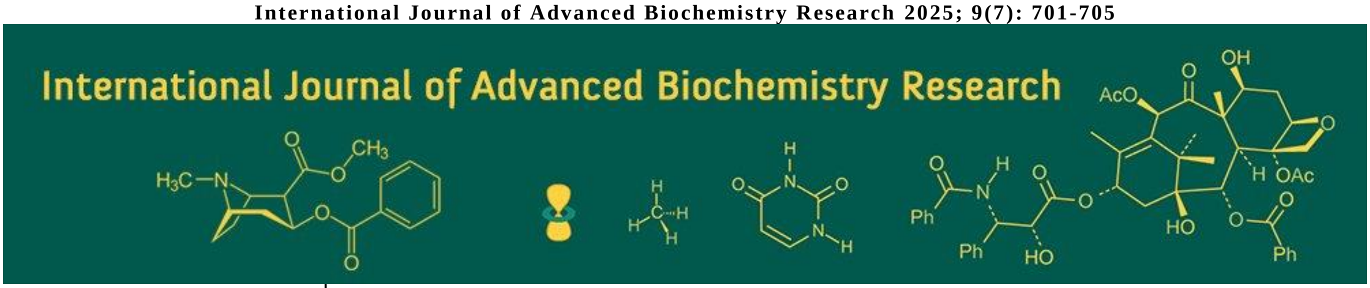
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Assessment of genetic variability, heritability and genetic advance in garden pea (*Pisum sativum* L. var. *hortense*) genotypes

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Abstract

The field experiment was conducted in the *Rabi* season of 2023-24 at the Vegetable Reseach Farm, Acharya Narendra Deva University of Agriculture and Technology, Ayodhya (U.P), by using 24 diverse genotypes of garden pea (*Pisum sativum* L. var. *hortense*). The experiment was organized using a randomized block design with three replications. All sixteen traits exhibited notable differences from genotype to genotype, indicating considerable genetic variation. Nonetheless, characteristics such as total soluble solids (TSS), seeds per pod, plant height and the first flower-producing node exhibited high GCV and PCV with slight variations, showing robust genetic regulation. The environmental impact was signaled by the finding that phenotypic coefficients of variation (PCV) often surpassed genotypic coefficients of variation (GCV). TSS (98.96%, 47.25%), reducing sugars (99.09%, 23.62%), average pod weight, plant height and seeds per pod all exhibited high heritability and significant genetic gain, implying additive gene action and potential for enhancement through direct selection. Pod yield showed the influence of both genetic and environmental factors, demonstrating moderate heritability (65.60%) and genetic improvement (12.51%). For upcoming breeding programs, the genotypes NDVP-21, NDVP-14, NDVP-13, NDVP-23 and NDVP-18 are recommended because of their outstanding yield and quality characteristics.

Keywords: Garden pea, genetic variability, heritability, GCV, PCV, genetic advance, pod yield, quality traits

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1. Introduction

The garden pea (*Pisum sativum* L. var. *hortense*) belongs to the Fabaceae family and has a chromosome number of 2n = 14. Blixt (1970) [1] asserts that the Mediterranean region is considered the primary hub of diversity for peas, while secondary hubs can be found in Ethiopia and the Near East. It is commonly eaten fresh or in processed variations like canned, frozen, or dried peas. Peas are particularly rich in vitamins such as vitamin C (ascorbic acid), vitamin K and folate. For instance, they provide about 65 mg of folic acid, 24.8 mg of vitamin K and 765 IU of vitamin A per 100 g (Thirupathi *et al.*, 2020) [13]. The plant has an upright growth habit, thin stems, a taproot system, compound leaves with tendrils and white, self-pollinated, papilionaceous flowers. India ranks third in global garden pea production, with an area of 611 thousand hectares and a total output of 6671 thousand metric tonnes. Among Indian states, Uttar Pradesh is the leading contributor, accounting for nearly 90% of the national production, covering 246.51 thousand hectares and yielding 3260.83 thousand tonnes (Ministry of Agriculture and Farmers Welfare, 2023-24). It enhance soil fertility via biological nitrogen fixation, which depends on phosphorus availability. Rhizobial cultures and balanced fertilization improve both yield and pod quality. To improve the productivity, development of better varieties is essential. This requires studying genetic variability and identifying yield-contributing traits. Evaluation of diverse genotypes helps in selecting superior lines. According to Vavilov (1951) [14], increased genetic variation enhances the likelihood of discovering superior genotypes. Genetic traits such as GCV, PCV, heritability and genetic gain are vital tools for estimating variability and guiding selection. Since genetic variability is less affected by environment than phenotypic variability, it provides a reliable base for crop improvement.

2. Materials and Methods

The study took place at the Main Experimental Station, Department of Vegetable Science, Acharya Narendra Deva University of Agriculture and Technology, Kumarganj, Ayodhya (U.P.). It is located in the Genetic Alluvial Plains of Eastern Uttar Pradesh, positioned between latitudes 24.470 and 26.560 N and longitudes 82.120 and 83.980 E. The area has a humid subtropical climate and sits at an elevation of 113 meters above mean sea level. The experimental samples comprised 24 genotypes gathered from various areas throughout India. The study was conducted in the Rabi season of 2023-24 utilizing a Randomized Block Design (RBD) with three replications to assess the performance of 24 genotypes. Every entry was grown in a 2 m × 2 m plot, with seeds sown in rows spaced 30 cm apart and 10 cm between each plant. All suggested agricultural practices and pest control methods were adhered to in order to promote a thriving crop. Data were gathered from five randomly selected plants of each genotype across all replications.

The values from the five plants were aggregated and divided by five to determine the average value. The data collected included days to 50% flowering, the initial flower-producing node, days to the first harvest, pod length (cm), average pod weight (g), pods per plant, seeds per pod, primary branches per plant, plant height (cm), crop duration, pod yield (q/ha), total soluble solids (°Brix), ascorbic acid (mg/100g), reducing sugars (%), non-reducing sugar (%) and total sugars (%). Data gathered on the aforementioned character will undergo the following procedures for statistical analysis. Analysis of variance (Panse and Sukhatme, 2000) [10]. Estimation of variation coefficients (Burton and de Vane, 1953) [2], estimation of heritability (Hanson *et al.*, 1956) [4] and genetic gain as a percentage of the mean (Johnson *et al.*, 1955) [5].

3. Results and Discussion

ANOVA was conducted on the data collected for sixteen characteristics among twenty-four genotypes. The average sum of squares related to genotypes exhibited highly significant differences for all traits, indicating substantial variation among the genotypes for the characters examined.

A notable degree of variability was observed across the genotypes, indicating substantial genetic diversity for every trait studied. The days to reach 50% flowering ranged between 37.33 days (NDVP-21) and 62.00 days (NDVP-250 C), yielding a mean of 52.07 days, the first flower-producing node varied from 5.53 (NDVP-21) to 12.47 (NDVP-250 C), with an average of 8.27. Additionally, the genotypes exhibited differences in the days to first picking, with ranging from 56.33 days (NDVP-21) to 80.33 days (NDVP-250 C), resulting in an average of 69.87 days, emphasizing the early maturity of NDVP-21 in both traits. Crop duration varied from 78.67 days (NDVP-21) to 98.33 days (NDVP-250 C), with a mean of 92.44 days. Regarding pod attributes, pod length ranged from 6.65 cm (NDVP-19) to 9.96 cm (NDVP-250), with an average of 8.97 cm. The typical weight of the pods ranged between 2.83 g (NDVP-16) and 5.96 g (NDVP-250), with an average of 4.97 g. Regarding yield-related traits, the number of pods per plant ranged from 5.20 (NDVP-19) to 12.07 (NDVP-18), with a mean of 9.16. The number of seed per pod ranged between 5.07 (NDVP-16) and 9.87 (NDVP-5), with an average of 7.36. The number of primary branches per plant ranged from 3.27 (NDVP-16) to 9.27 (NDVP-250), with a mean of 5.23. For quality attributes, the total soluble solids (TSS) content varied from 4.00°Brix (NDVP-1, NDVP-6) to 13.37°Brix (NDVP-17), with a mean of 7.21°Brix. The ascorbic acid levels varied from 18.21 mg/100g in NDVP-11 to 24.88 mg/100g in NDVP-21, with a mean of 21.28 mg/100g. The range of reducing sugars was from 1.85% in NDVP-9 and NDVP-16 to 2.83% in NDVP-18 and NDVP-20, with an average of 2.31%. For non-reducing sugars, values ranged from 2.27% in NDVP-6 to 5.44% in NDVP-17, leading to an average of 2.91%. Total sugar content ranged from 4.27% in NDVP-6 to 8.98% in NDVP-17, with a mean of 5.43%, signifying notable differences in sweetness and highlighting NDVP-17 as the sweetest variety. Pod yield varied from 72.17 q/ha in NDVP-16 to 106.75 q/ha in NDVP-21, averaging 96.39 q/ha, which reflects a wide range of yields and promising potential across the genotypes. Based on overall mean performance across yield and quality traits, the genotypes NDVP-21, NDVP-14, NDVP-13, NDVP-23 and NDVP-18 were identified as superior. These genotypes are recommended for use in future breeding programs aimed at improving productivity and quality in garden pea.

Table 1: Analysis of variance (Mean squares) s for sixteen characters in garden pea.

S. No.	Characters	Source of variation		
		Replication	**Treatments**	**Error**
	D.F.	**2**	**23**	**46**
1	Days to 50% flowering	3.43	81.80**	7.53
2	First flower producing node	0.77	7.02**	0.21
3	Days to first picking	3.43	80.94**	12.87
4	Plant height (cm)	78.36	406.89**	18.79
5	Crop duration (days)	13.85	73.29**	22.92
6	Pod length (cm)	0.152	2.115**	0.195
7	Average pod weight (g)	0.005	1.662**	0.065
8	Number of pods per plant	0.421	3.770**	0.236
9	Number of seeds per pod	0.872	4.059**	0.148
10	Number of primary branches/plant	0.352	0.180**	0.044
11	TSS (° Brix)	0.14	15.53**	0.05
12	Ascorbic acid (mg/100g)	0.09	8.15**	0.25
13	Reducing sugars (%)	0.002	0.243**	0.001
14	Non-reducing sugars (%)	0.016	0.263**	0.015
15	Total sugars (%)	0.014	0.545**	0.017
16	Pod yield (q/ha)	12.51	184.18**	27.4

*, ** significant at 5% and 1% level, respectively

3.1 Genotypic and Phenotypic Coefficient of Variation

The assessment of genetic diversity among sixteen garden pea genotypes showed significant differences in all examined characteristics. Phenotypic coefficient of variation (PCV) values were reliably greater than genotypic coefficient of variation (GCV) values, indicating that environmental factors significantly affect trait expression. Estimates of GCV and PCV variability are crucial for assessing the extent of genetic influence a trait possesses. A slight difference between GCV and PCV suggests a greater likelihood for effective phenotypic selection and a dominance of genetic factors. Table-2 presents the estimates of genotypic and phenotypic coefficients of variation for sixteen traits of garden pea genotypes.

The total soluble solids (TSS) exhibited the highest genetic coefficient of variation (GCV) at 23.06% and a phenotypic coefficient of variation (PCV) at 23.18%, with a slight difference, suggesting a strong genetic impact and the potential for direct selection. Similar patterns were found for the first flower producing node (GCV: 17.15%, PCV: 17.94%), plant height (GCV: 16.25%, PCV: 17.40%) and the number of seeds per pod (GCV: 15.52%, PCV: 16.37%), all of which displayed significant genetic diversity with little environmental impact, highlighting their potential for genetic enhancement. These findings correspond closely with the observations noted by Gudadini *et al.* (2017) [3], Yadav *et al.* (2020) [15] and Meena *et al.* (2021) [8], who similarly found elevated GCV and PCV for these characteristics in garden pea, indicating that the small difference between them supports their validity for direct phenotypic selection.

In comparison, traits like crop duration (GCV: 4.43%, PCV: 6.82%) and the number of primary branches per plant (GCV: 5.84%, PCV: 8.18%) showed comparatively low genetic coefficient of variation (GCV) values along with notable discrepancies between the phenotypic coefficient of variation (PCV) and GCV, suggesting a greater influence of environmental factors and reduced selection efficiency. Kumar *et al.* (2022) [7] and Katoch *et al.* (2018) [6] observed comparable results, noting greater disparities between PCV and GCV for characteristics such as days to maturity and the count of branches per plant, emphasizing their responsiveness to environmental variations. Pod yield showed moderate degrees of genetic (GCV: 7.50%) and phenotypic (PCV: 9.26%) variability, indicating that both genetic and environmental factors are influential. Singh *et al.* (2019) [12] and Meena *et al.* (2021) [8] noted moderate levels of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) regarding pod yield, highlighting the need for a strategy that improves multiple traits for its advancement.

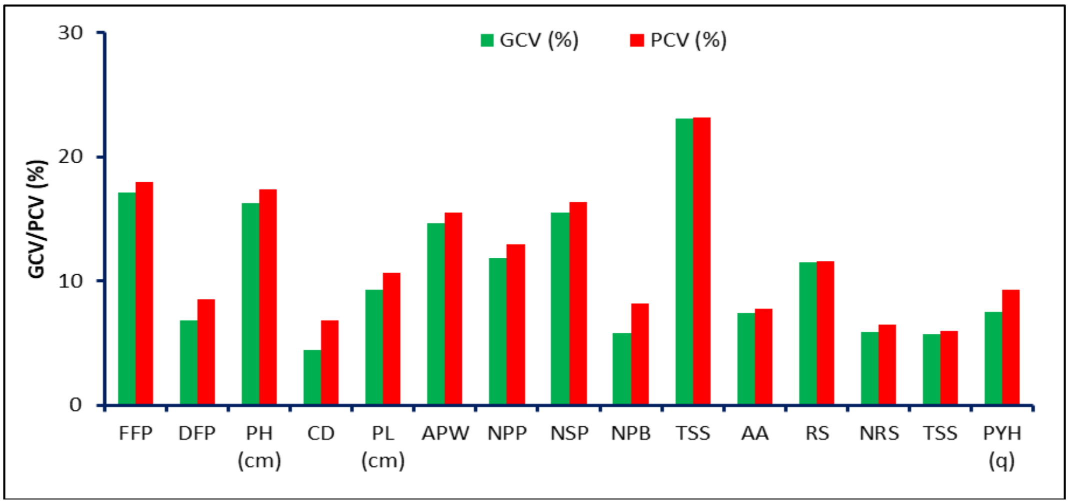

Fig 1: Impact of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) for sixteen traits of garden pea

3.2 Heritability and Genetic Advance

Heritability is a crucial genetic metric in plant breeding that evaluates the extent to which the variation in a trait can be attributed to genetic factors. Broad-sense heritability (H^2), encompassing additive, dominance and epistatic variances, is crucial for forecasting the success of selection, especially in self-pollinating crops such as garden pea where both additive and non-additive genetic influences are involved in the inheritance of traits.

In the present study, significant heritability estimates (>60%) were found for reducing sugars (99.09%), total soluble solids (TSS) (98.96%), seed count per pod (89.79%), average pod weight (89.19%), plant height (87.32%) and pods per plant (83.30%). These heightened values indicate that these traits are largely shaped by genetic influences with minimal effect from environmental factors. Moreover, the connection between elevated heritability and significant genetic improvement as a proportion of the mean in these traits suggests that additive gene action prevails, which implies that direct selection would be quite efficient. Common findings were executed by Meena *et al.* (2021) [8], Yadav *et al.* (2020) [15] and Gudadini *et al.* (2017) [3], who found significant heritability and genetic progress for total soluble solids, plant height, pod weight and seed count per pod, suggesting these traits as optimal for phenotypic selection in garden pea.

Characteristics like the number of primary branches per plant (50.86%) and the days to first picking (63.82%) exhibited moderate heritability (30-60%), suggesting that their expression was influenced by both genetic and environmental factors. Although selection for these characteristics can occur, the possible genetic improvement may be slower and more uncertain. These results align with the observations of Katoch *et al.* (2018) [6] and Kumar *et al.* (2022) [7], who indicated moderate heritability and genetic advancement for characteristics associated with maturity and branching, implying that multi-environment assessments combined with additional breeding strategies might improve selection efficiency. Characteristics with low heritability (<30%) are mainly influenced by environmental variables, making direct phenotypic selection unproductive.

In the current study, most agronomic and quality characteristics demonstrated moderate to high heritability, suggesting considerable potential for genetic improvement. The detection of significant heritability along with substantial genetic progress for traits like TSS, reducing sugars, average pod weight, pods per plant and seeds per pod indicates that these traits are affected by additive gene action and can therefore be enhanced using simple selection techniques. These findings correspond with the research of Singh *et al.* (2019) [12] and Sharma *et al.* (2016) [11], who emphasized that characteristics demonstrating substantial heritability and genetic progress are the most dependable indicators for attaining genetic enhancement through direct selection.

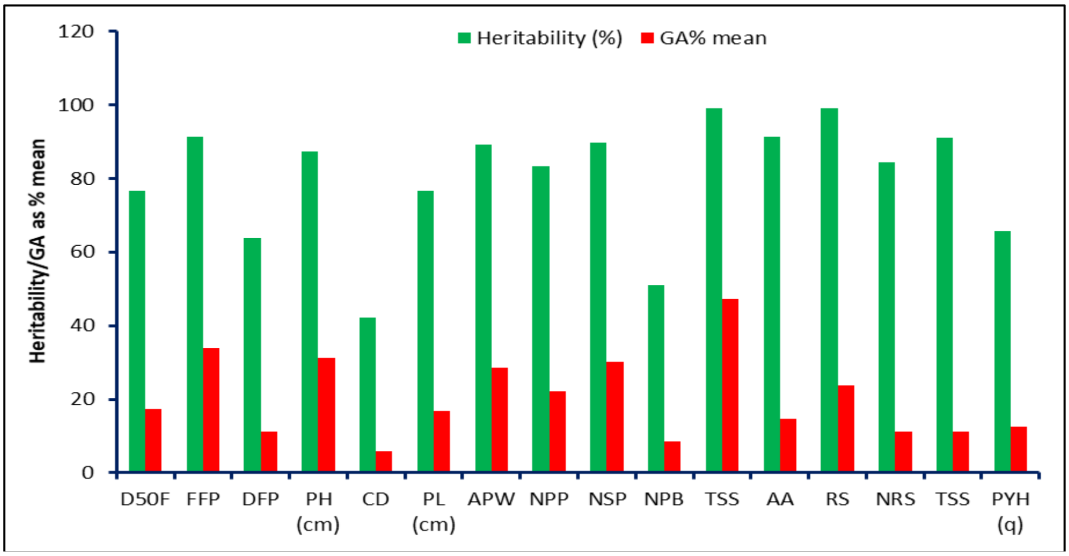

Fig 2: Impact of Heritability (%) and genetic advance in percent of mean for sixteen characters of garden pea.

Table 2: Estimation of range, grand mean, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), Heritability in broad sense and GA (in percent of mean) for sixteen characters of garden pea.

Characters	Mean	Min	Max	GCV (%)	PCV (%)	Heritability (%)	GA% mean
Days to 50% flowering	52.07	37.33	62.00	9.56	10.91	76.67	17.24
First flower producing node	8.78	5.53	12.47	17.15	17.94	91.42	33.79
Days to first picking	69.65	56.33	80.33	6.84	8.56	63.82	11.25
Plant height (cm)	69.97	52.63	90.04	16.25	17.40	87.32	31.29
Crop duration	92.44	78.67	98.33	4.43	6.82	42.28	5.94
Pod length(cm)	8.58	6.65	9.71	9.32	10.65	76.66	16.82
Average pod weight(g)	4.97	2.83	5.96	14.68	15.54	89.19	28.55
Number of pods per plant	9.16	7.67	12.33	11.84	12.98	83.30	22.27
Number of seeds per pod	7.36	5.07	9.27	15.52	16.37	89.79	30.29
No Primary branches/plant	3.65	3.20	4.00	5.84	8.18	50.86	8.57
TSS(°Brix)	9.85	5.23	13.37	23.06	23.18	98.96	47.25
Ascorbic acid (mg/100g)	21.78	19.78	24.99	7.45	7.80	91.25	14.66
Reducing sugars (%)	2.47	1.85	2.83	11.52	11.57	99.09	23.62
Non-Reducing sugars (%)	4.85	4.27	5.44	5.92	6.44	84.40	11.20
Total sugars (%)	7.32	6.12	7.98	5.73	6.00	90.95	11.25
Pod yield (q/ha)	96.39	72.17	106.75	7.50	9.26	65.60	12.51

5. Conclusion

The research showed considerable genetic diversity across all characteristics in 24 genotypes of garden pea. The existence of extremely significant variations among genotypes revealed by ANOVA underscores considerable genetic diversity, essential for effective selection and improvement of crops. Genotypes like NDVP-21, NDVP-14, NDVP-13, NDVP-23 and NDVP-18 have demonstrated excellent results regarding pod yield and quality attributes, positioning them as strong candidates for forthcoming breeding programs. The elevated levels of GCV, PCV, heritability and genetic advance for key properties like TSS, reducing sugars, pod weight, seed per pod and plant height indicate that these traits are predominantly shaped by additive gene action and can be significantly improved via direct phenotypic selection. Characteristics showing moderate to low heritability and genetic advancement, like the quantity of primary branches and total crop duration, are mainly influenced by environmental factors and may require indirect selection or advanced breeding methods. The findings of this study offer valuable knowledge regarding the genetic potential of garden pea genotypes and lay a strong foundation for developing high-yield and nutritionally improved cultivars suited for diverse agro-climatic conditions.

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