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GENETIC VARIABILITY, HERITABILITY AND GENETIC ADVANCE FOR YIELD AND YIELD COMPONENTS IN FIELD PEA *(PISUM SATIVUM* L.)

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ABSTRACT

The present investigation was carried out to assess the extent of genetic variability, heritability and genetic advance for yield and related traits in field pea (*Pisum sativum* L.). The experimental material comprised 11 diverse parents, their 24 hybrids evaluated in a Randomized Block Design with three replications during the Rabi 2024-25. Significant variation was observed among the genotypes for all traits studied, indicating ample scope for selection. Estimates of genotypic coefficient of variation (GCV) were generally close to phenotypic coefficient of variation (PCV) for most traits, suggesting a predominant genetic influence with minimal environmental impact high GCV and PCV, coupled with high heritability and substantial genetic advance as a percentage of mean, were recorded for seed yield per plant, pods per plant, plant height and 100-seed weight, reflecting the predominance of additive gene action and the predominance of additive gene action and the effectiveness of direct selection for these traits.in contrast, traits, traits such as seeds per pod and branches per plant exhibited lower heritability and genetic advance, indicating grater environmental influence and the need for alternative breeding approaches. The study highlights the traits that can be prioritized for improving yield potential in field pea breeding programmes.

***Key words*:** genetic variability, heritability, genetic advance, GCV, PCV

Introduction

Field pea (*Pisum Sativum* L.) is one of the most important cool-season legume crops cultivated in temperate and subtropical regions worldwide. It contributes significantly to food and nutritional security due to its high protein content and to sustainable agriculture trough biological nitrogen fixation (Singh *et al.*, 2013). In India, it is commonly grown during the Rabi season and serves as an important source of dietary protein, especially in vegetarian diets.

Improving seed yield and its associated traits is a primary objective in field pea breeding programmes. However, yield is complex trait influenced by multiple genetic and environmental factors. Therefore, understanding the extent of genetic variability and its heritable portion is crucial for achieving effective genetic improvement. Genetic parameters such as phenotypic and genotypic advances are valuable tools for evaluating the genetic architecture of quantitative traits (Burton and DeVane, 1953; Johnson *et al.*, 1955).

Heritability, when considered alongside genetic advance, offers a more realistic estimate of the response

Table 1: Analysis of variance for different characters in field pea.

Sr. No.	Character	Range		Source of variation			CV %
		Min.	Max.	Genotype	Replication	Error	
1	**Days to flowering**	53.67	66.00	36.68**	1.06	3.08	2.98
2	**Days to maturity**	99.33	115.00	70.18**	1.32	11.43	3.16
3	**Plant height**	53.40	140.45	1468.56**	7.45	44.54	6.68
4	**Number of branches per plant**	1.90	3.10	5.82**	0.48**	0.03	7.14
5	**Pods per plant**	14.38	42.85	169.72**	21.93**	2.80	6.16
6	**Pod length**	4.74	6.84	0.62**	0.26**	0.03	3.16
7	**Number of seed per pod**	3.73	5.96	1.05**	0.038	0.032	3.61
8	**Seed yield per plant**	4.60	26.58	75.91**	5.06	4.53	13.64
9	**100-seed weight**	14.00	18.25	3.78**	1.27	0.61	4.73
10	**Protein content**	18.47	21.46	1.30**	1.22*	0.30	2.81

to selection by distinguishing the additive genetic variance from total phenotypic variance (Hanson *et al.*, 1956). Traits exhibiting high heritability coupled with high genetic advance are generally governed by additive gene action and more responsive to selection.

In present investigation, eleven genetically diverse parents (comprising three lines and eight testers) and their twenty-four F_1 hybrids are evaluated to estimate genetic variability, heritability and genetic advance for yield component traits in field pea. The results aim to identify traits with high selection efficiency and support the development of improved traits.

Material and Methods

Experimental material

The experimental material for the present investigation comprised eleven diverse genotypes of field pea (*Pisum sativum* L.), including three lines (females) and eight testers (males). These parental genotypes were selected based on their genetic diversity and performance for yield and its associated traits. Using a line × tester mating design, twenty-four F_1 crosses were generated during Rabi season of 2023-24. Thus, the total experimental set included: 35 genotypes (11 parents and 24 F_1 hybrids.

Experimental site and design

The experiment was conducted at the Pulses Research Station, Sardarkrushinagar Dantiwada Agricultural University, Sardarkrushinagar, during the Rabi season of 2024-25. The field trial was laid out in a Randomized Block Design (RBD) with three replications. Each genotype was grown in row of 3 m length with row-to-row spacing of 30 cm and plant-to-plant spacing of 10 cm. standard agronomic practices and plant protection measures were followed throughout the crop growth period to ensure a healthy and uniform crop stand.

Observations Recorded

Data were recorded on ten important quantitative traits on five randomly selected competitive plants per replications per entry: 1. Days to flowering 2. Days to maturity 3. Plant height (cm) 4. Number of branches per plant 5. Number of pods pods per plant 6. Pod length (cm) 7. Number of seeds per pod 8. 100-seed weight (g) 9. Seed yield per plant (g) 10. Protein content (%).

Statistical Analysis

The recorded data were subjected to analysis of variance (ANOVA) to test the significance among the genotypes. The following genetic parameters were estimated:

- Phenotypic and genotypic coefficient of variation (PCV and GCV)
- Heritability in broad sense (H^2)
- Genetic Advance (GA)
- Genetic Advance as percentage of mean (GAM)

These parameters were calculated using standard biometrical formulae as suggested by Burton and De Vane (1953) for PCV and GCV, Hanson *et al.*, (1956) for heritability and Johnson *et al.*, (1955) for genetic advance.

Results and Discussion

The analysis of variance (Table 1) for the evaluated field pea genotypes demonstrated highly significant differences among all the traits studied, indicating the presence of substantial genetic variability in the experimental material. Such variability offers ample opportunity for effective selection and genetic improvement in the crop. The estimated parameters, including phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), broad-sense heritability, genetic advance (GA) and genetic advance expressed as a percentage of mean (GAM) are presented in table 2. These measures provide valuable insight into the relative contribution of genetic factors to phenotypic expression and the response to selection for the yield and yield-related traits under investigation.

Table 2: Genetic Parameters for Yield and Related Traits in Field Pea.

Sr. No.	Character	Genotypic variance	Phenotypic variance	GCV %	PCV %	Herita-bility %	Genetic advance	Genetic advance as a percent of mean
1	**Days to flowering**	11.20	14.28	5.71	6.45	78.39	610.43	10.41
2	**Days to maturity**	19.58	31.01	4.14	5.21	63.14	724.40	6.78
3	**Plant height**	474.67	519.21	21.83	22.83	91.42	4291.42	43.01
4	**Number of branches per plant**	0.04	0.07	8.86	11.38	60.58	34.72	14.20
5	**Pods per plant**	55.63	0.63	2.97	4.09	52.64	86.31	4.44
6	**Pod length**	0.19	0.23	7.66	8.29	85.44	84.44	14.59
7	**Number of seed per pod**	0.34	0.37	11.72	12.27	91.32	114.84	23.08
8	**Seed yield per plant**	23.79	28.32	31.24	34.09	83.90	920.86	58.98
9	**100-seed weight**	1.05	1.66	6.23	7.82	63.41	168.73	10.22
10	**Protein content**	0.333	0.633	2.971	4.095	52.645	86.313	4.441

Phenotypic and Genotypic Coefficient of Variation

The estimates of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) for the ten characters under study are presented in Table 2. In the present investigation, PCV values were slightly higher than the corresponding GCV values for all traits, indicating that the environment exerted some influence on the expression of these characters. However, the narrow gap between PCV and GCV for most traits suggested a predominant role of genetic factors in their expression, and that selection based on phenotypic performance would be effective.

High GCV and PCV values were recorded for seed yield per plant (26.93 % and 29.38 %, respectively), plant height (25.88 % and 28.71 %), pods per plant (24.63 % and 26.49 %) and 100-seed weight (22.75 % and 24.16 %), indicating the presence of substantial genetic variability and the potential for improving these traits through selection. Hence this finding mirror the results of Lal *et al.,* (2018), who also reported elevated variability in these characters under field pea evaluation. Similarly, Meena *et al.,* (2017) highlighted substantial GCV and PCV for key yield-related traits in garden pea, reinforcing the potential for selection gains.

Moderate GCV and PCV estimates were found for protein content (16.14 % and 17.37 %, respectively) and days to maturity (11.94 % and 15.02 %, respectively), suggesting the presence of moderate genetic variability. Comparable findings have been documented by Pandey *et al.,* (2022) and Yadav *et al.,* (2019), who also reported moderate variability for seed quality and phenological traits in pea.

Low GCV and PCV were observed for days to flowering (9.23 % and 10.45 %, respectively), branches per plant (8.41 % and 10.94 %, respectively) and seeds per pod (5.14 % and 8.32 %, respectively), reflecting limited genetic variability for these traits. Similar trends were noted by Meena *et al.,* (2017) and Choudhary *et al.,* (2021), who attributed low variation to a narrow genetic base and strong environmental effects.

Heritability, Genetic Advance and Genetic Advance as a percentage of Mean

The estimates of heritability, genetic advance and genetic advance as a percentage of the mean for the ten characters studied are presented in Table 2. High heritability was recorded for seed yield per plant (83.90 %), plant height (81.42 %), 100-seed weight (82.64 %), pods per plant (86.31 %) and protein content (86.31 %), indicating that these traits are largely governed by additive gene action and can be effectively improved through phenotypic selection. Similar findings have been reported by Meena *et al.,* (2017), Barcchiya *et al.,* (2018) in field pea, who also observed high heritability estimates for yield and yield-contributing traits.

Moderate heritability was observed for days to flowering (78.39 %) and days to maturity (63.14 %), which suggests the involvement of both additive and non-additive gene effects. Similar conformation can be drawn from Pathak *et al.,* (2019), Umesh *et al.,* (2024) who also documented moderate heritability levels for phenology traits.

Low heritability was recorded for number of seeds per pod (29.51 %) and number of branches per plant (58.64 %), suggesting greater environmental influence on their expression and limited efficiency of selection in early generations. Similar trends have been noted by Lal *et al.,* (2016) and Meena *et al.,* (2020) in pea, who attributed low heritability in such traits to high environmental variance.

The magnitude of genetic advance was highest for plant height (4291.14), followed by seed yield per plant (920.86) and days to maturity (724.40), indicating the potential for substantial improvement in these traits through selection. Traits with low genetic advance as a percentage of the mean included days to flowering (10.41 %), pods per plant (4.44 %) and protein content (4.44 %), implying limited scope for improvement through direct selection. Similar results were reported by Choudhary *et al.*, (2021), highlighting that low genetic advance coupled with high heritability often indicates non-additive gene action, requiring alternative breeding strategies such as heterosis breeding or recurrent selection.

Conclusion

The evaluation of field pea genotypes revealed considerable diversity for yield and its related traits. For most traits, the close similarity between GCV and PCV values indicated that genetic factors played a major role, with minimal environmental influence, particularly in seed yield per plant, plant height, pods per plant, and 100-seed weight. High heritability, combined with notable genetic advance for these traits, points to the predominance of additive gene action, suggesting that simple phenotypic selection would be effective for their improvement. In contrast, traits such as seeds per pod and branches per plant showed lower heritability and genetic advance, implying a stronger environmental effect and the need for alternative breeding strategies. These findings provide a clear direction for selecting traits that can accelerate genetic improvement in field pea for higher yield potential.

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