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## Genetic variability, heritability and genetic advance studies in vegetable pea [*Pisum sativum var. hortense* L.]

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### Abstract

A field experiment was carried out during *Rabi* season 2022-23 to assess the genetic variability, heritability and genetic advance among 15 genotypes of vegetable pea in randomized block design (RBD). Observations on thirteen characters *viz.*, days for first flower emergence, days to 50 percent flowering, days to first pod formation, days to first pod picking, plant height (cm), 100 seed weight, shelling %, average pod weight (g), pod length (cm), number of seeds per pod, yield per plant (grams/plant), yield per plot (kg/plot) and yield per hectare (tons/ha) were taken for the assessment. The results of ANOVA showed significant differences among the genotypes for all the characters indicating the existence of wide spectrum of variability among the genotypes. The phenotypic coefficient of variation (PCV) were comparatively higher than genetic coefficient of variation (GCV). The high estimates of the PCV were obtained for yield per plot followed by yield and yield per plant, whereas estimation of GCV was high in case of yield and yield per plant. High heritability was recorded for all the characters under study except average pod weight. The highest genetic advance as percent of mean was exhibited by yield per plant (g) followed by yield (t/ha), plant height (cm) and days to first flower emergence. So, these characters should be preferred during selection of traits in different breeding and crop improvement programs to develop high yielding and more successful Varieties.

**Keywords:** Variability, GCV, PCV, heritability, genetic advance

### Introduction

One of the most essential legume vegetables produced worldwide is the garden pea (*Pisum sativum var. Hortense* L.),  $2n=2x=14$ , which is a member of the Leguminosae subfamily Fabaceae. Being a cold season crop, it is extensively grown throughout the tropics and subtropics during the winter. It is also cultivated as a summer crop on the hills. The fragile, immature seeds that are picked for use as vegetables are the main reason it is grown. When creating an efficient breeding technique intended to take capitalise on the inherent variability of the original population, it is of the utmost importance that one considers elements such as genotypic and phenotypic coefficients of variation, heritability and advance, certificate of association between the various characters, and the direct impact of yield-contributing characters on total yield. While genetic variability is stable and more beneficial to a plant designer for use in selection or hybridization, phenotypic variability changes depending on the external variables. Therefore success of any breeding programme for its improvement depends on the existing genetic variability in the base population and on the efficiency of selection (Kumari *et al.*, 2008) [18]. Heritability indicates the proportion of phenotypic variance that is due to genotypes which is heritable. It serve as a useful guide to breeders as the selection for trait having high heritability will be effective and improvement will be brought through selection. The genetic advance is an improvement in the genetic value new population as compared to original one. It will be possible to decide various breeding programmes for improvement of different characters based on the study of heritability and genetic advance (Kumari *et al.*, 2012) [19]. Keeping this in view, an attempt was made in the present investigation to assess the magnitude of variability, heritability and genetic advance for different characters in Vegetable Pea.

### Materials and Methods

The investigation was carried out during the month of *Rabi* (October-February) season of 2022-2023 at the Agricultural Sciences and Allied Industries, Rama University, Agricultural Research, Uttar-Pradesh.

The experimental material consisted of fifteen genotypes of pea namely *viz.*, Ageta, Arkel, AP-1, AP-3, Asauji, KashiUday, Kashi Nandini, Kashi Shakti, Arka Priya, Arka Sampurna, Arka Apoorva, VL-17, Jawaharmatar 3, Jawaharmatar 4 and Pusa Pragati. The experiment was laid out in Randomized block design (RBD) with three replications. The observations were recorded on five randomly selected plants from each treatment on thirteen characters *viz.*, Days for first flower emergence, days to 50 percent flowering, days to first pod formation, days to first pod picking, plant height (cm), 100 seed weight, shelling %, average pod weight (g), pod length (cm), number of seeds per pod, yield per plant (grams/plant), yield per plot (kg/plot) and yield per hectare (tons/ha).

### Statistical Analysis of parameters

The analysis of variance for the setup of the experiment was conducted according to Panse and Sukhatme (1967). According to Burton and De Vane (1953) [4], both the genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were calculated in %. Heritability in the most general manner ( $h^2_b$ ), defined as the proportion of genotypic variation to total variance (phenotypic variance), was calculated using the formula provided by Hanson *et al.* (1956) [56]. Genetic advance as percent mean has been calculated using a technique developed by Johnson *et al.* (1955) [13].

### Results and Discussion

Analysis of variance was conducted to eliminate the variation due to causes other than genotypes from total variation. The analysis of variance carried out for all the 13 characters is depicted in Table 1. All the characters studied showed highly significant differences among all genotypes. The ANOVA revealed highly significant variation among the genotypes ( $p < 0.01$ ) for all the eleven characters under study. This substantial variability among the genotypes for all the characters might be endorsed to their various sources of collection as well as environmental and  $G \times E$  components. These results are in accordance with the findings of Guleria *et al.* (2009) [9], Lal *et al.* (2011) [20], Kumar *et al.* (2013) [15], Supe *et al.* (2013) [31], Kumar *et al.* (2015) [16], Georgieva *et al.* (2016) [6], Kumar *et al.* (2017) and Barcchiya *et al.* (2018) [3].

As determined through the phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability ( $h^2$ ), and genetic advances among the fifteen genotypes of pea, variance for each of the thirteen characters is shown in Table 2. The magnitude of GCV in the present investigation was lower than the equivalent PCV for all characters, demonstrating the influence of environmental factors on character expression (Ghosh *et al.* 2010) [7]. The fact that there was not much of a difference between GCV and PCV indicates that genetic factors as compared to environmental factors played a more significant part in determining how characters express themselves. As a result, the selection could be determined by phenotypic performance that provides potential for crop improvement. The high estimates of the PCV (>30%) were obtained for yield per plot (38.98) followed by yield (37.61) and yield per plant (34.89), while all the other characters under study showed moderate (10-30%) estimates indicating that these characters were more influenced by the environment. The estimation of GCV was high (>30%) in case of yield (34.75) followed by yield per

plant (34.13) however moderate estimates (10-30%) were shown by rest of the characters except pod length (7.28) which showed low estimate (<10%) of GCV. These results are similar to those reported by Singh and Singh (2006) [29], Sharma and Bora (2007) [26], Kumari *et al.* (2008) [18], Harshawardhan *et al.* (2010) [11], Singh *et al.* (2011) [28], Kumar *et al.* (2013), Jaiswal *et al.* (2015) [16], Georgieva *et al.* (2016) [5], Katoch *et al.* (2016) [14], Gudadinni *et al.* (2017) [8] and Kumar *et al.* (2019) [17].

Heritability is a measure of genetic relationship between parent and progeny and has been widely used in determining the degree to which a character may be transmitted from parents to off springs. Estimation of heritability in broad sense gives the extent of heritable component of variation. High heritability in broad sense is helpful in identifying appropriate character for selection and enables the breeder to select superior genotypes on the basis of phenotypic expression of quantitative characters. Heritability (in broad sense) was found to range from 77.00 for average pod weight (g) to 97.50 percent for plant height (cm). The highest heritability was recorded in case of average pod weight (97.50) followed by days to 50% flowering (95.40), days to first flower emergence (95.20), yield per plant (95.10), days to first pod formation (93.50), days to first pod picking (90.40), pod length (87.00), 100-seed weight (86.30), number of seeds per pod (85.30), yield (85.30), yield per plot (83.10) and shelling percent (80.40). However, moderate heritability was found in the case of average pod weight (77.00) only. Similar results were noticed by Ahmad *et al.* (2014) [2], Kumar *et al.* (2015) [16], Georgieva *et al.* (2016) [6], Afreen *et al.* (2017) [11], Gudadinni *et al.* (2017) [8], Tambolkar *et al.* (2017) [32], Kumar *et al.* (2019) [17] and Singh *et al.* (2019) [30]. The high values of broad sense heritability for the above characters expressed that they were less influenced by environmental conditions. It reflected that the phenotypes were the true representative of their genotypes and selection based on phenotypic performance would be reliable (Table 2).

Taking into account how much a trait is passed on and how it changes due to genetics and the surroundings can help improve how well selection works. Estimates of heritability alone are not enough for a selection program to work. Because of this, it is important to study both heritability and genetic progress. The genetic progress may or may not be proportional to predictions of genetic variability and heritability, because both high heritability and high genetic variability are needed to get a bigger genetic gain (Kumari *et al.*, 2008) [18]. The estimates of genetic advance as percent of the mean ranged from 11.61 in case of number of seeds per pod to 68.78 percent in case of yield per plant (g). The highest genetic advance as percent of mean was exhibited by yield per plant (68.78) followed by yield (66.12), plant height (58.21) and days to first flower emergence (40.04). Moderate genetic advance as percent of mean was found for days to 50% flowering (36.16), days to first pod formation (35.44), 100-seed weight (26.89) and yield per plot (26.61). The lowest genetic advance as percent mean was recorded for the characters days to first pod picking (22.89), shelling percent (18.79), average pod weight (18.31), pod length (16.48) and number of seeds per pod (11.61). These results were as per the guidelines agreement with Choudhary *et al.* (2010) [5] for the characters like plant height, pod yield per plant and number of pods per plant. Kumar *et al.* (2015) [16] also found the similar findings for the characters like pod length, 100

seed weight and shelling percentage. Pal and Singh (2013) [21] found the similar finding for the characters like plant height, days to first flowering and pod yield per plant. Siddika *et al.* (2013) [27] also found the similar results in pea for the characters like 100 green seed weight, plant height etc.

Similar results were also noticed by Rakesh *et al.* (2007) [22], Sardana *et al.* (2007) [24], Sanjay *et al.* (2008) [23], Singh *et al.* (2011) [28], Dagla *et al.* (2013), Kumar *et al.* (2013) [15], Singh *et al.* (2019) [30] and Yumkhaibam *et al.* (2019) [33].

**Table 1:** Analysis of variance for 13 characters in Pea (*Pisum sativum* L. var. *hortense*)

SL. No.		Mean Sum of Squares		
		Replication	Treatments	Error
	Degree of freedom	(2)	(14)	(28)
1	Plant height(cm)	8.28	1160.89	9.67
2	100 seed weight	7.93	82.10	4.12
3	Number of seeds per pod	4.44	3.25	1.62
4	Average pod weight (g)	4.94	2.44	0.87
5	Days to first flower emergence	18.39	267.79	4.46
6	Days to 50% flowering	7.04	290.71	4.63
7	Days to first pod formation	31.11	325.42	7.37
8	Days to first pod picking	16.46	273.44	9.33
9	Pod length (cm)	5.32	2.62	1.55
10	Shelling percent	0.51	69.42	5.23
11	Yield per plant(g)	3.83	431.42	6.37
12	Yield per plot(kg)	0.33	2.89	1.16
13	Yield (tons/ha)	11.84	18.22	0.99

**Table 2:** Coefficient of variation, heritability, genetic advance and genetic advance as % of mean for 13 characters in Pea

S. No.	Characters	Mean	Range		Variance		Heritability (%)	Genetic advance (as % of mean)
			Min.	Max.	GCV	PCV		
1	Plant height (cm)	68.45	48.95	111.67	28.61	28.97	97.50	58.21
2	100 seed weight	36.27	31.50	44.07	14.05	15.12	86.30	26.89
3	Number of seeds per pod	6.59	5.00	8.33	11.21	22.29	85.30	11.61
4	Average pod weight (g)	4.98	3.66	6.33	14.53	23.66	77.00	18.31
5	Days to first flower emergence	46.98	33.00	61.00	19.94	20.44	95.20	40.04
6	Days to 50% flowering	54.32	40.00	65.50	17.97	18.40	95.40	36.16
7	Days to first pod formation	57.88	44.66	73.40	17.78	18.39	93.50	35.44
8	Days to first pod picking	80.27	63.50	97.66	11.68	12.29	90.40	22.89
9	Pod length (cm)	8.20	5.75	9.66	7.27	16.83	87.00	16.48
10	Shelling percent	45.45	36.83	51.66	10.17	11.35	80.40	18.79
11	Yield per plant(g)	34.87	16.50	54.50	34.13	34.89	95.10	68.78
12	Yield per plot(kg)	3.38	2.00	5.50	22.44	38.98	83.10	26.61
13	Yield (tons/ha)	6.89	2.83	11.33	34.74	37.61	85.30	66.12

## Conclusion

Present study of variation indicated substantial variability among all the genotypes as all the characters under study significantly differed from each other. Characters such as yield per plant, plant height, days to first flower emergence, days to 50% flowering, days to first pod formation, average pod weight and days to first pod picking showed high to moderate estimates of GCV, PCV, heritability and genetic advance (as percent of mean). The characters showing high values for GCV, PCV, heritability and genetic advance should be preferred during selection of traits in different breeding and crop improvement programs. Further, these characters should be considered during selection for higher yield as well, in pea. The most promising genotypes which showed high values for the above mentioned important characters can be further selected and utilized to develop high yielding and more successful varieties.

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