed the highest genetic advancement. Consequently, this demonstrates the presence of additive gene action for these traits, which is advantageous and should be considered when selecting cultivars to enhance yield. These traits need to be taken into account.

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