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## Genetic variability analysis for various morphological traits in field pea (*Pisum sativum* L.)

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### Abstract

Field pea (*Pisum sativum* L.) oldest cultivated, most important nutritious food legume of the world and a major pulse crop of winter season. The present investigation was carried out to access genetic variability parameters for better understanding of genetic architecture of seed yield and its attributes in field pea. Twelve parents (9 lines + 3 testers) of field pea were crossed in L x T mating design and the parents along with their 27 hybrids were grown in randomized block design with three number of replication during *rabi* 2020-21. Narrow differences between PCV and GCV of different traits implying apparent variability present among genotypes not only due to genetic factor but also environment play a crucial role in expression of these traits. Low heritability coupled with low genetic advance were observed for most of traits expect days to maturity, height of first pod and plant height suggesting that these traits are genetically controlled by non-additive gene action and heterosis breeding would be rewarding for these traits.

**Keywords:** Genetic advance, GCV, heritability, PCV, seed yield

### Introduction

Field pea (*Pisum sativum* L.,  $2n=2x=14$ ) is one of the most important food legume crop of family Leguminosae; tribe Fabeae that is widely grown throughout the world including India, North America, Australia, Pakistan, West Europe and South America (Saxena *et al.*, 2013) [22]. It is a self-pollinated crop and its centre of origin is not precisely known but it is considered to be the native of Ethiopia, the Mediterranean and Central Asia (Blixt, 1970) [4]. It is extensively grown pulse crop in temperate climates due to its high nutritional profile such as a rich source of protein (25.10%) coupled with slowly digestible starch (61.80%), essential minerals (Ca, P and Fe), high fibre content (13.40%), and low fat content (Sharma *et al.*, 2023; Haque *et al.*, 2015) [23, 8]. As field pea is a leguminous crop, it maintains soil fertility by coexisting symbiotically with *Rhizobium* species of bacteria and fixing atmospheric free nitrogen into the soil (Rohilla *et al.*, 2022) [21]. In many parts of the world, it plays a significant role in agro-ecological cropping systems as a relay crop (Ali and Sarker, 2013) [1]. Therefore, it is imperative to agricultural systems from an economic as well as agronomic perspective (Yang *et al.*, 2018) [27].

Field pea is a multi-functional crop that may be used as green forage, forage dry matter, forage meal, silage, haylage, immature grain, mature grain, straw and green manure (Mihailovic and Mikic (2010) [13] and Ravindranet *et al.* (2010) [20]. India occupies sixth place in field pea production with an area of 6.4 lac hectares, production 8.8 lac tons and productivity of 1375 kg/ha in 2020-21 (Anonymous, 2022) [2]. Uttar Pradesh, Madhya Pradesh, Jharkhand, Odisha, Manipur, Assam, Bihar, West Bengal, Chhattisgarh and Rajasthan are the major field pea growing states in India. Unfortunately, the productivity of field pea is very low in India as compared to the world's productivity due to the narrow genetic base and use of limited variability to improve the local varieties (Kumar *et al.*, 2004) [11]. There is urgent need to increase the seed yield though yield is a multiplex trait that depends upon a number of other contributing traits and their association (Rao *et al.*, 1990) [19]. Thus information regarding genetic architecture between yield and its attributes will help in determining the selection criteria to improve yield, thus enhancing scope of success of breeding programs (Sunayana *et al.*, 2017) [26]. Thus, knowledge about the magnitude of genetic variability present for different traits along with its heritable component is of prime importance for achieving the desired goals of any breeding programme. As, for the development of stable varieties, there must be a presence of large genetic diversity in the populations under study (Gupta *et al.*, 2022) [7].

Heritability provides the information about index of transmissibility and measures the selection value for a trait in different progenies, while genetic advance is useful in determining the actual gain anticipated under selection (Ogunniyan and Olakojo, 2015) [14]. Hence, the current investigation was undertaken to estimate the genetic variability, heritability and genetic advances among yield and yield contributing traits for field pea genotypes.

### Materials and Method

Nine female lines (Pant P-243, DDR-23, HFP 715, IPF 14-13, IPF 14-16, RFP 2009-2, Pant P-200, RFPG 79, Aman) were crossed with three male testers (HFP 1545, HFP 1426, GP02/1108) in line  $\times$  tester design during *rabi* 2019-20. The 12 parents along with their 27 crosses were evaluated for thirteen quantitative traits in Pulses Research Area, Department of Genetics and Plant Breeding, CCS, Haryana Agricultural University, Hisar during *rabi* 2020-21. The experimental site situated at 29.10° N latitude and 75.46° E longitude at an elevation of 215.2 meter above mean sea level is characterized by extreme temperatures (low and high), dryness and scanty rainfall. The experiment was laid down in randomized block design with three replicates, with plot size of a single row of 4m length with 45 x 15cm spacing. Data on number of primary and secondary branches plant<sup>-1</sup>, nodes plant<sup>-1</sup>, plant height of 1<sup>st</sup> pod, plant height, pods plant<sup>-1</sup>, seeds pod<sup>-1</sup>, 100-seed weight, biological, seed yield and harvest index were recorded on five competitive randomly selected

plants while on days to flowering and maturity, the observations were recorded on the plot basis. The analysis of variance for each character was carried out by using the method described by Panse and Sukhatme (1985) [15]. The genetic variability parameters *i.e.* genotypic coefficients of variation (GCV) and phenotypic coefficients of variation (PCV) were calculated as per Burton and de Vane (1953) [5]. Heritability in narrow sense for each character was calculated according to Singh and Chaudhary (1985) [7], whereas expected genetic advance was calculated at 5 per cent selection intensity for each character as per Johnson *et al.* (1955) [10]. Data were analyzed using statistical software INDOSTAT.

### Results and Discussion

The mean squares were highly significant ( $P < 0.01$ ) for each of the thirteen variables studied suggesting sufficient amount of variability present in the experimental material. The conscientious study of analysis of variance, mean, standard errors and critical difference (CD) revealed significant differences among the genotypes for all thirteen traits of field pea indicating thereby existence of considerable genetic variability (Table 1). So, the vast range of variation present among these genotypes gives ample scope to plant breeder for selection of superior and desired genotypes for continued crop improvement. Singh *et al.*, 2017 [24]; Pratap *et al.*, 2021 [17]; Bahadur and Devi, 2021 [3] also reported significant variation among field pea genotypes for different traits.

**Table 1:** Analysis of variance for 13 quantitative traits in field pea

Characters	Mean	Range		S.E	CD (5%)	CD (1%)	Source of variation and mean squares		
		Min.	Max.				Replication DF (2)	Treatment DF (38)	Error DF (76)
DF	76	70	93	0.41	0.83	1.09	0.179	30.29**	0.258
DM	124	120	140	0.68	1.36	1.79	11.61**	20.95**	0.69
NPB	2.59	1.8	3.33	0.22	0.44	0.58	0.60**	0.25**	0.73
NSB	1.34	0.4	3.47	0.34	0.68	0.90	0.34	1.34**	0.17
NN	13.19	10.87	16	0.87	1.74	2.30	13.20**	4.52**	1.14
Ht. of 1 <sup>st</sup> pod	37.44	18.33	56	2.79	5.57	7.38	138.64**	373.81**	11.72
PH	69.27	30	109	4.91	9.80	13.02	96.444	1978.30**	36.33
100-SW	15.79	12.65	18.12	0.36	0.73	0.96	0.91*	4.17**	0.2
NPP	25.04	15.93	42.53	2.64	5.26	6.97	1.56	99.70**	10.46
NSP	4.89	3.87	5.8	0.25	0.51	0.67	0.22	0.77**	0.1
BY	29.77	13.37	49.5	2.50	4.48	5.94	1.482	183.41**	7.6
SYP	13.97	5.7	24.77	1.15	2.28	3.03	3.309	46.43**	1.98
HI	47.05	31.27	57.61	2.38	4.73	6.27	20.07	105.03**	8.47

\*, \*\* significant at 5% and 1%, respectively, DF-Days to 50% flowering; DM-Days to maturity; NPB-Number of primary branches per plant; NSB- Number of secondary branches per plant; NN-Number of nodes per plant; Ht. of 1<sup>st</sup> pod-height; Height of first pod; PH-Plant height; 100-SW-100-seed weight; NPP-Number of pods per plant; NSP-Number of seeds per pod; BY-Biological yield per plant; SYP-Seed yield per plant; HI- Harvest index.

### Genetic variability analysis

The overall magnitude of GCV was observed lower than that of PCV for all 13 traits with varying degree implying that environment has a role in expression of these traits among the studied genotypes. Earlier, similar results of slightly higher PCV than GCV were observed by Meena *et al.*, 2017 [12]; Pathak *et al.*, 2019 [16]; Bahadur and Devi, 2021 [3] in field pea. As per Deshmukh *et al.* (1986) [6] a value greater than 20% of PCV and GCV is considered to be high, whereas value 10-20% and < 10% are to be regarded as medium and low, respectively. Based on this categorization, a close observation of experimental results revealed a high estimate of PCV and GCV, respectively for number of secondary

branches plant<sup>-1</sup> (50.03%, 46.66%), plant height (37.07%, 29.35%), height of first pod (29.82%, 36.73%), seed yield plant<sup>-1</sup> (28.16%, 21.78%), biological yield plant<sup>-1</sup> (26.26%, 25.71%) and number of pods plant<sup>-1</sup> (23.02%, 27.55%). However, a moderate PCV were observed for harvest index (12.58%), number of primary branches plant<sup>-1</sup> (11.08%) and number of seeds pod<sup>-1</sup> (10.4%), whereas only one trait (harvest index) showed moderate GCV with a value of 12.06%. A low value of PCV and GCV, respectively were exhibited by number 100-seed weight (7.47%, 7.28%), days to 50% flowering (4.21%, 4.19%), days to maturity (2.13%, 2.09%) and number of nodes plant<sup>-1</sup> (8.05%, 9.31%). Narrow sense heritability ( $H^2_{ns}$ ) represents the genetic

strength of the traits and indicates the efficiency of selection, whereas genetic advance in percentage (expected) of mean (GAM) serve as indicator of efficacious and systematic progress of selection. As per Johnson *et al.* (1955) <sup>[10]</sup> heritability in narrow sense and the expected genetic advance as percentage of mean has direct correspondence with the magnitude of additive gene effects, therefore, simple selection would be effective for all the traits having high heritability. The heritability and GAM in the present investigation varied from 0.16% to 82.92% and 0.05% to 16.88%, respectively as shown in Table 2. Low magnitude of  $H^2_{ns}$  coupled with low GAM were observed for most of traits except days to

maturity, height of first pod indicating pre-dominant control of non-additive gene action and hence heterosis breeding would be rewarding for their genetic improvement whereas, moderate  $H^2_{ns}$  along with low GAM were observed for days to maturity and height of first pod while plant height exhibited high heritability with moderate GAM indicating that these characters might be governed by non-additive gene action and high heritability might be exhibited due to favourable influence of environment. Similar studies on heritability and genetic advance in field pea made by Jeberson *et al.*, 2016 <sup>[9]</sup>; Pathak *et al.*, 2019 <sup>[16]</sup>; Pratap *et al.*, 2021 <sup>[17]</sup>; Pujari *et al.*, 2021 <sup>[18]</sup> were in partial agreement with our findings.

**Table 2:** Estimates of variability parameters for quantitative traits in field pea

Character	Variance			Coefficient of variation (%)		Heritability(n.s)	Genetic advance as 5% of mean
	$\sigma^2_p$	$\sigma^2_g$	$\sigma^2_e$	Genotypic	Penotypic		
DF	10.099	10.012	0.086	4.19	4.21	16.26	0.67
DM	6.985	6.754	0.231	2.10	2.13	55.10	1.29
NPB	0.082	0.058	0.024	9.31	11.08	0.16	0.01
NSB	0.446	0.388	0.058	46.66	50.03	9.38	0.09
NN	1.507	1.127	0.380	8.05	9.31	6.44	0.12
Ht. of 1 <sup>st</sup> pod	124.603	120.697	3.907	29.35	29.82	45.90	5.09
PH	659.432	647.322	12.110	36.73	37.07	82.92	16.80
100-SW	1.389	1.323	0.067	7.28	7.47	6.48	0.11
NPP	33.232	29.747	3.485	21.78	23.02	22.15	1.55
NSP	0.258	0.226	0.033	9.72	10.4	6.88	0.05
BY	61.137	58.605	2.532	25.71	26.26	20.70	1.68
SYP	15.478	14.818	0.660	27.55	28.16	10.36	0.46
HI	35.009	32.185	2.824	12.06	12.58	6.12	0.48

\*, \*\* significant at 5% and 1%, respectively, DF-Days to 50% flowering; DM-Days to maturity; NPB-Number of primary branches per plant; NSB- Number of secondary branches per plant; NN-Number of nodes per plant; Ht. of 1<sup>st</sup> pod-height; Height of first pod; PH-Plant height; 100-SW-100-seed weight; NPP-Number of pods per plant; NSP-Number of seeds per pod; BY-Biological yield per plant; SYP-Seed yield per plant; HI- Harvest index.

## Conclusion

The understanding of variability present among the genotypes of a crop species is of utmost importance for their genetic improvement to produce high yielding cultivars. Thus we investigated 39 genotypes for 13 quantitative traits to examine the genetic variability present, phenotypic and genotypic associations and various traits contributing directly or indirectly to yield in field pea. High magnitude of PCV and GCV was observed for number of secondary branches plant<sup>-1</sup> followed by plant height, height of 1<sup>st</sup> pod, seed yield plant<sup>-1</sup>, biological yield plant<sup>-1</sup> and number of pods plant<sup>-1</sup> implied that adequate variability is present for almost all the traits. Low heritability coupled with low genetic advance were observed for most of traits expect days to maturity, height of first pod and plant height suggesting that these traits are genetically controlled by non-additive gene action and heterosis breeding would be rewarding for these traits. The present study's findings on genetic advance, heritability, and variability showed potential for increasing field pea yield through selection using variables like the genetic coefficient of variation, heritability, and GA. These results have significance when creating an effective breeding programme because breeders may employ additive gene effects, transgressive segregation, and heterosis to increase yield when there is enough genetic variability.

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