

## GENETIC VARIABILITY PARAMETERS OF YIELD AND QUALITY ATTRIBUTES IN VEGETABLE PEA (*Pisum sativum* L.)

Jaskanwal SINGH and R.K. DHALL

Department of Vegetable Science, Punjab Agricultural University, Ludhiana-141004, INDIA

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A field experiment was conducted to study the genetic variability, heritability and genetic advance of 24 morphological traits and three biochemical traits in 47 genotypes of vegetable pea. The analysis of variance showed significant differences among genotypes for all the characters under study. Highest coefficient of variation was observed for number of podding nodes per plant and highest phenotypic and genotypic coefficients of variation were recorded for seed yield per plant followed by number of primary branches per plant and green pod yield per plant. Very high heritability estimates were observed for days to last pod picking (97.63) followed by plant height (97.40), days to first pod picking (96.78) and shelling percentage (95.56) while genetic advance as percentage of mean was found high for seed yield per plant (65.95) and primary branches per plant (58.40). High heritability along with moderate to high genetic advance was predicted in case of pod weight and number of seeds per pod, which indicated the role of additive gene action for the inheritance of these traits and therefore, selection could be used for improving these traits.

*Key words:* genetic advance, heritability, quality, variability, vegetable pea, yield

### INTRODUCTION

Vegetable Pea (*Pisum sativum* L.) is a cool season crop and occupies 459 thousand hectare area in India and shares 21 percent production of the world. In Punjab, it is second

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*Corresponding author:* R.K.Dhall, Department of Vegetable Science, Punjab Agricultural University, Ludhiana-141004, Punjab, India. Ph (M): +91-8283840078, E-mail: [rajinderkumar@pau.edu](mailto:rajinderkumar@pau.edu)

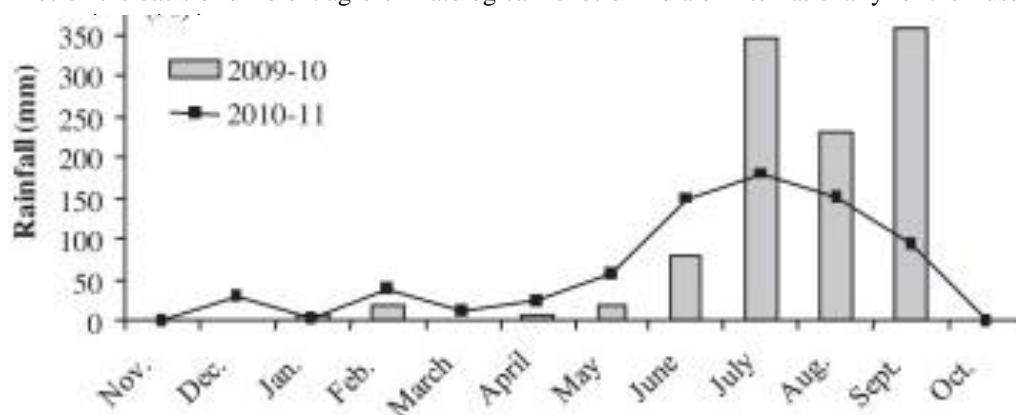
largest crop after potato and cultivated on 31.3 thousand hectare area. The average area increase was 2.9% from 2006 to 2015, but a jump of 41% was witnessed during last three years in the Punjab (NHB, 2016). It indicates that pea has potential for enhancement of area and production in the state but its productivity is still low due to lack of high yielding and multiple disease resistant cultivars. Hence, there is an urgent need to evaluate the new germplasm of vegetable pea to select high yielding and disease resistant genotypes which can be adopted as such for commercial production or can be incorporated in the future breeding programmes for improvement of yield and quality traits.

Crop improvement depends largely on availability of genetic variability in breeding material, their effective evaluation and utilization. Moreover, genetic variation is valuable for understanding gene function. The variability parameters especially heritability and genetic gain are reliable indicators for improvement of characters in a particular genetic material through selection. Since, the selection for highly heritable characters is more effective, therefore, heritability can be used in predicting the gain for a given selection intensity and expected genetic gain further gives the idea of the extent of improvement in a character through simple selection. The present study therefore, was taken up to estimate the parameters of variability in pea so that the desired targets are achieved.

## MATERIALS AND METHODS

### *Plant materials*

Forty seven vegetable pea (*Pisum sativum* L.) germplasm comprising breeding lines, accessions and cultivated varieties were selected from germplasm collection of two hundred lines on the basis of different agro-climatological zones of India or internationally for their use in



### *Morphological traits*

Five plants were selected randomly from each genotype, in each replication and were used for recording observations. For morphological characterization the genotypes were evaluated for twenty four morphological traits and three biochemical traits *viz.* early plant vigour, days to first flowering, days to 50% flowering, first blossom node, number of primary branches per plant, plant height (cm), days to first pod picking, days to last pod picking, number

of nodes per plant, number of podding nodes per plant, number of pods per plant, number of pods per node (one/two/both), grain filling period (days), number of seeds per pod, number of locules per pod, 100 seed weight (g), pod weight (g), pod length (cm), pod width (cm), pod thickness (cm), green pod yield per plant (g), seed yield per plant (g), shelling percentage, crude protein (%), soluble protein (%) and total sugars (%). Early plant vigour for 25 days old plants was recorded and ranked as 1 (poor), 2 (good) and 3 (very good). Plant growth habit recorded at the end of vegetative growth was ranked as 1 (erect), 2 (semi-erect), 3 (spreading) and 4 (bushy) whereas Number of pods per node was recorded and ranked as 1 (single pod per node), 2 (double pods per node) and 3 (mixed podding). Crude protein content was estimated by Kjeldahl method of nitrogen estimation (MCKENZIE and WALLACE, 1954). Soluble protein content was estimated by Lowry's method (LOWRY *et al.*, 1951). Total sugar (%) content was estimated by DUBIOS *et al.*, 1956. The mean values of five plants, for each replication, in 47 accessions were used for analysis of variance. The analysis of variance for forty seven genotypes was carried out for twenty four morphological and biochemical traits planted in Randomized Block Design.

#### Statistical analysis

Analysis of variance and error variance was tested for homogeneity (GOMEZ and GOMEZ, 1984). The genotypic and phenotypic coefficients of variation were calculated as per formula suggested by BURTON and DEVANE (1953). Heritability (broad sense) was calculated by the formula as suggested by ALLARD (1960). Genetic gain was genetic advance as per cent of mean, calculated by the method of JOHANSON *et al.*, (1955). The parameters of variability were estimated using following method given by BURTON and DEVANE (1953).

$$\text{Genotypic coefficient of variation (GCV)} = \frac{\sigma_g}{\bar{X}} \times 100$$

$$\text{Phenotypic coefficient of variation (PCV)} = \frac{\sigma_p}{\bar{X}} \times 100$$

$\sigma_p$  and  $\bar{X}$  represent the genotypic standard deviation, phenotypic standard deviation and population mean, respectively.

The heritability broad sense ( $h^2_{bs}$ ) was calculated using the following formula (ALLARD 1960), where,  $\sigma_g^2$  is genotypic variance and  $\sigma_p^2$  is phenotypic variance.

$$h^2 (bs) = \frac{\sigma_g^2}{\sigma_p^2} \times 100$$

The expected genetic advance (GA) was calculated as  $GA = k \times h^2 \times \sigma_p$   
Where,  $k = 2.06$  (selection differential at 5% selection intensity).

$$\text{Genetic advance (\% of mean)} = \frac{GA}{\bar{X}} \times 100$$

## RESULTS AND DISCUSSION

Vegetable pea genotypes under study were examined to assess the amount of variability present among different genotypes in respect to a number of morphological and biochemical traits.

### *Mean performance*

The mean performance of 47 pea genotypes along with range, character mean and critical difference for 27 studied traits is presented in Table 1.

### *Early plant vigour*

Out of the total genotypes, 10, 22 and 15 genotypes respectively were found to be poor, good and very good for early plant vigour (Table 1). GP-2, VRPMR-9, VRPMR-11, VRP-4, VRP-6, VRP-22, 09/PMVAR-2, 09/PMVAR-5, 09/PMVAR-6, KS-268, JM-5, PMR-19, PMR-20, PMR-62 and Arka Ajit were found very good for early plant vigour.

### *Days to first flowering*

Early flowering varieties tend to give early marketable yield which can fetch early price advantage. Similarly late maturing varieties also have the same advantage i.e. to capture late season market (SINGLA *et al.*, 2009). The data presented in Table 1 clearly indicated that statistically there were highly significant differences among all genotypes for days to first flowering. Days to first flowering ranged from 48.33 to 79.17 with mean value of 66.38 days (SE=1.07, SD=7.35). VRP-6 was reported to be early in first flowering (48.33 days), followed by 09/PMVAR-8 (48.67 days), VRP-22 (49.00 days) and PMR-62 (51.17 days) while 08/PMVAR-3 (79.17), VRPMR-9 (78.33), 09/PMVAR-5 (78.17) and RE-89 (78.83) takes maximum days for first flowering.

### *Days to 50% flowering*

Days to 50 per cent flowering ranged from 53.50 to 91.50 with mean value of 76.65 days (SE=1.14, SD=7.84). VRP-6 was reported to be early for appearance of 50% flowering (53.50 days), followed by 09/PMVAR-8 (56.00 days), VRP-22 (57.33 days) and 09/PMVAR-7 (63.00 days) while 09/PMVAR-5 takes maximum days for first flowering (91.50) followed by 08/PMVAR-3 (89.50) and VRPMR-11 (86.17). All the genotypes differ significantly from each other for days to 50% flowering.

### *First blossom node*

The genotypes which bear the flower at relatively lower node tend to yield better than the plants which bear flower at higher nodes. Such genotypes also mature early. So, plants which set flower at lowest node are preferred for early yields (DHALL and BRAR, 2015). Data showed that all the genotypes differ significantly from each other for first blossom node. For first blossom node values ranged from 9.22 to 14.00 and mean value was 11.39 (SE=0.15, SD= 1.06). Lowest first blossom node was observed in C-96 (9.22) followed by GS-10 (9.44), VRP-6 (9.72), 09/PMVAR-7 (9.80) and PB-89 (9.89) while highest first blossom node was observed in VRPMR-9 (14.00).

Table 1. Mean performance of vegetable pea (*Pisum sativum* L.) genotypes for various morphological and biochemical traits

Genotype	Early Plant vigour <sup>a</sup>	Days to first flowering	Days to 50% flowering	First blossom node	Number of primary branches per plant	Plant height (cm)	Plant growth habit <sup>b</sup>	Days to first pod picking	Days to last pod picking
GP-2	3	62.67	70.00	12.06	1.94	71.40	2	114.50	126.50
GP-3	2	66.67	75.67	11.56	1.78	79.73	1	124.83	132.33
GP-5	2	74.17	82.00	12.22	2.39	82.47	2	131.17	143.00
JP 501 A/2	2	62.83	77.33	11.72	5.00	135.31	3	127.00	146.17
VRPMR-9	3	78.33	89.33	14.00	3.11	109.06	3	128.33	137.83
VRPMR-11	3	72.17	86.17	11.89	3.78	88.64	3	130.00	139.83
VRP-4	3	63.50	74.33	11.42	3.17	91.31	2	125.50	140.83
VRP-6	3	48.33	53.50	9.72	1.89	58.45	1	126.33	133.83
VRP-7	2	62.83	73.33	11.97	2.72	90.60	2	126.17	134.00
VRP-22	3	49.00	57.33	9.94	2.33	65.35	2	112.67	127.50
09/PMVAR-2	3	72.00	82.67	11.25	3.50	85.26	1	134.00	152.33
09/PMVAR-5	3	78.17	91.50	11.89	2.11	86.65	1	134.83	152.00
09/PMVAR-6	3	71.83	82.67	12.28	3.00	90.24	3	133.83	152.17
09/PMVAR-7	2	52.33	63.00	9.80	1.33	83.04	2	123.17	130.67
09/PMVAR-8	2	48.67	56.00	10.14	1.28	89.99	1	124.67	133.00
PB. 87	2	66.83	74.67	11.05	2.06	83.78	2	124.83	143.17
PB. 88	2	70.17	81.83	11.11	1.67	101.83	1	130.17	137.73
PB. 89	1	65.00	72.00	9.89	1.94	90.00	2	115.76	128.67
C-96	2	65.50	75.67	9.22	2.28	73.39	3	122.00	132.17
C-308	2	67.67	77.50	11.78	2.06	97.61	2	119.50	130.33
C-400	2	69.17	81.33	10.72	1.56	83.61	2	125.17	135.17
KS-205	2	61.17	69.33	10.56	1.83	92.07	1	124.67	134.33
KS-268	3	64.67	72.50	12.22	2.11	177.50	3	133.83	144.00
08/PMVAR-1	2	62.50	77.33	10.64	1.94	99.51	1	135.33	143.84
08/PMVAR-3	1	79.17	89.50	11.89	2.33	97.15	2	126.50	137.17
08/PMVAR-4	2	62.50	74.00	11.47	2.11	102.26	1	130.00	139.67
08/PMVAR-5	2	67.83	77.67	11.64	1.44	100.34	2	130.00	139.83
JM-1	1	72.33	83.17	11.30	2.89	91.53	3	133.83	142.83
JM-5	3	69.00	78.17	13.33	2.78	169.37	3	134.83	152.17
NDVP-8	1	67.67	76.17	11.56	1.72	83.78	1	127.17	137.00
NDVP-10	1	63.17	73.83	11.39	2.56	85.36	3	126.33	136.33
PMR-4	2	72.83	81.00	12.42	3.00	95.48	2	133.17	141.67
PMR-19	3	63.50	80.00	10.06	2.28	89.73	2	127.17	136.33
PMR-20	3	61.33	73.00	10.61	2.94	98.03	4	123.00	142.33
PMR-62	3	51.17	70.50	13.72	2.28	87.45	4	128.50	146.83
CHP-I	1	75.50	83.17	11.67	1.89	78.67	3	125.83	141.83
CHP-II	1	71.83	84.83	12.06	3.50	109.58	3	125.83	141.83
VP-5	2	71.83	82.00	13.31	1.50	88.13	2	126.33	141.50
VP-215	2	70.50	78.33	11.31	3.00	92.61	2	130.50	140.33
VL-8	1	65.33	76.33	12.72	1.89	115.78	1	127.33	136.33
PEW-9	1	67.67	78.33	10.94	1.61	98.72	4	124.83	142.67
Arka Ajit	3	65.17	77.17	11.06	2.56	91.38	3	128.67	134.67
Angoori	2	64.83	73.17	11.94	2.33	85.90	1	126.83	145.83
GS-10	2	63.67	70.83	9.44	1.89	77.28	2	119.33	132.17
Aryaveer	2	69.17	79.17	10.55	2.56	91.29	3	117.50	129.83
RE-89	1	75.83	84.67	10.78	2.00	89.41	2	125.50	134.17
Prachi	2	72.00	80.33	11.17	2.39	95.13	1	127.17	144.83
Mean	----	66.38	76.65	11.39	2.34	94.44	----	126.68	138.77
Range	1/2/3	48.33-79.17	53.50-91.50	9.22-14.00	1.28-5.00	58.45-177.50	1/2/3/4	112.67-135.33	126.50-152.33
CD (5%)	----	4.38	4.82	1.22	0.38	8.07	----	1.55	1.66
CD (1%)	----	5.76	6.34	1.60	0.50	10.6	----	2.03	2.18

<sup>a</sup>1= poor, 2=good, 3= very good ; <sup>b</sup>1= erect, 2= semi-erect, 3= spreading, 4= bushy

Table 1. Continued

Genotype	Number of nodes per plant	Number of podding nodes per plant	Number of pods per node <sup>c</sup>	Number of pods per plant	Grain filling period (days)	Number of seeds per pod	Number of locules per pod	100 seeds weight (g)	Pod weight (g)
GP-2	31.89	10.83	2	21.61	44.50	7.83	8.11	41.12	4.45
GP-3	24.06	10.69	3	14.22	49.17	6.50	8.06	30.19	4.31
GP-5	51.34	17.92	3	20.72	49.17	6.22	7.61	39.97	3.87
JP 501 A/2	69.33	18.44	3	24.75	49.67	5.31	6.31	26.04	3.56
VRPMR-9	55.27	14.33	3	19.94	39.00	6.89	7.11	39.18	3.69
VRPMR-11	62.39	19.12	2	38.50	43.83	6.56	6.95	40.52	3.90
VRP-4	59.72	25.65	3	31.44	51.17	5.83	7.06	27.35	4.08
VRP-6	35.73	13.72	1	13.72	72.83	6.17	6.89	32.43	4.90
VRP-7	66.50	25.00	3	29.00	52.83	6.61	7.83	37.13	3.77
VRP-22	49.21	23.72	3	29.42	55.33	6.33	6.89	36.63	4.56
09/PMVAR-2	55.61	31.00	3	33.33	51.33	5.94	6.67	40.73	5.29
09/PMVAR-5	33.78	15.00	1	15.00	43.33	6.56	7.00	38.68	4.49
09/PMVAR-6	61.34	26.79	3	31.76	51.17	5.76	7.44	37.56	3.38
09/PMVAR-7	46.94	18.89	1	18.89	60.17	5.83	7.17	25.97	4.05
09/PMVAR-8	33.67	15.17	1	15.17	68.67	6.28	7.18	33.06	4.79
PB. 87	53.98	26.44	3	30.56	50.17	5.50	5.89	37.26	4.30
PB. 88	46.16	15.17	2	30.17	48.33	6.28	8.33	35.48	5.52
PB. 89	38.78	17.06	2	34.17	43.67	8.61	9.00	43.37	5.66
C-96	45.72	27.11	3	31.06	46.33	5.39	6.28	32.92	4.10
C-308	36.69	13.22	2	26.00	42.00	7.53	7.92	37.13	4.33
C-400	29.64	11.67	3	16.17	43.83	6.11	6.61	35.17	4.04
KS-205	35.33	15.27	1	15.27	55.33	6.78	7.83	32.61	4.90
KS-268	44.50	16.78	3	19.38	61.33	6.28	6.94	30.84	4.57
08/PMVAR-1	46.81	22.66	3	27.14	58.00	6.83	7.22	40.27	5.40
08/PMVAR-3	54.76	22.20	3	22.74	37.00	7.56	8.72	35.68	4.22
08/PMVAR-4	45.67	21.06	3	23.77	56.00	6.44	6.67	29.75	4.04
08/PMVAR-5	36.02	12.50	3	17.00	52.33	6.89	8.11	37.67	4.31
JM-1	53.27	16.94	3	19.99	50.67	5.57	6.56	33.80	4.02
JM-5	75.97	19.94	3	25.56	56.67	5.42	6.97	27.86	3.23
NDVP-8	35.34	13.03	3	16.41	51.00	6.44	7.67	44.77	4.55
NDVP-10	57.58	22.17	3	25.19	52.50	5.06	6.95	34.61	4.11
PMR-4	53.32	25.00	3	29.46	52.77	4.78	6.83	23.72	3.31
PMR-19	51.39	21.39	3	25.00	47.17	4.72	5.45	30.95	3.54
PMR-20	65.55	25.44	3	30.51	50.00	5.50	6.56	33.69	3.41
PMR-62	50.00	25.83	3	28.91	58.00	5.50	6.89	41.75	4.54
CHP-I	46.44	24.94	3	31.07	42.67	5.28	6.50	35.31	3.95
CHP-II	77.61	26.33	3	29.11	41.50	6.33	6.72	30.73	3.28
VP-5	40.71	13.50	2	26.78	48.50	4.39	5.94	37.13	3.90
VP-215	47.61	20.44	3	23.31	49.00	6.39	8.11	39.69	4.42
VL-8	49.72	17.94	2	35.72	48.50	5.33	7.06	38.04	3.95
PEW-9	37.82	13.11	3	17.44	50.33	5.94	7.50	39.05	4.60
Arka Ajit	46.07	15.06	3	20.22	49.67	6.28	6.83	32.03	3.74
Angoori	42.67	20.16	3	23.91	46.17	6.22	7.44	36.60	3.80
GS-10	34.36	14.11	3	17.48	46.67	7.17	9.06	35.19	4.99
Aryaveer	43.64	18.56	3	22.33	46.33	5.28	7.17	33.21	4.36
RE-89	48.17	22.16	3	26.01	42.50	5.67	7.39	32.32	3.52
Prachi	42.83	23.88	3	26.56	45.33	5.61	7.83	38.70	5.44
Mean	47.89	19.30	----	24.51	50.04	6.12	7.22	35.19	4.24
Range	24.06-77.61	10.69-31.00	1/2/3	13.72-38.50	37.00-72.83	4.39-8.61	5.45-9.06	23.72-44.77	3.23-5.66
CD (5%)	5.60	3.27	----	3.84	3.74	0.33	0.78	2.59	0.23
CD (1%)	7.36	4.30	----	5.05	4.92	0.43	1.026	3.41	0.30

<sup>c</sup> 1= one pod/ node, 2= two pods/node, 3= mixed (one and two pods/ node)

Table 1. Continued

Genotype	Pod length (cm)	Pod width (cm)	Pod thickness (cm)	Green pod yield per plant (g)	Seed yield per plant (g)	Shelling percentage	Crude protein (%)	Soluble Protein (%)	Total Sugars (%)
GP-2	8.72	1.13	0.99	96.57	46.71	48.38	26.84	4.54	28.59
GP-3	7.71	1.42	0.99	62.01	26.62	42.88	21.26	3.04	25.40
GP-5	7.90	1.57	1.00	79.76	29.69	37.22	23.37	3.09	23.31
JP 501 A/2	6.17	1.08	0.93	88.23	34.22	38.77	18.74	3.23	17.58
VRPMR-9	8.36	1.23	1.01	74.08	35.86	48.38	20.19	3.73	20.16
VRPMR-11	8.41	1.25	1.00	151.22	74.46	49.22	21.65	4.04	25.51
VRP-4	7.60	1.27	0.91	128.51	62.53	48.62	19.11	3.54	13.84
VRP-6	7.84	1.41	0.96	66.86	31.54	47.21	21.63	3.05	17.69
VRP-7	8.93	1.44	1.03	109.52	53.15	48.56	20.83	4.10	13.31
VRP-22	7.93	1.29	1.05	133.60	64.26	48.11	21.37	4.14	19.47
09/PMVAR-2	8.11	1.42	1.07	175.96	86.24	49.02	21.68	3.47	16.64
09/PMVAR-5	7.20	1.54	0.99	67.77	29.11	42.93	23.36	3.46	22.20
09/PMVAR-6	7.66	1.13	0.95	106.73	46.96	44.00	18.70	2.92	19.88
09/PMVAR-7	7.65	1.30	0.95	75.33	31.73	42.13	18.90	3.80	20.15
09/PMVAR-8	7.75	1.36	0.89	72.63	33.06	45.52	26.64	5.70	27.68
PB. 87	7.79	1.33	1.00	131.27	59.89	45.63	19.05	3.92	20.77
PB. 88	8.12	1.37	0.99	166.08	78.70	47.38	24.10	4.81	21.10
PB. 89	9.34	1.28	1.08	192.88	95.98	49.76	25.55	5.49	28.78
C-96	8.56	1.12	0.96	126.18	50.69	40.17	19.05	3.57	18.07
C-308	7.82	1.23	0.99	113.64	55.95	49.21	21.15	3.26	19.98
C-400	7.68	1.29	0.98	65.09	31.07	47.74	20.91	4.12	20.22
KS-205	8.39	1.38	1.00	74.95	29.44	39.30	20.52	4.13	19.05
KS-268	8.33	1.41	0.93	88.40	34.80	39.39	21.26	3.04	18.73
08/PMVAR-1	8.81	1.48	1.13	146.71	62.18	42.39	19.84	3.59	14.39
08/PMVAR-3	8.97	1.29	0.98	95.31	44.62	46.80	18.90	3.76	13.73
08/PMVAR-4	8.44	1.44	0.95	95.89	41.26	43.03	24.48	5.89	18.79
08/PMVAR-5	7.55	1.29	1.01	73.16	36.44	49.81	24.64	4.59	19.30
JM-1	6.47	1.16	0.99	79.96	29.43	36.80	18.79	2.26	21.15
JM-5	6.75	1.25	0.87	82.86	32.24	38.94	19.92	3.07	23.31
NDVP-8	7.26	1.18	0.97	74.18	33.28	44.81	21.54	3.81	21.20
NDVP-10	8.07	1.30	0.99	103.12	51.68	50.12	22.91	3.53	18.18
PMR-4	6.77	1.07	0.91	97.11	45.26	46.60	21.90	3.44	20.07
PMR-19	6.89	1.21	0.89	88.07	42.01	47.69	22.26	4.53	17.60
PMR-20	6.99	1.37	0.83	103.63	47.28	45.60	22.92	4.13	15.57
PMR-62	8.39	1.27	1.03	130.49	61.75	47.31	23.07	4.09	24.40
CHP-I	8.01	1.32	1.01	122.08	48.45	39.68	19.85	3.50	16.27
CHP-II	7.53	1.21	0.90	95.30	41.87	43.93	20.58	3.55	17.10
VP-5	7.39	1.18	1.00	104.14	44.01	42.28	20.00	2.92	13.51
VP-215	8.19	1.26	1.02	103.02	45.44	44.11	17.09	1.98	22.21
VL-8	7.46	1.29	0.93	140.71	54.44	38.70	19.47	3.69	13.17
PEW-9	8.03	1.28	1.05	80.33	30.37	37.81	21.90	3.48	21.42
Arka Ajit	8.45	1.29	0.89	75.74	36.50	48.21	22.90	3.90	26.57
Angoori	8.59	1.15	0.99	90.59	44.36	48.95	23.47	3.26	21.09
GS-10	9.09	1.22	0.96	87.25	42.81	49.06	24.55	5.47	26.75
Aryaveer	7.95	1.38	1.07	97.60	47.10	48.26	23.36	4.26	25.53
RE-89	7.86	1.22	1.00	90.91	42.59	46.83	22.70	4.24	24.40
Prachi	9.00	1.61	1.15	143.45	67.61	47.13	23.15	3.47	24.31
Mean	7.94	1.30	0.98	103.17	46.71	44.99	21.62	3.80	20.38
Range	6.17-9.34	1.07-1.61	0.83-1.15	62.01-192.88	26.59-95.98	36.80-50.12	17.09-26.84	1.98-5.89	13.17-28.59
CD (5%)	0.59	0.91	0.66	16.58	7.58	0.42	1.87	0.66	1.65
CD (1%)	0.78	1.20	0.86	21.81	9.97	0.55	2.46	0.86	2.17

*Number of primary branches per plant*

Number of primary branches is an important yield affecting character. The plants in which primary branches are more generally tend to yield more than plants with less primary

branches (DHALL and BRAR, 2015). Number of primary branches per plant ranged from 1.28 to 5 with mean value of 2.34 (SE=0.10, SD=0.71) and all the genotypes differ significantly for number of primary branches per plant. Majority of the genotypes had 1.89 to 3.00 primary branches per plant. The genotypes 09/PMVAR-8 and 09/PMVAR-7 were reported to have lowest number of primary branches i.e. 1.28 and 1.33 respectively while JP 501 A/2 had the highest number of primary branches (5.00).

#### *Plant height*

Plant height is an important character because yield increases with an increase in plant height (DHALL and BRAR, 2015) The data presented in Table 1 clearly indicated that there were significant differences among various genotypes for plant height, ranged from 58.45-177.50 cm. The genotype KS-268 had the maximum plant height (177.50 cm), followed by JM-5 (169.37 cm), JP501A/2 (135.31) and VL-8 (115.78). Minimum plant height was observed in genotype VRP-6 (58.45 cm). The average value for the plant height was 94.44 cm (SE= 3.06, SD=20.96).

#### *Plant growth habit*

Plant growth habit recorded at the end of vegetative growth and 13 genotypes were found to be erect, 18 as semi-erect, 13 as spreading while only three genotypes (CHP-I, PMR-62 and Arka Ajit) were found to be bushy for growth habit. Erect plants were found to be late in maturity while bushy plants were early in maturity.

#### *Days to first pod picking*

Days to first pod picking reflects earliness. Generally early maturing varieties are preferred because of price advantage during early season (SINGLA *et al.*, 2009). All the genotypes were found to have significant differences for days to first pod picking. Days to first pod picking ranged from 112.67 to 135.33 with mean value 126.68 (SE=0.76, SD=5.21). The genotype VRP-22 was found to be early for first pod picking (112.67) followed by GP-2 (114.50), PB-89 (115.76), GS-10 (117.50) and Angoori (119.33). The genotypes 08/PMVAR-1 (135.33), 09/PMVAR-5 (134.83) and JM-5 (134.83) takes maximum days for first pod picking.

#### *Days to last pod picking*

Days to last pod picking is important character for overall earliness of variety as well as in case of late maturing varieties for their economic advantage during end of season as prices generally goes up late in the season (SINGLA *et al.*, 2009). All the genotypes were found to have significant differences for days to last pod picking. Days to first pod picking ranged from 126.50 to 152.33 with mean value 138.77 (SE=0.96, SD=6.55). The genotype GP-2 was found to be early for last pod picking (126.50) followed by VRP-22 (127.50), PB-89 (128.67), GS-10 (129.83) and C-308 (130.33). The genotypes 09/PMVAR-2 (152.33), 09/PMVAR-6 (152.17) and JM-5 (152.17) takes maximum days for last pod picking.

#### *Number of nodes per plant*

All the genotypes differ significantly for number of nodes per plant. Number of nodes per plant ranged from 24.06 to 77.61 with mean value of 47.89 (SE=1.69, SD=11.59). The highest number of nodes per plant were observed in the genotype CHP-II (77.61) followed by



JM-5 (75.97), JP501A/2 (69.33) and VRP-7 (66.50). Minimum number of nodes per plant was found in the genotype GP-3 (24.06).

#### *Number of podding nodes per plant*

Number of podding nodes per plant is an important yield component. So, plants with higher number of podding nodes are desirable for selection. In the present investigation considerable amount of variation was observed for number of podding nodes per plant, ranging from 10.69 to 31.00 (SE=0.75, SD=5.15) and mean value was 19.30. Maximum podding nodes per plant were observed in genotype 09/PMVAR-2 (31.00) followed by C-96 (27.11), 09/PMVAR-6 (26.79), PB-87 (26.44) and CHP-II (26.33). The genotype GP-3 was found with minimum number of podding nodes per plant (10.69).

#### *Number of pods per node*

Number of pods per node is an important character affecting yield and plants with double podding are preferred more than single or mixed podding type (DHALL and BRAR, 2015). Three genotypes (VRP-7, 09/PMVAR-8 and PB. 87) were found to have single podding habit, 7 genotypes (GP-3, VRP-4, PB. 89, C-96, C-400, VP-215 and PEW-9) had double podding habit, while all others were having both single or double (mixed) pods per node.

#### *Number of pods per plant*

Number of pods per plant is an important yield component (DHALL and BRAR, 2015). In present investigation significant differences have been observed for number of pods per plant which showed a good possibility of selection for this character. Number of pods per plant ranged from 13.72 to 38.50 with mean value 24.51 (SE=0.91, SD=6.26). Maximum number of pods per plant was observed in genotype VRP-11 (38.50) followed by VL-8 (35.72), PB.89 (34.17) and 09/PMVAR-2 (33.33). Minimum number of pods per plant was observed in VRP-6 (13.72).

#### *Grain filling period (days)*

All the genotypes differ from each other for grain filling period (Table 1). Grain filling period for all the genotypes ranges between 37.00-72.83 days with mean value of 50.04 (SE=1.00, SD=6.87). The lowest grain filling period was found in 08/PMVAR-3 (37.00) followed by VRP-9 (39.00), CHP-II (41.50), C-308 (42.00) and RE-89 (42.50). The highest grain filling period was found in VRP-6 (72.83).

#### *Number of seeds per pod*

This is an important character and influences quality and quantity of shelled peas. Data presented in Table1 showed that all the genotypes differ from each other for number of seeds per pod. The highest number of seeds per pod was found in PB-89 (8.61) followed by GP-2 (7.83), 08/PMVAR-3 (7.56), C-308(7.53) and GS-10 (7.17). The lowest number of seeds was found in the genotype VP-5 (4.39). The character for all the genotypes ranges from 4.39-8.61 with mean value of 6.12 (SE=0.12, SD=0.82).

#### *Number of locules per pod*

It is an important character to estimate number of missing seeds per pod by comparison with number of seeds per pod. All the genotypes differ from each other for number of locules per

pod. Number of locules per pod ranged from 5.45 to 9.06 with mean value 7.22 (SE=0.11, SD=0.76). Maximum number of locules per pod were observed in GS-10 (9.06) followed by PB-89 (9.00), 08/PMVAR-3 (8.72) and PB-88 (8.33). Minimum number of locules per pod was observed in PMR-19 (5.45) and PB-87 (5.89).

#### *100 seeds weight (g)*

All the genotypes differ from each other for 100 seed weight, which ranged from 23.72 to 44.77 with mean value 35.19 g (SE=0.09, SD=0.61). The highest 100 seed weight was found in the genotype NDVP-8 (44.77g) followed by PB-89 (43.37g), PMR-62 (41.75g) and GP-2 (41.12g). The lowest 100 seed weight was observed in the genotype PMR-4 (23.72g).

#### *Pod weight (g)*

Pod weight is another important yield component and needs due consideration while making selection for yield (GAUTAM *et al.*, 2017). All the genotypes differ significantly for pod weight. Range for pod weight varied from 3.23-5.66 g with mean value of 4.24g (SE=0.09, SD=0.61). Maximum pod weight was found in PB-89 (5.66g) followed by PB.88 (5.52g), Prachi (5.44g) and 09/PMVAR-2 (5.29g). Minimum pod weight was observed in the genotypes JM-5 (3.23g) and CHP-II (3.28g).

#### *Pod length (cm)*

Pod length is also one of the important traits affecting pod yield. Generally it is assumed that more is the pod length, more will be the number of seeds (GAUTAM *et al* 2017). All the genotypes differ significantly for pod length. Range for pod length varied from 6.17 to 9.34 cm with mean value of 7.94 cm (SE=0.10, SD=0.70). Maximum pod length was found in PB-89 (9.34 cm) followed by GS-10 (9.09 cm), Prachi (9.00 cm) and 08/PMVAR-3 (8.97 cm). Minimum pod weight was observed in the genotypes JP501A/2 (6.17 cm) and JM-1 (6.67 cm).

#### *Pod width (cm)*

All the genotypes differ significantly for pod width. Pod width for all the genotypes ranges between 1.07 to 1.61 cm mean value of 1.30 cm (SE= 0.02, SD=0.12). Maximum pod width was found in genotype Prachi (1.61 cm) followed by 09/PMVAR-2 (1.54 cm), 08/PMVAR-1 (1.48 cm) and 08/PMVAR-4 (1.44 cm) and minimum pod width was observed in the genotypes PMR-4 (1.07 cm) and JP501A/2 (1.08 cm).

#### *Pod thickness (cm)*

All the genotypes differ significantly for pod thickness. Range for pod thickness varied from 0.83 to 1.15 cm with mean value of 0.98 cm (SE=0.01, SD=0.06). Maximum pod thickness was found in the genotype Prachi (1.15 cm) followed by 08/PMVAR-1 (1.13 cm), PB-89 (1.08 cm), Aryaveer (1.07 cm) and 09/PMVAR-2 (1.07 cm). Minimum pod thickness was observed in genotype PMR-20 (0.83 cm).

#### *Green pod yield per plant (g)*

Yield is the prime objective of any breeding program. A lot of variability for green pod yield was observed indicating huge scope for improvement in pod yield per plant (GAUTAM *et al.*, 2017). Data presented in table 2 revealed significant difference between genotypes for green

pod yield per plant, indicating scope for improvement in pod yield on per plant basis. Green pod yield per plant ranges between 62.01 to 192.88 g with mean yield of 103.17 g (SE=4.46, SD=30.53). The highest yield was recorded in PB-89 (192.88g) followed by 09/PMVAR-2 (175.96g), PB-88 (166.08g) and VRPMR-11 (151.22g). Lower yield was obtained from genotypes GP-3 (62.01g) and C-400 (65.09g).

#### *Seed yield per plant (g)*

Data presented in table 2 revealed significant difference between genotypes for seed yield per plant. Seed yield per plant ranged from 26.62 to 95.98 g with mean value of 46.71 g (SE=2.29; S.D=15.67). The highest yield was recorded in genotype PB-89 (95.98g) followed by 09/PMVAR-2 (86.24g), PB-88 (78.70g) and VRPMR-11 (86.24g). Lower seed yield per plant was obtained from genotypes GP-3 (26.62g) and 09/PMVAR-5 (29.11g).

#### *Shelling percentage*

It is an important character which directly influences seed yield and it ranged from 36.80 to 50.12 % (Table 2). Highest shelling percentage was found in genotypes NDVP-10 (50.12 %), PB-89 (49.76 %), VRPMR-11 (49.22 %), C-308 (49.21 %) and GS-10 (49.06 %). The lowest shelling percentage was found in JM-1 (36.80 %). The mean value was 44.99 % (SE=0.57, SD=3.94).

#### *Crude protein (%)*

Content of crude protein is a qualitative attribute which varied from 17.09 to 26.84 with mean value of 21.62 (SE=0.32, SD=2.19). All the genotypes differ significantly for crude protein content. The highest crude protein content was recorded in the genotype GP-2 (26.84) followed by 09/PMVAR-8 (26.64) and PB-89 (25.55) and minimum crude protein content was found in genotype VP-215 (17.09).

#### *Soluble protein (%)*

Soluble protein percentage is an important biochemical trait varied from 1.98 to 5.89 with mean value of 3.80 (SE=0.12, SD=0.79). All the genotypes differ significantly for soluble protein content. The highest soluble protein content was found in the genotype 08/PMVAR-4 (5.89) followed by 09/PMVAR-8 (5.70) and PB-89 (5.47). Minimum soluble protein content was found in genotype VP-215 (1.98).

#### *Total sugars (%)*

All the genotypes differ significantly for total sugar content. Range for total sugar percentage varied from 13.17 to 28.78 with mean value of 20.38 (SE=0.60, SD=4.13). The highest total sugar content was found in PB-89 (28.78), GP-2 (28.59) and 09/PMVAR-8 (27.68). Minimum total sugar content was found in VL-8 (13.17).

#### *Analysis of variance*

From the analysis of variance, it was observed that mean squares due to genotypes were highly significant (1% level of significance) for all the traits studied (Table 2), indicating thereby the presence of genetic variability in the experimental material. The difference between PCV and GCV of various characters was very little indicating the greater role of genetic factors in the

expression of characters with less influence of environment and offering ample scope for improvement.

Table 2. Analysis of variance for different characters studied in vegetable pea

Character	Mean Sum of Squares			F-ratio		CD (5%)	
	Replicates (2)	Genotypes (46)	Error (92)	Replicates	Genotypes	Replicates	Genotypes
Days to first flowering	136.12	165.61**	7.28	18.70	22.74	1.11	4.38
Days to 50% flowering	167.16	188.21**	8.83	18.93	21.31	1.21	4.82
First blossom node	2.30	3.45**	0.57	4.55	6.05	0.31	1.22
Primary branches per plant	0.56	1.53**	0.55	9.99	27.44	0.96	0.38
Plant height	6.53	1346.40**	24.76	2.44	54.38	NS	8.07
Days to first pod picking	2.00	83.30**	0.91	2.19	91.05	NS	1.55
Days to last pod picking	1.76	131.35**	1.05	1.67	124.82	NS	1.66
Number of nodes per plant	193.08	411.43**	11.91	16.20	34.52	1.41	5.60
Number of podding nodes per plant	58.38	81.43**	4.06	14.37	20.04	0.82	3.27
Total pods per plant	68.79	120.16**	5.60	12.28	21.44	0.79	3.84
Grain filling period	134.54	144.57**	5.32	24.27	27.16	0.94	3.74
Number of seeds per pod	0.57	2.06**	0.42	1.36	48.87	NS	0.33
Number of locules per pod	0.10	1.77**	0.23	0.04	7.56	NS	0.78
100 seed weight	32.18	67.66**	2.56	12.54	26.37	0.65	2.59
Pod weight	0.14	1.14**	0.20	0.38	56.35	NS	0.23
Pod length	0.23	1.48**	0.13	1.77	11.23	NS	0.59
Pod width	0.13	0.45**	0.31	0.06	14.17	NS	0.91
Pod thickness	0.05	0.12**	0.16	2.33	7.32	0.23	0.66
Green pod yield per plant	35.58	2856.17**	104.44	0.34	27.35	NS	16.58
Seed yield per plant	5.68	752.87**	21.82	0.26	34.50	NS	7.58
Shelling percentage	0.71	47.51**	0.69	1.04	690.46	NS	0.42
Crude proteins	2.05	14.72**	1.33	1.54	11.06	NS	1.87
Soluble proteins	1.02	1.91**	0.17	2.19	11.57	0.21	0.66
Total sugars	26.68	52.35**	1.04	25.58	50.20	0.41	1.65

\*\* Significant at 1% level of significance.

#### Components of variation

The range of mean values based on phenotypic expression could represent only a rough estimate of the variation or magnitude of divergence present among different genotypes. The estimates of genotypic and phenotypic coefficients of variation are more reliable estimates of extent of genetic variability present within the experimental material. As the estimates of phenotypic variability cannot differentiate between genetic and environmental effects and also in order to study the genotypic properties of population, it is necessary to divide the phenotypic or observed variation into heritable (variation due to genotype) and environmental components. For this purpose, phenotypic and genotypic coefficients were estimated and the results pertaining to the phenotypic and genotypic coefficients of variation are presented in Table 2. A relative amount of variation in genotypes for different characters can be judged by comparing the coefficients of genotypic and phenotypic variation.

#### Coefficients of variation (%)

The range of mean values could present a rough estimate about the magnitude of divergence present among different genotypes but the estimate of genotypic and phenotypic coefficients are of greater use in determining the extent of variability present within the material. The highest coefficient of variation (Table 3) was observed in number of podding nodes per plant (10.44) suggesting high degree of variation in the studied genotypes for this character. It

was followed by primary branches per plant (10.08), seed yield per plant (10.00), green pod yield per plant (9.91), total pods per plant (9.66), number of nodes per plant (7.21), number of locules per pod (6.71) and first blossom node (6.63). The lowest coefficient of variation was observed in number of pod weight (3.35) and number of seeds per pod (3.36).

Table 3. Estimation of CV, PCV, GCV, heritability, genetic advance and GA as percent of mean for different characters in pea

Character	Coefficient of variation (CV)	Phenotypic coefficient of variation (PCV)	Genotypic coefficient of variation (GCV)	Heritability in broadsense (%)	Genetic advance (GA)	Genetic advance as percent of mean
Days to first flowering	4.06	11.67	10.94	87.88	14.03	21.13
Days to 50% flowering	3.88	10.81	10.09	87.13	14.87	19.40
First blossom node	6.63	10.86	8.60	62.75	1.60	14.04
No. of primary branches per plant	10.08	31.59	29.94	89.81	1.37	58.44
Plant height (cm)	5.27	22.52	22.22	97.40	42.50	45.18
Days to first pod picking	0.76	4.20	4.14	96.78	10.62	8.38
Days to last pod picking	0.74	4.81	4.75	97.63	13.41	9.67
Number of nodes per plant	7.21	25.63	24.95	94.75	23.89	50.03
Number of podding nodes per plant	10.44	28.30	26.31	86.39	9.72	50.37
Number of pods per plant	9.66	27.00	25.21	87.20	11.89	48.50
Grain filling period (days)	4.61	14.37	13.62	89.71	13.29	26.57
Number of seeds per pod	3.36	13.83	13.41	94.10	1.64	26.80
Number of locules per pod	6.71	11.98	9.93	68.63	1.22	16.94
100 seed weight (g)	4.55	14.00	13.24	89.43	9.07	25.79
Pod weight (g)	3.35	14.78	14.40	94.86	1.22	28.89
Pod length (cm)	4.58	9.61	8.45	77.33	1.21	15.31
Pod width (cm)	4.34	10.08	9.10	81.44	0.22	16.92
Pod thickness (cm)	4.15	7.32	6.03	67.88	0.10	10.23
Green pod yield per plant (g)	9.91	30.98	29.36	89.74	59.11	57.30
Seed yield per plant (g)	10.00	34.88	33.42	91.78	30.81	65.95
Shelling percentage	0.58	8.86	8.84	95.56	8.17	18.17
Crude proteins (%)	5.34	11.13	9.77	77.03	3.82	17.67
Soluble proteins (%)	6.23	22.77	20.10	77.90	1.39	36.54
Total sugars (%)	5.01	20.90	20.90	94.03	8.27	40.58

#### *Phenotypic coefficient of variation (%)*

Data presented in Table 3 indicated wide range of phenotypic variability in the studied germplasm. Phenotypic coefficients of variation expressed in percentages ranged from 4.20 to 34.88. The maximum expression of phenotypic coefficient of variation was for seed yield per plant (34.88) followed by primary branches per plant (31.59), green pod yield per plant (30.98), number of podding nodes per plant (28.30) and total pods per plant (27.00) indicating better scope of phenotypic selection to enhance total yield. Phenotypic coefficient of variation was moderate for total sugars (20.90), pod weight (14.78) and grain filling period (14.37). The minimum expressions of phenotypic coefficients of variation were observed for days to first pod

picking (4.20), days to last pod picking (4.81), pod thickness (7.31), shelling percentage (8.86) and pod length (9.61). Similar findings were earlier reported in vegetable pea for seed yield per plant (SARDANA *et al.*, 2007; NISAR *et al.*, 2008), primary branches per plant (SINGH, 1990), green pod yield per plant (SHINDE, 2000; SINGH 2001; PAL and SINGH 2013; GEORGIEVA *et al.*, 2016) and number of podding nodes per plant and total pods per plant (ARUMUGAM *et al.*, 1977; CHAUDHARY and SHARMA, 2003; SHARMA and SHARMA, 2013). Low phenotypic coefficient of variation were observed for days to maturity (SINGH, 2001), days to first pod picking, pod length and shelling percentage (SHARMA *et al.*, 2007; SHARMA and SHARMA, 2013) shelling percentage and pod thickness (CHAUDHARY and SHARMA, 2003).

#### *Genotypic coefficient of variation (%)*

As the estimates of phenotypic coefficient of variation cannot differentiate between the genetic effects and environmental effects, so the study of genetic coefficient of variation is effective in partitioning out the real genetic differences. In the experimental material, genotypic variability for all the characters under study ranged from 4.14 to 33.42 (Table 3). Maximum expressions of genotypic coefficient of variation were observed in seed yield per plant (33.42) followed by primary branches per plant (29.94), green pod yield per plant (29.36), number of podding nodes per plant (26.31) and total pods per plant (25.21). In previous study was reported high genotypic coefficient of variation for pod yield per plant and total pods per plant (SHARMA *et al.*, 2007; SINGH, 2001; PAL and SINGH, 2013; GEORGIEVA *et al.*, 2016), for number of primary branches per plant (SOLANKI *et al.*, 1988; SINGH, 2001) and for number of podding nodes per plant (SUREJA and SHARMA, 2000). Genotypic coefficient of variation was moderate for total sugars (20.90), soluble proteins (20.10), pod weight (14.40) and 100 seed weight (13.24). The minimum expressions of genotypic coefficients of variation were observed for days to first pod picking (4.14), days to last pod picking (4.75), pod thickness (6.03), pod length (8.45) and shelling percentage (8.84). Low genotypic coefficient of variability for shelling percentage, pod length and days to maturity (SINGH, 2001; SHARMA and SHARMA 2013), days to first pod picking and pod length (SHARMA *et al.*, 2007, SHARMA and SHARMA, 2013) and pod thickness (SINGH, 1990) were also reported.

There were narrow differences between magnitude of phenotypic and genotypic coefficients of variation in all the characters studied, indicating low environmental influence in expression of these characters, which implies that phenotypic variability is a reliable measure of genotypic variability (NANDPURI *et al.*, 1973). So, selection for improvement of the trait is possible and effective on the phenotypic basis.

#### *Heritability in broad sense (%)*

Heritability is a measure of genetic relationship between parent and progeny and has been widely used in determining the degree to which a character may be transmitted from parents to offsprings. Estimation of heritability in broad sense gives the extent of heritable component of variation. Knowledge of degree of heritability for the character permits a rational choice of breeding methods to be followed for its improvement and helps to estimate the genetic gains from selection (GAUTAM *et al.*, 2017). The results pertaining to heritability, genetic advance and percentage genetic advance are presented in Table 3.

In the present study heritability is expressed as percentage ranged from 62.75 to 97.40. Very high heritability estimates were observed for days to last pod picking (97.63), plant height

(97.40), days to first pod picking (96.78), shelling percentage (95.56), pod weight (94.86) and number of seeds per pod (94.10). High heritability estimates were obtained for pod width (81.44), pod length (77.33), number of locules per pod (68.63) and pod thickness (67.88). Our results are consistent with results of other authors (SINGH, 2001; SHARMA *et al.*, 2007; CHAUDHARY and SHARMA, 2003; SARDANA *et al.*, 2007).

#### *Genetic advance (as percent of mean)*

Selection for a particular trait is made on the basis of phenotype, which is produced by the joint action of genotype and environment. Therefore, the phenotypic superiority of selected plants or families over the original population is not solely due to their genotypic superiority. It may be due to favorable environmental conditions, so only heritability estimates are not reliable. Genetic advance in such cases gives a good idea for actual position (JOHNSON *et al.*, 1955) as it provides information about improvement in the mean genotypic value of the selected families over base population. Genetic advance depends upon the heritability of the character under selection, genetic variability of the genotypes and intensity of selection (SINGH, 2005). A highly heritability coupled with high genetic advance gives effective criteria for selection.

In the present investigation as shown in Table 3, the highest genetic advance as percentage of mean was predicted high for seed yield per plant (65.95) followed by primary branches per plant (58.40) and green pod yield per plant (57.30). Some authors were also reported high genetic advance for green pod yield per plant (SOLANKI *et al.*, 1988; KORLA and SINGH, 1988; SINGH, 2001 and CHAUDHARY and SHARMA, 2003). Moderate genetic advance estimates were obtained for pod weight (28.89), grain filling period (26.57), number of seeds per pod (26.80) and 100 seed weight (25.79). The results are in agreement with the findings of GUPTA *et al.*, (1998) and NISAR *et al.*, (2008). Low genetic advance was observed for days to first pod picking (8.38), days to last pod picking (9.67) and pod length (15.31). CHAUDHARY and SHARMA (2003) and SHARMA *et al.* (2007) were also found a low genetic advance for pod length and GUPTA *et al.* (1998) and CHAUDHARY and SHARMA (2003) for days to maturity. SARDANA *et al.*, (2007) and NISAR *et al.*, (2008) reported high genetic advance for seed yield per plant and primary branches per plant.

From the present investigation, it is clear that characters like seed yield per plant, pod weight and green pod yield per plant have high heritability and higher genetic advance which indicated that the expression of these characters was governed by additive gene action. So these characters can be easily improved by selection methods. Higher heritability coupled with moderate genetic advance was expressed in number of seeds per pod. Higher heritability estimates and low genetic advance were obtained for days to first pod picking, days to last pod picking and pod length implies that these traits are most probably governed by non-additive gene action. The high heritability estimates obtained for above characters might be due to favorable effect of environment rather the genetic constitution and in such cases there is little scope for selection.

#### CONCLUSIONS

Genetic variability, heritability and genetic advance studies were carried out for yield and yield contributing characters for forty-seven diverse genotype of pea. The results revealed a wide range of phenotypic variation, along with high heritability in pea. High genotypic and phenotypic co-efficient of variation were recorded for seed yield per plant followed by primary branches per plant, green pod yield per plant, number of podding nodes per plant and total pods per plant

indicating better scope of phenotypic and genotypic selection to enhance total yield. Likewise, high heritability along with moderate to high genetic advance as percent of means was recorded for pod weight and number of seeds per pod, which indicated the role of additive gene action for the inheritance of these traits and therefore, selection could be used for improving these traits.

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**GENETIČKA VARIJABILNOST PARAMETARA PRINOSA I OSOBINA KVALITETA  
GRAŠKA (*Pisum sativum* L.)**

Jaskanwal SINGH I R.K. DHALL

Department za povrtarstvo, Punjab Poljoprivredni Univerzitet, Ludhiana-141004, Indija

**Izvod**

Eksperiment u polju je postavljen u cilju ispitivanja genetičke varijabilnosti, heritabilnosti i genetičkog napredka za 24 morfološke osobine i 3 biohemijeks osobine u 47 genotipova graška. Analiza varijanse je pokazala značajne razlike između genotipova za sve ispitivane osobine. Veći koeficijent variranja je dobijen za broj nodusa po biljci i visi fenotipski i genetički koeficijent varijacije je dobijen za prinos semena po biljci praćen brojem primarnih grana po biljci i prinos zelenih mahuna po biljci. Veoma visoka heritabilnost je dobijena za dane do pojave poslednje mahune (97.63) sledi viisna biljke (97.40), dani do pojave prve mahune (96.78) i procenat (95.56) dok genetički napredak kao procenat sredine je nađen visok za prinos semena po biljci (65.95) i primarne grane po biljci (58.40). Visoka heritabilnost zajedno sa umerenim do visokim genetičkim napredkom je predviđena u slučaju težine mahune i broja semena po mahuni, što ukazuje na ulogu aditivne akcije gena za nasleđivanje ovih osobina i zato, selekcija se može koristiti za poboljšanje ovih osobina.

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