

Original Research Article

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Studies on Genetic Variability, Heritability and Genetic Advance in Table Pea (*Pisum sativum* var. *hotense* L.)

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ABSTRACT

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An experiment was conducted to estimate genetic variability, heritability and genetic advance of eight parent and 28 f_1 's of table pea during 2018-19 and 2019-20 at HRC, SVP&T, Meerut (UP) 250110. The observations were recorded on various yield and yield contributing characters. Analysis of variance showed the significant variability for all the studied characters. High heritability was recorded for all characters except width of pod (55.84 %) which was medium heritability. High GCV and PCV were recorded in seed yield per plant and number of pods per plant which indicates the presence of high genetic variation. High heritability coupled with high genetic advance observed for the traits viz. plant height, seed yield per plant, number of pods per plant, length of first fruiting node, days to 50% flowering, number of first fruiting node, length of pod and number of seeds per pod which indicates presence of additive gene action and demands for population improvement by selection. The genotypes with specific characters can be utilized for hybridization programme.

Introduction

The pea (*Pisum sativum* L.) is the most important grain legume crop grown worldwide, used as food and fodder. 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.

Table Pea ($2n = 2x = 14$), a member of family Fabaceae is an important vegetable crop. It is

native to Europe and West Asia, while its wild prototype came from Ethiopia (De Candolle, 1886). 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 20-30%, 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 fiber and antioxidant compounds (Urbano *et al.*, 2003)

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 was conducted at Horticulture Research Centre (HRC), Sardar Vallabhbhai Patel University of Agriculture and Technology, Meerut (UP) 250110 during *Rabi* season 2018-19 & 2019-20. The experimental material consisted of eight genotypes of pea namely viz., AP-3, KashiNandini, Arkel, VL-7, PMR-53, KashiUday, PC-531 and AP-1 were crossed in half diallele mating design and obtained 28 F₁ crosses. All the 28F₁'s along with parents were grown in Randomized Complete Block Design with three replications. Observations were recorded on five randomly selected plants from each treatment on nine characters viz., days to 50% flowering, plant height (cm), number of first fruiting node, length of first fruiting node (cm), number of pods per plant, length of pod (cm), width of pod (cm), no. of seeds per pod, 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 (1967), phenotypic and genotypic

coefficients of variation were estimated by given by Burton (1952) and Johnson *et al.*, (1955) and heritability in broad sense was estimated as per formula given by Allard (1960). The expected genetic advance was calculated by using formula as suggested by Allard (1960) and Robinson *et al.*, (1949).

Results and Discussion

All the characters showed significant variability among the all the characters observed among parents (except length of pod) and F₁ Hybrids, suggest presence of sufficient variability in the parents and F₁ Hybrids (Table 1).

The genotypic coefficient of variation, phenotypic coefficient of variation, heritability genetic advance and genetic advance as percent of mean also are present in Table 2. The magnitude of phenotypic coefficient of variation (PCV) were higher than the genotypic coefficient of variation (GCV) 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 Siddika *et al.*, (2013), Ahmad *et al.*, (2014), Iqbal *et al.*, (2015), Katoch *et al.*, (2016), Pandey *et al.*(2017), Barcchiya *et al.*, (2018). Results from the present study in this context indicated that PCV and GCV were high (more than 20%) observed for seed yield per plant, number of pods per plant. Similar findings were also reported by Tiwari and Lavanya (2012), Afreen *et al.*, (2017), Ali *et al.*, (2018), Singh *et al.*(2019),while moderate (10-20%) for plant height, number of first fruiting node, days to 50% flowering, length of pod and length of first fruiting node Similar findings were also reported by Georgieva *et al.*, (2016), Gudadinni *et al.*, (2017) and low (<10%) for number of seeds per pod and width of pod. Similar findings were also reported by Kaur *et al.*, (2018).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 studied. Out of nine characters eight characters observed for high heritability viz plant height (99.88%), seed yield per plant (99.79 %) number of pods per plant (99.32%), length of first fruiting node (99.24%), days to 50% flowering (98.45 %), number of first fruiting node (97.71%), length of pod (92.91%) and number of seeds

per pod (90.06%). Similar results were noticed by Ceyhan *et al.*, (2012), Siddika *et al.*, (2013), Jaiswal *et al.*, (2015), Kumar *et al.*, (2015), Thakur *et al.*, (2016), Georgieva *et al.*, (2016), Tambolkar *et al.*, (2017). Moderate heritability (30-60%) was observed for width of pod (55.84 %) similar results were noticed by Katiyar *et al.*, (2014). 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.

Table.1 Analysis of variance for parent and hybrids for nine quantitative traits

SV	Df	DF	PH	NFFN	LFFN	NPP	LP	WP	NSP	SY
REP	2	0.45	0.22	0.11	0.10	0.02	0.16	0.0013	0.01	0.11
Treatment	35	104.87**	515.62**	10.91**	28.57**	20.33**	3.60**	0.0069**	0.911**	167.92**
PAR	7	199.37**	868.94**	6.65**	43.48**	33.92**	0.73	0.0128**	1.06**	341.88**
F1	27	78.72**	437.87**	10.58**	23.94**	16.17**	2.73**	0.0055**	0.81**	127.21**
PVF1	1	149.22**	141.90**	49.73**	49.16**	37.55**	47.28**	0.0056**	2.71**	49.44**
EROR	70	0.55	0.21	0.08	0.07	0.05	0.09	0.0014	0.03	0.12

DF-Days to 50% flowering, PH-Plant height (cm), NFFN-Number of first fruiting node, LFFN- Length of first fruiting node, NPP-No. of pods per plant, LP-Length of pod, WP-Width of pod, NSP-No. of seeds per pod, SY-Seed yield per plant (g). SV- Source of variation, *df*- Degrees of freedom, *, ** significant at 5% and 1% level, respectively

Table.2 Variability parameters for yield and yield attributing characters in Table pea

S.No.	Characters	Heritability (%)	Genetic Advance	GA value % means	GCV (%)	PCV (%)
1	DF	98.45	12.05	28.19	13.79	13.90
2	PH	99.88	26.99	35.97	17.47	17.48
3	NFFN	97.71	3.87	35.56	17.46	17.67
4	LFFN	99.24	6.33	20.53	10.00	10.04
5	NPP	99.32	5.34	43.28	21.08	21.15
6	LP	92.91	2.15	22.57	11.37	11.80
7	WP	55.84	0.07	4.42	2.87	3.84
8	NSP	90.06	1.06	13.75	7.03	7.41
9	SY	99.79	15.39	49.51	24.06	24.08

DF- Days to 50% flowering, PH-Plant height (cm), NFFN- Number of first fruiting node, LFFN- Length of first fruiting node, NPP- No. of pods per plant, LP- Length of pod, WP- Width of pod, NSP- No. of seeds per pod, SY- Seed yield per plant (g)

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 (49.51 %), number of pods per plant (43.28 %), plant height (35.97%), number of first fruiting node (35.56%), days to 50% flowering (28.19%), length of pod (22.57%), length of first fruiting node (20.53) while moderate (10-20%) for number of seeds per pod (13.75%) and Low (<10%) was found in width of pod (4.42 %).

Similar results were reported by Choudhary *et al.*, (2010), Yadav *et al.*, (2010), Singh *et al.*, (2011), Kumar *et al.*, (2013), Kumari *et al.*, (2012) and Gudadinni *et al.*, (2017) and Low (<10%) was found in width of pod. thereby, suggesting average response for selection based on *per se* performance.

In present investigation high heritability coupled with high genetic advance observed for plant height, seed yield per plant, number of pods per plant, length of first fruiting node, days to 50% flowering, number of first fruiting node, length of pod and number of seeds per pod.

High heritability coupled with moderate genetic advance observed for number of seeds per pod while moderate heritability coupled with low genetic advance for width of pod.

Some of these characters have also been reported earlier by Singh and Singh (2006), Sharma *et al.*, (2007), Singh *et al.*, (2011), Kumari *et al.*, (2012), Katiyar *et al.*, (2014), Pandey *et al.* (2015), Pandey *et al.*, (2017), Barcchiya *et al.*, (2018).

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.

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