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Study on Genetic Variability, Heritability and Genetic Advace in Vegetable Pea (*Pisum sativum* var. *hortense* L.) Genotypes

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ABSTRACT

Keywords

Phenotypic coefficients of variation (PCV), Genotypic coefficients of variation (GCV), Heritability, Genetic advance.

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The present investigation conducted with the using 40 genotypes of vegetable pea to study the extent of variability and genetic divergence among the genotypes for growth yield and quality attributes. The study was conducted in the Randomized block design with 3 replications. The study revealed that mean sum of squares due to genotypes for 18 quantitative characters was highly significant for all traits indicating ample variation among the genotypes. The estimates of phenotypic coefficients of variation (PCV) were higher than genotypic coefficients of variation (GCV) for all the traits. High magnitudes of variability were observed in case of number of pods per plant, primary branches per plant and pod yield per plant, with of pod. High heritability coupled with high genetic advance in per cent of mean were observed for number of pods per plant, primary branches per plant and pod yield per plant indicating scope of high selection response. High estimate of heritability along with high genetic advance in per cent of mean provides good scope for further improvement in advance generations.

Introduction

Vegetable pea (*Pisum sativum* var. *hortense* L.), belongs to Fabaceae family, is one of the most popular vegetable crop grown all over the world, both for fresh market and the food processing industry. It has a prominent place among vegetables due to its high nutritive value, particularly proteins and other health building substances like carbohydrates vitamin A, vitamin C, calcium and phosphorus. There is a very less work has employed regarding the crop improvement of vegetable pea. Critical analysis of the genetic variability is a prerequisite for initiating any crop improvement programme and for adoption of appropriate selection techniques. The adequate information on extent of variability parameters may be helpful to improve the yield by selecting the yield component traits because yield is a complex trait, whose manifestation depends on the component traits. Generally, the estimates of heritability (h2) of traits are environment specific). The higher the heritable variation, the greater will be the possibility of fixing the characters by selection methods. Therefore present investigation was carried out to assess the genetic variability and nature of association between yield and yield components in vegetable

The study of genetic parameters like genotypic and phenotypic coefficient of variation, heritability, genetic advance and genetic advance as per cent of mean provide a clear data about extent of variability present in a plant population and a relative measure of efficiency of selection of genotypes based on phenotype in a highly variable population.

The present investigation was carried out to ascertain magnitude and extent of genotypic and phenotypic coefficient of variation, heritability, genetic advance and genetic advance as per cent of mean in 40 different genotypes for 18 traits under Faizabad conditions.

Materials and Methods

The experimental material comprised forty genotypes of vegetable pea collected from different places in India and being maintained at Main Experiment Station, Vegetable Science farm, N. D. University of Agriculture and Technology, Narendra Nagar (Kumarganj), Faizabad (U.P.). The experiment was carried out at Vegetable Research Farm, Narendra Deva University of Agriculture and Technology, Narendra Nagar (Kumarganj), Faizabad (U.P.) during Rabi season of 2014-2015.The experimental was conducted in Randomly Block Design with 3 replications to assess the performance of 40 (including 7 check) genotypes. Seed of each genotype were sown in a plot measuring 3.0 x 0.90 meter at spacing of 30 cm and 10 cm were maintained between row to row and plant to plant, respect

Observations were recorded on 5 randomly selected plants from each genotype in each replication. The observations recorded on the 5 plants were summed up and divided by 5 to get mean value. The procedure is described under the respective sub-heads. The observations was recorded on characters *viz.*, days to 50 % flowering, plant height, number of nodes per plant, intermodal length, node at first flower appears, node at first pod appears, primary branches per plant, circumference of pod, width of pod, number of pods per plant, length of pod, number of seeds per pod, 100seed weight, number of seeds per 100gm, number of pod per 100g, shelling percentage, total soluble solids and pod yield per plant.

The experimental data was compiled by taking the mean value of the 40 genotypes of garden pea for eighteen yield and its components traits from all the three replications.

Then it was subjected to the following statistical analyses: Analysis of variance for the design of experiment (Panse and Sukhatme, 1967), estimation of coefficient of variation (GCV and PCV) (Burton and de Vane, 1953). Heritability and Genetic advance in per cent of mean (Johnson *et al.*, 1955) and genetic divergence of forty genotypes of vegetable pea was worked out using Mahalanobis (1936) D^2 statistics. The 18 quantitative characters in pea were included for these analyses.

Results and Discussion

The analysis of variance for different characters had been presented in table 1. The mean sum of square due to genotypes was highly significant for all characters. In other words, the performances of the genotypes with respect to these characters were statistically different; suggesting that, there is ample scope for selection in the available genotypes of vegetable pea. The results are with conformity of earlier researcher like, Chaudhary and Sharma (2003) and Gupta *et al.*, (2006).

The estimate of genotypic coefficient of variation is of prime importance to breeder because genetic variance alone, does not allow a decision as to which characters were showing the highest degree of variability. Therefore, accurate relative comparison can be made with the help of phenotypic and genotypic coefficient of variation. In general, the phenotypic coefficients of variability were higher than the genotypic coefficient of variability for all characters under study, which indicated that environment played very important role in the expression of the traits.

The highest phenotypic and genotypic coefficient of variation values (>20%) (Table 2) were observed for number of pods per plant, primary branches per plant and pod yield per plant, width of pod. Similar, results have been reported by Chaudhary *et al.,* (2010) and Singh *et al.,* (2012). The moderate phenotypic and genotypic coefficient of variation values (15-20%) were observed days to 50% flowering, intermodal length, plant height, node at first flower appears, number of seed per pod. Similar, results have been reported by Srivastava *et al.,* (2009) and Lal *et al.,*(2011).

The phenotypic and genotypic coefficients of variations values (<15%) were lower for number of seed per 100g, circumference of pod, node at first pod appears, number of pod per plant, number of node per plant, T.S.S.(%), 100g seed weight, length of pod, shelling percentage.

Table.1 Analysis of variance (mean sum of squares) for 18 characters in vegetable pea

S. No	Characters	Source of variation		
		Replications	**Treatments**	**Error**
	d.f.	**2**	**39**	**78**
1.	Days to 50% flowering	0.77	312.89**	7.93
2.	Plant height (cm)	6.21	719.60**	11.99
3.	Number of nodes per plant	2.49	17.01**	1.07
4.	Internodal length (cm)	0.06	1.51**	0.21
5.	Node at first flower appears	0.57	9.32**	0.78
6.	Node at first pod appears	0.17	8.05**	0.65
7.	Primary branches per plant	0.02	1.04**	0.06
8.	Circumference of pod (cm)	0.03	0.70**	0.11
9.	Width of pod (cm)	0.02	0.25**	0.03
10.	Number of pods per plant	1.07	54.38**	1.59
11.	length of pod (cm)	0.18	1.14**	0.45
12.	Number of seeds per pod	0.24	2.69**	0.51
13.	100 seed weight (g)	2.30	48.29**	4.60
14.	Number of seeds per 100 g	4.86	2991.73**	7.27
15.	Number of pods per 100 g	0.31	43.17**	2.86
16.	Shelling percentage (%)	3.65	15.64**	3.21
17.	T.S.S. (%)	0.23	7.62**	0.67
18.	Pod yield per Plant (g)	0.67	311.02**	4.65

*, ** - significant at 5 % and 1 % probability level, respectively.

Table.2 Estimates of range, grand mean, phenotypic (PCV), genotypic (GCV), and environmental (ECV) coefficient of variation, heritability in broad sense, genetic advance (Ga) and genetic advance in per cent of mean for 18 characters in vegetable pea

S. No.	Characters	Range		Grand mean	PCV (%)	GCV (%)	ECV (%)	Heritability (h^2_{bs}) in broad sense (%)	Genetic advance	Genetic advance in per cent of mean
		Lowest	Highest							
1.	Days to 50% flowering	40.33	72.00	53.55	19.54	18.82	5.26	92.80	20.00	37.35
2.	Plant height (cm)	50.43	117.66	86.63	18.17	17.72	3.99	95.20	30.86	35.62
3.	Number of nodes per plant	14.66	25.00	19.83	12.73	11.61	5.22	83.20	4.33	21.82
4.	Internodal length (cm)	2.38	7.07	4.40	18.32	14.95	10.58	66.60	1.10	25.15
5.	Node at first flower appears	9.10	15.60	11.85	16.08	14.23	7.48	78.30	3.07	25.94
6.	Node at first pod appears	10.20	16.40	12.52	14.10	12.53	6.48	78.90	2.87	22.93
7.	Primary branches per plant	1.23	3.20	1.94	32.14	29.47	12.82	84.10	1.08	55.67
8.	Circumference of pod (cm)	2.80	4.98	3.81	14.59	11.59	8.88	63.00	0.72	18.93
9.	Width of pod (cm)	0.68	2.00	1.30	25.13	20.82	14.07	68.60	0.46	35.53
10.	Number of pods per plant	7.53	20.06	13.59	32.22	30.85	9.29	91.70	8.27	60.85
11.	length of Pod (cm)	7.40	9.80	8.54	9.68	5.60	7.89	33.50	0.57	6.68
12.	Number of seeds per pod	5.54	9.90	7.33	15.17	11.63	9.74	58.80	1.34	18.38
13.	100 seed weight (g)	30.46	45.73	37.89	11.55	10.06	5.66	76.00	6.85	18.08
14.	Number of seeds per 100 g	150.82	245.33	212.95	14.86	14.81	1.26	99.30	64.73	30.39
15.	Number of pods per 100 g	21.86	35.33	28.76	14.03	12.74	5.88	82.40	6.85	23.83
16.	Shelling percentage (%)	40.00	51.66	44.24	6.13	4.60	4.05	56.30	3.14	7.11
17.	T.S.S. (%)	12.02	19.26	14.55	11.87	10.45	5.63	77.50	2.76	18.96
18.	Pod yield per Plant (g)	24.56	56.30	40.55	25.47	24.91	5.31	95.60	20.35	50.19

Low GCV and PCV for these traits indicated that the genotypes taken in the present study were similar for these traits. The values of ECV were low for almost characters.

The heritability in broad sense (%) ranged from 33.50 in case of length of pod and 99.30 from number of seeds per 100g. High estimate of heritability were recorded for 8 characters *viz.* number of seed per 100g (99.30%), pod yield per plant, plant height, days to 50% flowering, number of pods per plant, primary braches per plant, number of nodes per plant and number of pods per plant 100g. The above estimates gave an indication that substantial genetic improvement can be achieved in these characters and indicating that these traits were little influenced by environment. These require low selection intensity for improvement. Similar results were also reported by Kumar *et al., (*2009) and Gupta *et al.,* (2006). High heritability does not mean a high genetic advance for a particular quantitative character. Johnson *et al.,* (1955) reported that heritability estimated along with genetic advance would be more rewarding than heritability alone in predicting the consequential effect of selection to choose the best individual.

High heritability coupled with high genetic advance in percent of mean (%), was shown by number of seeds per 100g and moderate pod yield per plant. Similar results were also reported by Srivastava *et al.,* (2009) and Dar *et al.*, (2013). This indicates the influence of non-additive gene action and environment in the expression of these traits which are less reliable for direct selection in crop improvement. So, breeder should adopt proper methods to utilize both additive and non-additive gene effects simultaneously. This highlights the fact that in variability studies one should not rely upon phenotype alone while making selection it is always better to consider PCV, GCV and high heritability coupled with high genetic percent of mean. Hence, the breeder should adopt suitable breeding methodology to utilize both additive and non-additive gene effects simultaneously since varietal and hybrid development will go a long way in the breeding programmes.

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