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Studies on heritability and genetic advance for the quantitative characters in Pea (*Pisum sativum* L.) in sodic condition

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Abstract

Pea (*Pisum sativum* L.) $2n = 2x = 14$, belongs to the family *Fabaceae*. It originated in central Asia, the Near East, Abyssinia and Mediterranean. In India huge range of variability is available in the land races or cultivars, in terms of qualitative as well as quantitative characters of pea. High heritability coupled with high genetic advance for days to 50% flowering and pods per plant. Whereas plant height had high estimates of heritability but genetic advance was low. The maximum positive direct effect on green pod yield per plant was expressed by plant height (cm) and pod length (cm) whereas, Internodal length (cm) showed negative direct effect on green pod yield per plant (g). It is suggested that selection for these traits will directly increase the green pod yield.

Keywords: Pea (*Pisum sativum* L.), Heritability, Genetic advance, Variability, Internodal length, Green pod yield.

Introduction

Pea ($2n=2x=14$) is strictly self-pollinated in nature. Stigma is receptive to pollen from several days prior to anthesis until one day or more after the flower wilts. Pollen is viable from the time of anther dehiscence until several days thereafter.

Pea can be grown on all kinds of soils but the best crop is harvested from well drained and fertile loam soil. Light soils are best for early crop whereas, heavy soils are found suitable for main crop and produces higher yield. Pea does best in a soil having pH 6.8 to 7.5. Pea does not thrive on acidic soils. The area of sodic soil in U.P. is 958 thousand ha. Anonymous (1998)^[1]. This area can be utilized by pea cultivation which is semi tolerance against this condition.

The possibility of improvement in any crop is measured by available variability in the crop. In past a number of pea varieties has been recommended by the central and state government for cultivation in eastern Uttar Pradesh. But no systematic work on evaluation of existing cultivars has been done so far. Genetic variability is essential for crop improvement programme for obtaining high yielding varieties. The screening of genetic variability is prerequisite to know the nature and magnitude of genetic variation and also the influence of environmental in the expression of yield and other traits. Greater the variability in the initial genetic material better would be the chance of selecting desirable type (Vavilov, 1959).

On other hand, yield is a complex character and is associated with some yield contributing characters. Yield is not only a polygenically controlled trait, but it is also directly or indirectly constituted by the associated yield characters.

Methods and Materials

The present investigation was carried out at Main Experiment Station, Department of Vegetable Science, Narendra Deva University of Agriculture & Technology, Kumarganj, Faizabad (U.P.) during Rabi -2009-10, to evaluate the heritability and genetic advance for the quantitative characters in pea (*Pisum sativum* L.) in sodic condition for yield and its component traits of 35 genotypes, with three replications in Randomized Block Design. Seed of each genotype were sown in a plot measuring 3.0 X 0.9 meter at spacing of 30 cm and 10cm were maintained between row to row and plant to plant respectively. The genotype NDVP-10 (31.93 g) significantly out yielded rest of the genotypes as well as check.

Results and Discussion

The prime objective of most of the plant breeding programme is to make an improvement in yield, but yield is a complex character and a combined result of a number of component traits.

Since yield is controlled polygenically and influenced greatly by the environmental fluctuations. Therefore, the selection of superior genotype based on yield alone would not be effective; one has to put attention on the component characters, which contribute yield in positive direction. In such a situation the available variability in the gene pool provides opportunity for selecting superior genotypes, which can be obtained through screening and evaluation. The knowledge of association between the characters helps to plant breeders in deciding the selection criteria. The identification of donor parents for important characters, assessment of genetic variation and diversity in the available genotypes and the information about characters association are required for successful breeding programmes.

Thus an attempt was made in the present investigation together the primary information on the magnitude of

variability and heritability, genetic advance with yield. The findings of present investigation consisting of thirty five genotypes of pea are discussed as follows for twelve characters.

Analysis of variance

The analysis of variance for different characters is presented in table 1. The mean sum of square due to replication was non-significant for all the characters but pod length and seeds per pod were significant. The variation due to treatment was highly significant for all characters except nod at 1st pod appear and seeds per pod. In other words the performances of the genotypes with respect of these characters were statistically different; suggesting that, there is ample scope for selection present in different traits for pea improvement.

Table 1: Analysis of variance (mean sum of square) for 12 characters in pea genotypes (2009-10).

Characters D.F.	Source of variation		
	Replication	Treatment	Error
	2	34	68
Days to 50% flowering	1.03	241.47**	4.13
Plant height (cm)	1.29	245.34**	4.29
Nodes/ plant	0.58	12.37**	1.23
Internodal length (cm)	0.003	0.25**	0.04
Node At First Pod Appears	0.12	7.06*	0.39
Branches/ Plant	0.20	0.81**	0.28
Pods/ Plant	2.17	11.20**	1.23
Pod length (cm.)	0.57*	0.42**	0.11
Shelling %	0.83	5.50**	0.98
Seeds/ Pod	1.62*	0.59*	0.33
100 Seed Weight (gm)	0.23	2.16**	0.13
Green Pod Yield/ Plant (gm)	1.08	18.82**	2.48

Heritability and genetic advance

Heritability in broad sense of a character is important to the breeder since it indicates the possibility and extent to which improvement is possible through selection. It also indicates direction of selection pressure to be applied for traits during selection because it measures relationship between parents and their progeny, hence widely used in determining the degree to which a character may be transmitted from parents to offspring. However, high heritability alone is not enough to make efficient selection in advanced generations unless accompanied by substantial amount of genetic advance (Burton, 1952) [2]. High estimates of heritability along with high genetic advance provide good scope for further improvement in advance generations. The result of present investigation revealed that low to high heritability estimates were present in all most all the characters. The heritability estimates for different characters ranged between 20.6 to 95 per cent Table 2. High heritability was recorded for days to 50 percent flowering followed by plant height, node at 1st pod appears, 100- seed weight, nodes per plant and pods per plant. Whereas green pod yield per plant and shelling percentage showed moderate level heritability. Low heritability was recorded for seeds per pod (20.6%) indicated more environmental effect due to presence of non-additive gene action in expression of characters. From this it was obvious that improvement of the characters exhibiting high heritability could be more efficiently by adopting normal selection procedures and for those having lower value, some other suitable breeding techniques, like population improvement programme would have to be adopted.

Heritability itself provides no indication of among of genotypic gain that will result from selection of best individuals. The genetic advance is commonly predicted as a product of heritability ratio and selection differentials. Johnson *et al.* (1955) [4] also advocated that heritability values alone in predicting the effectiveness of selection are not enough. Panse (1957) mentioned that where high heritability value is accompanied by high genetic advance. The progress realised by selection would be greater due to presence of additive gene action simple selection would be most appropriate. In present study, high heritability coupled with genetic advance in percent of mean was recorded for days to 50% flowering, branches per plant, plant height indicating that these traits were less influenced by environment.

On the other hand, the traits namely plant height, node at 1st pod appears and pods per plant had high heritability and moderate genetic advance also revealed the additive gene action for those traits. The high heritability coupled with low genetic advance for nodes per plant and green pod yield per plant might be due to the presence of low genetic advance for Internodal length and branches per plant is due to the presence of additive and non- additive gene effects. The low heritability association with low genetic advance for seeds per pod and pod length revealed that non-additive gene action was prevailing for these characters. Similar results were also reported by Korla and Singh (1988) [5], Dube and Lal (1988) [3] for seeds per pod and shelling percentage. While Supe and Patil (2010) [8] studied also support the result for branches per plant. In the study of Singh *et al.* (2007) [7] highest heritability was recorded for plant height.

Table 2: Estimates of range, grand mean, coefficient of variation (PCV & GCV), heritability (in broad sense) and Genetic advance for 12 characters of pea genotypes.

S. No.	Characters	Range		Grand Mean	PCV	GCV	ECV	Heritability (B S) (%)	Genetic advance in % of mean
		Lowest	Highest						
1	Days to 50% flowering	36.33	68.00	57.15	15.97	15.56	3.56	95	31.25
2	Plant height (cm)	68.90	122.73	82.51	11.15	10.86	2.51	94.9	21.80
3	Nodes/plant	18.00	27.67	22.78	9.77	8.46	4.88	75	15.09
4	Internodal length (cm)	3.02	4.33	3.65	9.39	7.21	6.00	59.1	11.42
5	Node at first pod appears	8.67	13.67	12.07	13.40	12.34	5.23	84.1	23.41
6	Branches/ plant	0.00	2.00	1.34	50.69	31.16	39.98	37.8	39.46
7	Pods/ plant	6.00	15.00	10.20	20.92	17.87	10.87	73	31.45
8	Pod length (cm.)	7.43	9.47	8.10	5.77	3.91	4.25	45.9	5.46
9	Shelling %	41.23	47.53	44.06	3.58	2.79	2.26	60.4	4.46
10	Seeds/ pod	6.33	8.33	6.91	9.39	4.26	8.36	20.6	3.97
11	100 seed weight (g)	15.00	18.90	16.77	5.37	4.91	2.18	83.6	9.25
12	Green pod yield/ plant (g)	21.67	31.93	26.49	10.63	7.93	5.95	68.7	15.05

Conclusion

Heritability in broad sense ranged from 20.6 to 95% which was in general high for all traits except seeds per pod and branches per plant. Whereas plant height had high estimates of heritability but genetic advance was low. High heritability coupled with high genetic advance was observed for days to 50% flowering and pods per plant indicating opportunity for high selection response.

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