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Genetic variability, heritability and genetic advance in vegetable pea (*Pisum sativum* L. var. *hortense*)

Maneesh Pandey*, V.B. Singh and G.C. Yadav, Pradip Pandey[1], and Yamuna Prasad Singh

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Vegetable pea (*Pisum sativum* L. var. *hortense*) belongs to family Leguminoceae sub family Fabaceae. Pea is an important legume vegetable, extensively cultivated in the temperate regions and restricted to cooler altitudes in the tropics and winter season in the sub-tropics. It is a self-pollinated crop having diploid chromosome number, 2n=14. It is highly nutritious and capable of fixing atmospheric nitrogen. Being most important to growers and consumer, there is an urgent need to increase its productivity to fulfill the increasing demands throughout the year. The information usually needed for developing high yield varieties in a particular species pertains to the extent of genetic variability for desirable traits in the available germplasm. Evaluation of germplasm is the basic tool for identification of improved genotypes. The great extent of natural variation present in various characters among the genotypes suggests good scope of improvement in economic traits. Large variability ensures better chance for selection of new genotypes. Variability parameters like genotypic and phenotypic coefficient of variation, heritability and genetic advance as well as degree of association between the various characters along with direct and indirect effect of yield contributing characters on yield, and genetic divergence among the genotypes for quantitative traits is of paramount significance in formulating an appropriate breeding strategy aimed to exploit the inherent variability of the original population.

The experiment was conducted at NDUAT, Faizabad, UP by using Randomized Complete Block Design with three replications during *Rabi* season of 2013 to assess the performance of 36 vegetable pea genotypes. Each genotype consisted of five rows and replicated thrice. Each entry was grown in the plot size of and 3.0×1.5 m. The line sowing was done with the spacing of 30 cm and 10 cm from seed to seed. All the recommended agronomic package of practices and plant protection measures were followed to raise a healthy crop. Observations were recorded on five randomly selected plants from each treatment in each replication for; (i) nodes at which first flower appears, (ii) days to 50% flowering, (iii) number of nodes per plant (iv) inter-nodal length (cm), (v) primary branches per plant, (vi) plant height (cm) (provide units), (vii) length of pod (cm), (viii) width of pod (cm), (ix) number of green pods per plant, (x) number of green pods per cluster, (xi) number of seeds per pod (xii) shelling percent (xiii) pod weight (g), (xiv) TSS of edible seeds (Brix), (xv) pod yield per plant (g). The mean squares for error was subtracted from the mean squares due to genotypes and the difference was divided by number of replications for obtaining the genotypic variance, which was calculated according to the method suggested by Burton (1952). Environmental variance is the mean squares due to error. Phenotypic variance was calculated by adding genotypic variance and environmental variance, which was suggested by Burton and de Vane (1953). Heritability in broad sense (h^2_{bs}) was calculated using the formula suggested by Burton and de Vane (1953).Genetic advance (GA) was estimated by the method suggested by Johnson et al. (1955).

The mean squares due to genotypes were highly significant for all the fifteen traits (Table 1), indicating significant differences among the genotypes with respect to all the traits under study. In general, the phenotypic coefficient of variability (PCV) was higher than the respective genotypic coefficients of variability (GCV) for all the characters which indicates that environment played an important role in the expression of the traits. The highest phenotypic and genotypic coefficient of variation was observed for plant height, green pod yield per plant, days to 50% flowering, shelling per cent and number of green pod per plant. Singh and Dhillon (2004) and Kumaran et al. (1995) also reported higher GCV and PCV for number of green pod per plant, weight of

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Department of Vegetable Science, Narendra Deva University of Agriculture & Technology, Kumarganj, Faizabad-224229, UP
[1]BBAU, Lucknow-226025, UP
*Corresponding author email: maneeshpandey9219@gmail.com

Table 1: Analysis of variance (mean squares) for fifteen quantitative characters in vegetable pea

Characters	Source of variation		
	Replications	Treatments	Error
d. f.	2	35	70
Nodes at which first flower appears	0.41	7.12**	0.67
Days to 50% flowering	5.12	265.01**	2.89
No. of nods per plant	0.53	26.88**	0.96
Intermodal length (cm)	0.63	3.61**	0.34
Primary branches per plant	0.31	0.71**	0.19
Plant height (cm)	133.97	1293.88**	42.89
Length of pod (cm)	0.70	1.74**	0.52
Width of pod (cm)	0.01	0.04**	0.03
No. of pods per plant	4.21	25.51**	2.61
No. of pods per cluster	0.51	0.45**	0.07
No. of seeds per pod	1.28	1.65**	0.54
Shelling (%)	1.14	38.36**	3.24
Pod weight (g)	0.55	2.65**	0.25
TSS	3.69	3.82**	0.93
Pod yield per plant (g)	270.92	383.22**	73.99

*, ** Significant at 5% and 1% probability levels, respectively

seed per pod, green pod yield per plant in his studies. Moderate PCV and GCV were estimated for inter nodal length, number of nodes per plant, nodes at which first flower appears and number of seeds per pod. The PCV and GCV were lower for pod weight. It may be due to the fact that the environment influenced the observed variance.

Table 2: Range, grand mean, phenotypic (PCV), genotypic (GCV), environmental (ECV) coefficient of variation, heritability in broad sense, genetic advance in per cent of mean (GA) for fifteen characters in vegetable pea

Characters	Range		Grand mean	Variability			Heritability in broad sense (%) (h^2_{bs})	Genetic advance (GA)	Genetic advance in per cent of mean (GA %)
	Lowest	Highest		PCV (%)	GCV (%)	ECV (%)			
Nodes at which first flower appears	7.33	12.77	9.42	18.08	15.83	8.69	76.69	2.874	30.507
Days to 50% flowering	40.33	69	51.90	18.35	18.05	3.28	96.77	19.15	36.90
No. of nods per plant	11.07	20.20	15.04	20.62	19.58	6.51	90.16	5.95	39.52
Inter-nodal length (cm)	3.37	7.73	5.68	21.06	18.40	10.24	76.35	2.048	36.08
Primary branches per plant	1.33	2.93	2.18	27.55	18.92	20.17	47.13	0.73	33.29
Plant height (cm)	49.13	121.00	80.71	26.57	25.30	8.11	90.67	41.36	51.25
Length of pod (cm)	6.40	10.13	8.30	11.59	7.68	8.68	43.89	1.10	13.24
Width of pod (cm)	1.63	2.10	1.87	9.41	2.90	8.95	9.48	0.05	2.93
No. of pods per plant	5.40	17.40	11.89	26.93	23.25	13.60	74.50	5.39	45.37
No. of pods per cluster	1.07	2.00	1.36	32.52	26.41	18.94	65.98	0.68	49.92
No. of seeds per pod	5.13	7.80	6.27	15.18	9.70	11.68	40.79	1.12	16.40
Shelling (%)	31.67	48.33	44.88	8.63	7.59	4.10	77.44	6.75	15.03
Pod weight (g)	3.27	6.92	4.78	21.40	18.69	10.44	76.29	1.75	36.64
TSS	11.43	15.87	13.82	9.97	7.04	6.98	49.96	1.76	12.72
Pod yield per plant (g)	22.88	78.59	49.86	26.71	20.34	17.25	58.04	18.79	37.68

The heritability in broad sense ranged from 9.48% for pod width to 96.77% for days to 50% flowering (Table 2). High estimates of heritability >75 % were recorded for all the characters except seed TSS (49.96%), primary branches per plant (47.13 %) and length of pod (43.89 %). Highest value of genetic advance in percent of mean was shown by plant height (51.25%), while pod width exhibited lowest (2.93%) which indicated opportunity for improvement through selection in available germplasm of vegetable pea. Singh and Dhillon (2004) found high heritability estimates for number of green pods per plant and number of primary shoots, respectively. Moreover, Gupta et al. (2006) reported high heritability for early yield per plant, while Lal et al. (2011) reported high heritability for plant height, biological yield, number of pods per plant and cluster per plant. Dar et al. (2013) also reported high heritability coupled with high genetic advance for most of the traits except plant height, number of nodes per plant and pod weight. A high estimate of heritability along with high genetic advance provides good scope for further improvement in advance generations. Thus, the degree of success in selection depends upon the magnitude of the heritability values.

In vegetable pea, high heritability coupled with high genetic advance was observed for days to 50% flowering, primary branches per plant, number of node per cluster, shelling percentage and TSS indicating that these traits could be improved through selection. Consideration of these traits for improvement will be helpful to in the development of new high yielding varieties with good pod quality.

References

Burton GW and de Vane EH (1953) Estimated heritability in tall replicated clonal material. Agron J 45: 474-478.

Dar SA, Ishfaq A, Ali G, Pir FA and Abu M (2013) Studey on genetic variability, heritability and genetic advance in pea (*Pisum sativum* L.). Ann Hort 6(1): 161-163.

Gupta AJ, Singh YV and Verma TS (2006) Genetic variability and heritability in garden pea (*Pisum sativum* L.). Indian J Hort 63 (3): 332-334.

Johnson HW, Robinson HF and Comstock RE (1955) Eatimates of genetic and environmental variability in soyabean. Agron J 47: 314-318.

Kumaran SS, Natrajan S and Thamburaj S (1995) Genetic variability in pea (*Pisum sativum* L.). South Indian Hort 43 (1-2): 10-13.

Lal GM, Meena ML and Singh C (2011) Assessment of genetic variability and interrelation between yield and its contributing components in pea (*Pisum sativum* L.). Environ Ecol 29 (3A): 1235-1239.

Singh N and Dhillon GS (2004) Genetic variability for pod yield and its contributing traits in pea (*Pisum sativum* L.). Haryana J Hort Sci 33 (3): 300-301.

Singh SM, Singh M, Singh MK, Kumar S, Dev P and Kumar V (2012) Genetic advancement in pea (*Pisum sativum* L.). Prog Agric 12 (1): 219-222.