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## Studies on genetic variability, heritability and genetic advance in pea (*Pisum sativum* L.)

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#### Abstract

The present investigation was carried out during *Rabi* season 2015-16 to study the genetic parameters, genetic variability, heritability and genetic advance for 62 pea genotypes. This experiment was laid out at Research Farm of Institute of Agricultural Sciences, Banaras Hindu University, Varanasi in a randomized block design with three replications. Data were recorded for nine characters. Analysis of variance revealed that the highly significant differences are present among the genotypes for all the characters under study. The genotypes exhibited wide range of variability for most of the traits. The genotype IC-203386, IPF-9931, PANTP-14 and IC-267182 showed high mean performance for yield. The analysis of genetic parameters revealed higher phenotypic and genotypic coefficient of variation was found for character plant height (1186.10% and 1152.77%) while moderate PCV and GCV found for character observation traits pod per plant (4.09% and 3.15%), 25 seed weight (0.52% and 0.40%), seed yield per plant (1.61% and 1.26%), pod length (0.39% and 0.33%), number of primary branches (0.09% and 0.028%) and seed per pod (0.41% and 0.21%). High heritability coupled with higher estimates of genetic advance as a per cent of mean observed for characters plant height, 25 seed weight, seed yield per plant, pod length and pod per plant, shows that simple selection could be practiced for improving these characters.

**Keywords:** Pea, variability, heritability, PCV, GCV and genetic advance

#### Introduction

The pea (*Pisum sativum* L.) is the most important grain legume crop grown worldwide, used as food, fodder and vegetable. The wide distribution of this crop is due to rich protein content, balanced amino acid composition, high digestibility and comparatively higher yield levels among other pulses. Pea ( $2n = 2x = 14$ ), a member of family Fabaceae is native to Europe and West Asia, while its wild prototype came from Ethiopia. In India, it is grown mainly as a winter vegetable in the plains of north and central parts and as a summer vegetable in the hilly regions of the country. Pea is the valued primarily for the nutritional quality having high protein as 7.2%, vitamin A - 5%, beta carotene 4%, and sufficient carbohydrates. Large proportion of peas are processed (canned, frozen or dehydrated) for consumption in off season. The crop is grown for its green pods and dried seeds and is known for its superior quality protein like lysine content, the limiting amino acid in cereals. Pea has great nutrient value and contains vitamin-A, B and C, along with minerals, dietary fibre and antioxidant compounds. Estimating the parameters of variability, especially heritability and genetic advance are important indicators for improvement of characters through selection whereas the selection for highly heritable characters is more effective for a successful breeding programme. 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 pea.

#### Materials and Methods

The investigation was conducted at Agricultural Research Farm, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi during *Rabi* season 2015-16. The crop was planted in a randomized block design with three replications. Each genotype was grown in three row plot of four meter length. Row-to-row and plant-to-plant distance was maintained at 60cm and 15cm, respectively. The experimental material consisted of sixty-two genotypes of pea obtained from different Institutions of India (Table-1). Observations were recorded on three randomly selected plants from each treatment on nine characters *viz.*, Plant height (cm), Number of primary branches per plant, Days to 50% flowering, Days to maturity, Number of pods per plant, Pod length (cm), Number of Seeds per pod, 25 seed weight (g), Seed yield per

plant (g). The mean data was used for statistical analysis. Analysis of variance was carried out as per the procedure given by Panse and Sukhtame (2000) [13], phenotypic and genotypic coefficients of variation were estimated by given by

Burton (1952) [14] and heritability in broad sense was estimated as per formula given by Allard (1960) [15]. The expected genetic advance was calculated by using formula as suggested by Allard (1960) [15].

**Table 1:** Pedigree and source of procurement of the sixty-two field pea (*P. sativum* L.) genotypes evaluated in the present study.

S. No	Name of the genotype	Pedigree	Source
1.	JPBB-3	Local genotype of JNKV Jabalpur	JNKV Jabalpur
2.	JPBB-4	Local genotype of JNKV Jabalpur	JNKV Jabalpur
3.	KPMR-669	Not available	NA
4.	KPMR-636	KPMR157 X DDR-4	CSAUAT, KANPUR
5.	KPMR615	DMR37 X P1463	CSAUAT, KANPUR
6.	KPMR-678	KPMR-186 X KPMR-157	CSAUAT, KANPUR
7.	KPMR-666	Not available	CSAUAT, KANPUR
8.	VL-42	VL Mater X P-388	VPKAS, ALMORA
9.	LMR-20	NA	JNKV Jabalpur
10.	PANT P-13	HFP-4 X FC-1	GBPUAT, PANTNAGAR
11.	DDR-27	HFP-4 X P-10	IARI, NEW DELHI
12.	DDR-23	HFP-4 X P-10	IARI, NEW DELHI
13.	DDR-49	Selection from ET-2255-1	IARI, NEW DELHI
14.	PANT P-20	HFP-4 X FC-1	GBPUAT, PANTNAGAR
15.	DDR-66	HFP-4 X P-1540	IARI, NEW DELHI
16.	PANT P-31	EC1 X FC1	GBPUAT, PANTNAGAR
17.	IPF-2-13	HFP-4 X EC-1	GBPUAT, PANTNAGAR
18.	IFP-2-13	NA	NA
19.	IFP-1-19	NA	NA
20.	IFP-1-22	NA	NA
21.	HUDP-18	NA	BHU, VARANASI, UP
22.	HUDP-15	PG-3 (PG-3 X S-143) FC-1	BHU, VARANASI, UP
23.	AMBIKA	DMR-7 X HUP-27	IGKV, RAIPUR
24.	PANT P-19	EC-324110 X FC1	GBPUAT, PANTNAGAR
25.	HUDP-27	NA	BHU, VARANASI, UP
26.	PANT P-101	Pusa-10 x FC1	GBPUAT, PANTNAGAR
27.	PANT P-12	(HFP-4 X P-1542)X(HFP4 X P-1540)	GBPUAT, PANTNAGAR
28.	IPF-9728	NA	NA
29.	KPMR-400	Rachna x HFP-4	CSAUAT, KANPUR
30.	IPF-400	NA	NA
31.	DDR-61	HFP-4 X KPMR-157	IARI, NEW DELHI
32.	JP-1193	NA	NA
33.	JP-861	NA	NA
34.	IPF-9414	NA	IGKV, RAIPUR
35.	IPF-9931	KPMR-10 X KIRAN	IGKV, RAIPUR
36.	IC-208380	NA	NBPGR, NEW DELHI
37.	IC-267182	NA	NBPGR, NEW DELHI
38.	IC-208186	NA	NBPGR, NEW DELHI
39.	IC-199776	NA	NBPGR, NEW DELHI
40.	IC-267171	NA	NBPGR, NEW DELHI
41.	Pant P-19	EC-324110 X FC-1	GBPUAT, PANTNAGAR
42.	Pant P-20	HFP-4 X FC-1	GBPUAT, PANTNAGAR
43.	Pant P-11	T-161 X FC-1	GBPUAT, PANTNAGAR
44.	HFP-9426	NA	NA
45.	HUP-1	KPMR-84 X EC 109194	BHU, VARANASI, UP
46.	Pant P-25	EC-324110 X FC-1	GBPUAT, PANTNAGAR
47.	HUP-9	NA	NA
48.	Pant P-14	HFP-4 X Longitee	GBPUAT, PANTNAGAR
49.	Pant P-20	HFP-4 X FC-1	GBPUAT, PANTNAGAR
50.	Ec-318761	NA	NBPGR, NEW DELHI
51.	EC-313639	NA	NBPGR, NEW DELHI
52.	EC-322745	NA	NBPGR, NEW DELHI
53.	EC-324118	NA	NBPGR, NEW DELHI
54.	EC-324121-II	NA	NBPGR, NEW DELHI
55.	EC-324132	NA	NBPGR, NEW DELHI
56.	IARI-3138	NA	IARI, NEW DELHI
57.	IARI-3191	NA	IARI, NEW DELHI
58.	IARI-2877	NA	IARI, NEW DELHI
59.	IARI-2876	NA	IARI, NEW DELHI
60.	IARI-2875	NA	IARI, NEW DELHI
61.	IARI-2875-II	NA	IARI, NEW DELHI
62.	JPBB-5	NA	JNKV Jabalpur

## Results and Discussion

The data pertaining to heritability and genetic advance of all the traits under consideration have been presented in Table-2. Results revealed that high heritability for plant height (97%) followed by days to 50% flowering (87%), days to maturity (87%), pod length (83%), seed yield per plant (78%), pod per plant (77%) and 25-seed weight (77%) were noticed during course of study. The genotypic coefficient of variability helps to measure of the range of genetic diversity for a specific character and to compare the genetic variability for the quantitative traits. The high genotypic coefficient of variability accompanied by high phenotypic coefficient of variability were observed for plant height for all the characters under study which is an indicator of additive gene effect influenced by environment on the expression of the traits. Similar finding were also reported by Arya *et al.* (2004)<sup>[1]</sup>. Moreover, PCV and GCV were observed higher for days to 50% flowering, days to maturity, plant height during investigation. Similar results were reported by Tiwari *et al.* (2001)<sup>[7]</sup>, Sharma *et al.* (2007)<sup>[8]</sup> in pea. The difference among the genotypic coefficient of variance and phenotypic coefficient of variance value for different characters indicated that the influence of environment in expressing the variability with traits. The estimates of heritability (>60%) in broad sense for nine characters were studied. Out of nine characters, eight characters were observed for high heritability *viz* seed yield per plant (97%), days to 50% flowering (87%), days to maturity (87%), number of pods per plant (83%), number of seeds per pod (78%), 25seed weight (77%), No of primary branches/plant (77%). Moderate heritability (30-60%) was observed for pod length (50%), plant height (30%). Similar results were obtained by Sureja and Sharma (2000)<sup>[12]</sup>, Mahanta *et al.* (2001)<sup>[4]</sup>, Salman *et al.* (2007)<sup>[5]</sup>, Sharma *et al.* (2013)<sup>[6]</sup>. The high heritability denotes high proportion of

genetic effects in the determination of these characters and can be adopted for improving seed yield. Seed yield the characters showing high heritability, could be owing to greater contribution of additive genetic components in the inheritance of these attributes. For an effective selection, the knowledge alone on the estimates of heritability is not sufficient and genetic advance if studied along with heritability is more useful. The genetic advance expressed as percentage of mean was high (>20%) for seed yield per plant (76.97%), Number of primary branches per plant (23.62%), 25-seed weight (23.54%), number of seed per pod (21.77%), number of pods perplant (20.40%).

In present investigation high heritability coupled with high genetic advance observed for pod per plant, pod Length, seed Yield Per plant, 25Seed weight, plant height. Similar results were reported by Sureja and Sharma (2000)<sup>[12]</sup>, Mahanta *et al.* (2001)<sup>[4]</sup>, Salman *et al.* (2007)<sup>[5]</sup>, Sharma *et al.* (2013)<sup>[6]</sup>. High heritability with low genetic advance was recorded for days to 50% flowering, days to maturity and moderate heritability and genetic advance recorded for seeds per pod. Some of these characters have also been reported earlier by Sharma *et al.* (2007)<sup>[8]</sup>, Singh *et al.* (2011)<sup>[10]</sup>, Kumari *et al.* (2009)<sup>[3]</sup>, Katiyar *et al.* (2009)<sup>[2]</sup>. High heritability with moderate genetic advance indicated the presence of both additive and non-additive gene effects; while high/low heritability with low genetic advance for width of pod indicated the importance of non-additive gene action. Hence, that characters obtained high heritability and high genetic advance could be used for selection will be effective for these traits. From the present study, it concludes that PCV and GCV were high seed yield per plant, number of pods per plant which indicated that high degree of variability in this character and suggested that possibility of yield improvement through selection of these trait.

**Table-2:** Estimations of mean, range coefficients of variability, heritability and genetic advance

Characters	Grand mean (x)	Range	Coefficients of variability PCV GCV		Heritability % in Broad sense	Genetic Advance (GA)	GA. In % of mean
Days to 50% flowering	71.58	57-76.00	8.24	7.18	87	5.15	7.20
Days to maturity	113.99	108.3-127.3	7.74	6.77	87	5.03	4.41
Plant height	89.58	38.0-154	1186.10	1152.77	30	0.19	12.08
No of primary branches/plant	1.58	1.1-2.22	0.09	0.028	77	3.21	23.62
Number of pods per plant	13.60	10-17.5	4.09	3.15	83	1.08	20.40
Pod length	5.32	3.85-6.32	0.39	0.33	50	0.66	15.37
Number of seeds per pod	4.34	3.13-5.86	0.41	0.21	78	2.05	21.77
25-seed weight	4.91	2.7-6.09	0.52	0.40	77	1.15	23.54
Seed yield per plant	9.41	7.12-11.8	1.61	1.26	97	68.95	76.97

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