Assessment of Genetic variability, Heritability and Genetic Advance for Quantitative Traits in Pea (*Pisum sativum*) Germplasm

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ABSTRACT: Pea is the most widely cultivated pulse crop in the state of Uttar Pradesh. The main aspect of increasing productivity is the selection of genotypes with higher yields and better quality. Crop improvement needs research and greater understanding of the diversity present in a population base of the crop so that plant breeders can take advantage of it. Fifty-four entries consisting of 10 lines and 4 testers were Line × Tester mating design. 40 F$_1$s used and evaluated in a randomized block design with three replications at the Horticulture Research Centre, Department of Vegetable Science, Sardar Vallabhbhai Patel University of Agriculture and Technology, Meerut during the *rabi season* of 2022-23. The analysis of variance showed significant differences among the genotypes for all the characters. For all twelve characters under investigated, the mean sum of squares contributes to treatment was found significant, indicating that the materials showed significant variability. The moderate value of phenotypic and genotypic coefficient of variances was recorded for branches per plant, plant height, pod yield per plant, days to first flowering and days to 50% flowering indicating that these traits is controlled by a combination of both additive and non-additive gene actions. The high heritability (broad sense) was revealed for all the characters except pod wight. The high genetic advance as % of mean was recorded for branches per plant, plant height, pod yield per plant and days to first flowering. Whereas, moderate for days to 50 % flowering, green pods per plant, number of seeds per pod, pod diameter, TSS Brix %, days to first green pod picking and pod length. The high heritability coupled with high genetic advance were governed by additive gene action and can be reliable targets for selection in breeding programs to develop improved pea varieties.

Keywords: Genetic variability, heritability, genetic advance, pea.

INTRODUCTION

Pea (*Pisum sativum*) is a highly esteemed legume crop, cherished for its culinary and nutritional value worldwide. As a rich source of proteins, carbohydrates, vitamins, and minerals, garden pea plays a crucial role in balanced diets, making it a vital component of global food security and sustainable agriculture (Bhattacharya *et al.,* 2019; Sankari *et al.,* 2014). However, amidst increasing population pressures and climate uncertainties, there is an urgent need to enhance garden pea productivity and adaptability to diverse agroclimatic conditions.

Genetic variability, heritability, and genetic advance serve as fundamental parameters in understanding the genetic basis underlying important agronomic traits and optimizing crop improvement strategies (Falconer and Mackay 1996; Singh and Chaudhary 1985). In the context of garden pea breeding, an accurate assessment of the extent of genetic variability and heritability for yield-related traits is vital for identifying superior genotypes and hastening the development of high-yielding cultivars.

Heritability estimates, on the other hand, elucidate the extent of genetic control over phenotypic variation in a given trait. High heritability values suggest a predominant genetic influence on the expression of the trait, making it more amenable to selection and breeding (Singh and Chaudhary 1985). Accurate heritability estimates play a pivotal role in choosing the most effective breeding strategy, be it phenotypic

selection or marker-assisted breeding, to enhance target traits effectively (Mohammadi *et al.,* 2015).

Genetic advance, a crucial parameter in plant breeding, quantifies the expected gain in a trait due to selection. Identifying genotypes with higher genetic advance for specific yield-related traits enables breeders to focus their efforts on the most promising individuals, expediting the development of improved cultivars (Johnson *et al.,* 1955). This parameter guides the prioritization of breeding lines and facilitates informed decision-making for crop improvement programs**.**

MATERIALS AND METHODS

The experiment was carried out using a Randomized Block Design (RBD) with three replications during *Rabi season* of 2022-2023 at the Horticulture Research Centre, Department of Vegetable Science, Sardar Vallabhbhai Patel University of Agriculture and Technology, Meerut. The experimental materials were consisted of fourteen genotypes of pea viz., VRP-22, Kashi Uday, AP-3, EC-598603, EC-395899, AP-1, Arka Priya, VRP-7, PC-531, Pant Matar-2, Pusa Pragati, Kashi Nandini, Kashi Mukti and Arkel. Out of fourteen genotypes, ten as lines viz., VRP-22, Kashi Uday, AP-3, EC-598603, EC-395899, AP-1, Arka Priya, VRP-7, PC-531 and Pant Matar-2 and four testers viz., Pusa Pragati, Kashi Nandini Arkel and Kashi Mukti were crossed in line x tester mating design and 40 F_1s.The experimental plot size was maintained uniformly for each parent and F_1 progenies to ensure consistent growing conditions. Proper care and management practices were followed throughout the experimental period to maintain optimal plant growth and health. During the crop growth and development stages, various yield-related traits were recorded for both parents and F_1 progenies. The following key traits were recorded for days to first flowering, days to 50% flowering, days to first pod picking, plant height, branches per plant, green pod per plant, pod weight, pod length, pod diameter, number of seeds per pod, TSS Brix % and pod yield per plant. The data obtained from the study were subjected to statistical analysis to compute the genetic coefficient of variation (GCV) using the method described by Panse and Sukhtame (1985). Additionally, the analysis of variance (ANOVA) was carried out following the procedure provided by Panse and Sukhtame (1985). Phenotypic and genotypic coefficients of variation were estimated based on the method proposed by Burton (1952). Furthermore, the heritability in the broad sense was estimated using the formula given by Allard (1960). The heritability in broad sense provides an understanding of the proportion of phenotypic variation that can be attributed to genetic factors. To assess the potential for improvement through selection, the expected genetic advance was calculated using the formula suggested by Johnson *et al.* (1955).

RESULTS AND DISCUSSION

Analysis of variance (Table1) showed highly significant differences among the genotypes for all the characters *viz.,* days to first flowering, days to 50 % flowering,

days to first green pod picking, plant height (cm), branches per plant, green pods per plant, pod weight (g), pod length (cm), pod diameter (mm), number of seeds per pod, TSS Brix % and pod yield per plant. This showed the genotypes' large range of variability and indicated that more genetic investigation and evaluation would be valuable. It has also been previously stated that there is this much genetic heterogeneity for the different attributes by Sharma and Bora (2013); Georgieva *et al.* (2016); Singh and Dhall (2018); Singh *et al.* (2019); Gupta *et al.* (2020); Ali *et al.* (2021).

The mean performance and range of parent and F_1s for 12 characters presented in Table 2. The study assessed the extent of variability among the pea entries in terms of range and phenotypic and genotypic coefficients of variation. A wide range of variability was observed for various important traits, such as days to first flowering, days to 50% flowering, days to first pod picking, plant height, branches per plant, green pods per plant, pod weight, pod length, pod diameter, number of seeds per pod, TSS Brix %, and pod yield per plant indicating significant potential for selection of suitable initial breeding materials to improve the crop. This variability offers an excellent opportunity for plant breeders to identify and focus on superior genotypes with desirable traits for further breeding and crop enhancement initiatives. Similar findings were also found by Singh *et al.* (2019); Gupta *et al.* (2020); Ali *et al.* (2021); Parveen and Saivamsireddy (2022).

Estimates of variability, heritability, and genetic advances for 12 characters studied are presented in Table 3 and Fig. 1 and 2. The values for genotype coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were observed for each character. Interestingly, both the phenotypic and genotypic coefficients of variation showed nearly similar values for all the characters studied. However, it is worth noting that the magnitude of the phenotypic coefficient of variation was consistently higher than that of the genotypic coefficient of variation.

The moderate genotypic and phenotypic coefficients of variance was recorded for the characters viz., branches per plant, plant height, pod yield per plant, days to first flowering and days to 50% flowering indicating that characters were influencing more by environment. Similar results were also reported early by Mishra *et al.* (2014); Jeberson *et al.* (2016).

The values for heritability estimates in broad sense were ranged from branches per plant (92.26 %) to pod weight (58.86 %). Most of the characters resulted high heritability in broad sense. Among the characters under studied, highest heritability was recorded for branches per plant, plant height, pod yield per plant, days to first flowering, days to 50 % flowering, green pods per plant, number of seeds per pod, pod diameter, TSS Brix %, days to first green pod picking and pod length whereas, moderate heritability was recorded in pod weight. The similar results were also earlier reported by Devi *et al.* (2017); Parveen and Saivamsireddy (2022). These findings suggest that these traits are strongly influenced by genetic factors and can be reliable targets

for selection in breeding programs to develop improved pea varieties. The identified high heritability traits could serve as valuable resources for breeders to enhance pea cultivars, ultimately contributing to increased agricultural productivity and food security.

Among the traits under investigation, branches per plant, plant height, pod yield per plant, and days to first flowering displayed the highest genetic advance values. These traits exhibited a substantial scope for improvement through selection, as their genetic variation contributed significantly to the observed phenotypic variation. These results indicate that these traits are predominantly governed by additive gene action, making them promising targets for breeding programs aiming to develop improved varieties with enhanced performance and yield Devi *et al.* (2017); Ali *et al.* (2021).

On the other hand, traits such as days to 50% flowering, green pods per plant, number of seeds per pod, pod diameter, TSS Brix %, days to first green pod picking, and pod length exhibited moderate genetic advances as percentages while, pod weight demonstrated the lowest genetic advance percentage. Similar findings were earlier reported by Ali *et al.* (2021). This suggests that these traits are influenced by both additive and non-additive gene actions, which may lead to a more complex inheritance pattern. High heritability coupled with high genetic advance was observed for branches per plant, plant height, pod yield per plant, days to first flowering, days to 50 % flowering showed that these traits were controlled by additive gene action, showing that direct selection of these traits would be effective and profitable for yield improvement.

Table 1: Analysis of variance (ANOVA) for parents and F₁s for 12 quantitative characters in Pea (*Pisum sativum* L.).

| Characters	d.f.	DFF	DFPF	DFGPP	PH (cm)	BPP	GPPP	PW (g)	PL (cm)	PD (mm)	NSPP	TBP	PYPP (g)
Replications	2	1.13	0.10	1.62	2.93	0.04	0.70	0.000	0.061	0.001	0.005	0.01	1.09
Genotypes	53	51.88**	55.22**	60.27**	117.42**	2.50**	4.20**	0.798**	0.991**	0.035**	1.293**	4.20**	210.69**
Error	106	2.50	2.84	6.70	6.26	0.06	0.22	0.078	0.102	0.003	0.098	0.46	8.93
Total	161	18.74	20.05	24.27	42.81	0.86	1.54	0.314	0.394	0.014	0.490	1.69	75.25

DFF=Days to first flowering DFPF=Days to 50% flowering DFGPP=Days to first green pod picking PH=Plant height (cm) BPP=Branches per plant GPPP=green pods per plant PW=Pod weight (g) PL=Pod length (cm) PD= Pod diameter (mm) NSPP=Number of seeds per pod TBP= TSS Brix % PYPP=Pod yield per plant (g)

**Table 2: List of mean and range performance of parents and F₁s.**

Sr. No.	Characters	Mean	Mean	
			Minimum	Maximum
1	Days to first flowering	38.91	34.83 (Kashi Uday × Kashi Nandani)	50.33 (EC-598609)
2.	Days to 50% flowering	42.60	38.33 (Pant Matar-2 × Kashi Nandani)	55.33 (EC-598609)
3.	Days to first green pod picking	64.38	59.00 (Arka Priya × Pusa Pragati)	76.33 (EC-598609)
4.	Plant height (cm)	62.27	47.33 (Kashi Nandani)	85.00 (Pant Matar-2)
5.	Branches per plant	6.44	4.00 (EC-598609)	8.00 (Kashi Mukti)
6.	Green pods per plant	12.49	8.33 (Arka Priya)	14.67 (AP-1 × Kashi Mukti)
7.	Pod weight (g)	6.58	5.83 (VRP-7)	7.24 (Pant Matar-2 × Kashi Nandani)
8.	Pod length (cm)	8.43	6.83 (VRP-7)	9.50 (Pusa Pragati)
9.	Pod diameter (mm)	1.50	1.26 (Pusa Pragati)	1.80 (Pant Matar-2)
10.	Number of seeds per pod	7.96	6.67 (VRP-22)	9.00 (EC-598609 × Pusa Pragati)
11.	TSS Brix %	16.32	14.70 (Kashi Nandani)	20.37 (Arkel)
12.	Pod yield per plant (g)	74.27	46.92 (Arka Priya)	90.36 (Pant Matar-2 x Kashi Mukti)

Table 3: Estimates of genetic variability for 12 quantitative characters in Pea (*Pisum sativum* L.).

Genotypes	Mean	Mean		var (g)	var (p)	Heritability (%)	GA	GA as % of mean	GCV (%)	PCV (%)
		Min.	Max.							
Days to first flowering	38.91	34.83	50.33	16.46	18.96	86.81	7.79	20.01	10.43	11.19
Days to 50% flowering	42.60	38.33	55.33	17.46	20.30	86.02	7.98	18.74	9.81	10.58
Days to first green pod picking	64.38	59.00	76.33	17.85	24.56	72.71	7.42	11.53	6.56	7.70
Plant height (cm)	62.27	47.33	85.00	49.69	56.16	88.47	13.66	21.93	11.32	12.03
Branches per plant	6.44	4.00	8.00	0.76	0.83	92.26	1.73	26.79	13.54	14.10
Green pods per plant	12.49	8.33	14.67	1.29	1.51	85.32	2.16	17.29	9.08	9.83
Pod weight (g)	6.58	5.83	7.24	0.11	0.19	58.86	0.52	7.95	5.03	6.56
Pod length (cm)	8.43	6.83	9.50	0.27	0.37	72.35	0.91	10.83	6.18	7.26
Pod diameter (mm)	1.50	1.26	1.80	0.01	0.01	75.46	0.19	12.43	6.95	8.00
Number of seeds per pod	7.96	6.67	9.00	0.35	0.45	77.11	1.07	13.39	7.40	8.43
TSS Brix %	16.32	14.70	20.37	1.25	1.71	73.08	1.97	12.06	6.85	8.01
Pod yield per plant (g)	74.27	46.92	90.36	67.25	76.19	88.28	15.87	21.37	11.04	11.75
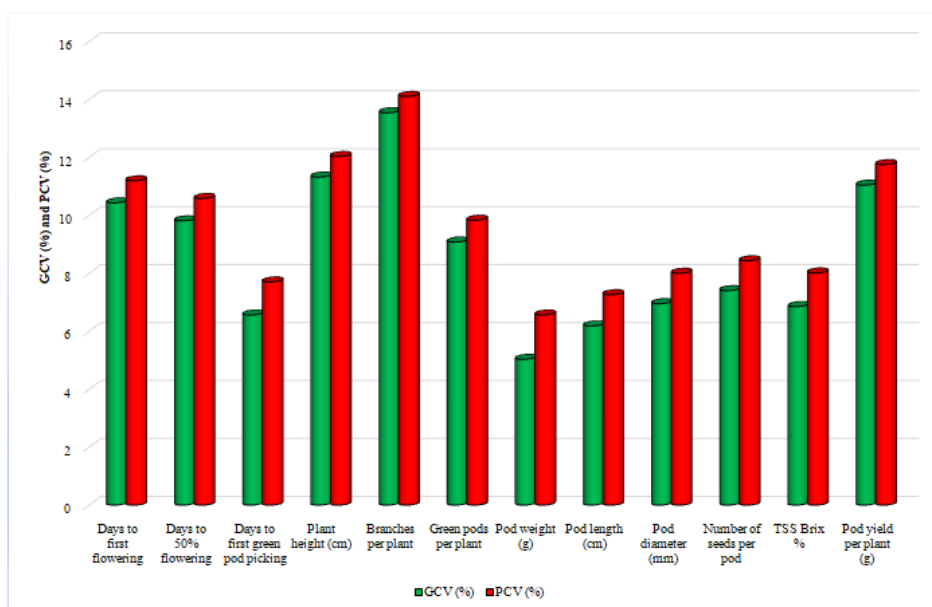
Fig. 1. Genotypic coefficient of variation and Phenotypic coefficient of variation.
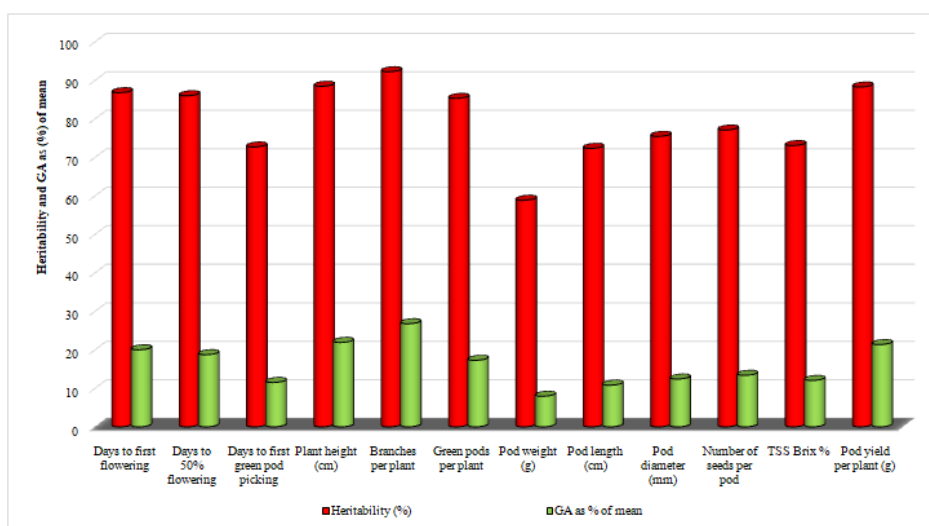
Fig. 2. Heritability and Genetic advance as (%) of mean.

CONCLUSIONS

The present study indicates a substantial degree of variability, heritability and genetic advance for these traits, suggesting that simple selection approaches could be effective in enhancing yield through these specific attributes.

FUTURE SCOPE

The present study provides a good information for the future scope of research and breeding efforts in pea (*Pisum sativum*) germplasm. The recognition of traits influenced by additive gene action and the understanding of environmental influences on specific traits offer promising opportunities for the development of improved pea varieties.

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