

Variability Studies in Pea (*Pisum Sativum* L.) with Respect of Growth, Yield and Yield Attributs Parameters

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Abstract: The variability studies in fifteen pea (Pisum sativum L.) genotypes at the Instructional-Cum-Research Farm, Department of Horticulture, College of Agriculture, Latur, during- 2014-15 under Rabi season. The highly significant differences were observed among the genotypes for the characters. Estimates of phenotypic and genotypic co-efficient of variance were plant height, number of branches, number of leaves, leaf area (dsm⁻¹), days to initiation of first flowering, number of clusters per plant, pod length (cm), number of seeds per green pod, green pod yield per plant (g), pod yield per plot (kg), pod yield per hectare (q), crop duration (days). The high heritability estimates with high genetic advances were obtained for plant height, Number of leaves, Leaf area (dsm⁻¹) with low genetic advances which indicated inadequate variability in the material.

INTRODUCTION

Pea (*Pisum sativum* L.) chromosome number 2n = 14 is one of the most important components of human diet and are perhaps the best source of almost all vitamins and minerals. They are right called as, "protective food" since they impart disease resistance to our body.

Evaluation of variability in the available germplasm is a pre-requisite for any breeding programme. The breeder selects better genotypes based on their phenotypic expression. The progress in breeding for economic characters that are mostly polygenically controlled and hence environmentally influenced is determined by the magnitude and nature of their genotypic variability. The estimates of phenotypic and genotypic variances for various characters and their heritability are important components in selecting the best genotypes. The heritability plays an important role in selection for the desirable characters. The estimates of heritability along with genetic advance are helpful in designing successful breeding programme.

MATERIALS AND METHODS

An experiment consisting of 15 Pea genotypes *viz.*, AP-1, PB-89, Arkel, Phule Priya, AP-3, Nilanga Local, Alandi Local, Aghawan Local, Man Local, Parbhani Local, Renapur Local, Jalna Local, Mudkhed Local, Partur Local and Aurangabad Local were carried out in Rabi 2014-15at the Instructional-Cum-Research Farm, Department of Horticulture, College of Agriculture, Latur. Each genotypes were consider as a treatment and planted in RBD in two replication. Observations were recorded on 5 randomly selected plants from each genotypes (plots) in both replications for 16 characters (Table 1). The mean values for 10 plots were subjected to statistical analysis (Panse and Sukhatme, 1985). The genotypic co-efficient of variance (GCV) and phenotypic co-efficient of variance (PCV), heritability and expected genetic advances was estimated as per Pallavi *et al.* (2013).

Genotypic and phenotypic coefficient of variation

Genotypic and phenotypic coefficients of variation were estimated by the formulae as suggested by Pallavi *et al.* (2013).

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$$\text{GCV} = \frac{\sqrt{\text{Genotypic variance}}}{\overline{X}} \times 100$$

Where, \overline{X} = the mean of character

$$PCV = \frac{\sqrt{Phenotypic variance}}{\overline{X}} \times 100$$

Where \overline{X} = the mean of character

Heritability estimates (h²)

In broad sense, it may be defined as the proportion of genotypic variance to phenotypic variance and heritability percentage in broad sense is calculated by the formulae as suggested by Pallavi *et al.* (2013).

$$h^2(b) = \frac{\sigma^2 g_i}{\sigma^2 p_i}$$

Where,

 h^2 (b) = Heritability in broad sense.

$$\sigma^2 g_i$$
 = Genotypic variance of character '*i*'.

 $\sigma^2 p_i$ = Phenotypic variance of character '*i*'.

Expected genetic advance (EGA)

$$EGA = \frac{VG}{\sqrt{VP}} \times K$$

Where,

VG = Genotypic variance

 \sqrt{VP} = Phenotypic standard deviation

K = Selection differential at %
 selection intensity.

Value of K = 2.06 at 5 % level,

Value of K = 2.64 at 1%

Expected genetic advance is expressed in percentage over mean.

EGA in % of mean =
$$\frac{\text{EGA}}{\overline{X}} \times 100$$

Where,

 \overline{X} = The mean of treatment

RESULTS AND DISCUSSION

The present investigation study the statistical analysis revealed highly significant difference found among the genotypes for all the characters studied (Table

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Sr. No.	Characters	Mean sum of squares				
		Replication (df=1)	Treatments (df=14)	Error (df=14)		
1	Plant height (cm)	6.9697	370.1551**	17.8417		
2	Number of branches/plant	0.0333	6.1733**	0.3904		
3	Number of leaves/plant	126.4853	7306.9219**	230.1081		
4	Leaf area/plant (dsm ⁻¹)	0.4788	358.4456**	12.3047		
5	Days to initiation of first flowering	4.0333	168.6333**	11.0333		
6	Days to 50% flowering	2.7000	163.3476**	20.2714		
7	Days to first picking	9.6333	333.5142**	61.2761		
8	Number of picking	0.0333	1.9904**	0.3904		
9	Number of cluster/plant	0.5880	110.4881**	3.7765		
10	Number of pod in cluster	0.0005	0.1333**	0.0224		
11	Pod length (cm)	0.1552	0.1333**	0.5398		
12	Number of seed/green pod	0.0388	3.4290**	0.3541		
13	Crop duration (days)	0.0333	208.2761**	63.6761		
14	Green pod yield/plant (g)	0.0013	0.8584**	0.0384		
15	Green pod yield/plot (kg)	2.1280	601.0173**	18.9543		
16	Green pod yield/ha (q) **Significant at 1% level	4.3624	131.1533**	9.3124		

 Table 1

 Analysis of variance for different characters studied in the genotypes of pea.

1.), which is indicated presence of wide variability in the material which can be used for further crop improvement through selection or by involving them in various crosses followed by conventional breeding methods. The mean, range, genotypic and phenotypic coefficients of variation, heritability and genetic advance for all the traits. The evaluated material exhibited a broad range variation and high mean values for different traits. Significant variability for various quantitative characters has been reported by various workers viz., Muhammad and Muhammad (2002), Dayal Prasad Babu and Suresh (2007), Sardana *et al.* (2007), Kumar *et al.* (2010) and Khan *et al.* (2013).

The range recorded for plant height was from 43.08 to 96.88 cm with an average value of 55.42 cm. The genotype Nilanga Local was found to be the highest plant height (96.88 cm), followed by Man Local (66.57 cm). The range recorded for number branches per plant was 4.00 to 9.10 with an average 6.06. The genotype Alandi Local was found to produce highest branches per plant (9.10) followed by Aghawan Local (8.30). The range recorded for number of leaves per plant was 101.80 to 281.80 and the average160.26. The genotype Man Local was found to produce highest number of leaves per plant (281.80) followed by Aghawan Local (250.00). The range recorded for leaf area per plant was 19.24 to 68.71, while, the average 31.95. The genotype Nilanga Local was recorded maximum leaf area per plant (68.71) followed by Man Local (50.61). The range recorded for days to first flower of 28.00 to 53.50 days was observed and the average 41.56 days, whereas, the genotypes Arkel and AP-3 were early to flower (28.00) followed by Man Local (33.00). The range recorded for days to 50% flowering at different genotypes from 34.00 to 61.00 days with the average 48.56. The genotype AP-3 took minimum of 34.00 days for 50% flowering followed by the genotypes Arkel (35.50 days).

Days to first picking ranged from 45.00 days to 86.00 days, with the average of 68.10 days. The genotype AP-3 took minimum days to first harvest of pod (45.00 days) followed by genotype AP-3 (45.50 days). The range recorded for number of picking 4.50 to 8.00, with the average of 6.23. The genotype Man Local (8.00) took maximum number of pickings followed by genotype Aghwan Local. The number of cluster per plant for all the fifteen genotypes ranged from 11.70 to 37.50, with the average of 18.95. The genotype Man Local took maximum number of cluster per plant (37.50) followed by genotype Aghwan Local (31.30). The maximum number of pods in cluster (2.00) in all genotypes and minimum number of pods in a cluster was recorded in genotype Jalna Local (1.00). The range recorded for length of pod was 3.92 to 8.02 cm, with the average length of pod 6.36 cm. Phule Priya was found recoded maximum length of pod (8.02 cm) followed by genotype Arkel (7.93 cm). The range recorded for number of seed per green pod was 3.76 to 8.06, with the average6.05. Phule Priya was found maximum number of seed per green pod (8.06 cm) followed by genotype PB-89 (7.18).

Range for the green pod yield per plant was recorded from 16.36 g to 45.53 g. The average yield per plant was found to be 27.34 g. The genotype Phule Priya produced maximum yield per plant (45.53 g) followed by genotype Arkel (39.68 g). The green pod yield per plot of all the fifteen genotypes were in the range of 1.10 kg to 3.50 kg. The average yield per plot was found 1.97 kg. The genotype, Phule Priva had recorded maximum yield per plot (3.50 kg) followed by genotype Arkel (3.00 kg). The green pod yield per hectare of all the fifteen genotypes ranged from 29.10 q. to 92.60 q. The average yield per hectare was found 52.21 quintal. The genotype Phule Priya produced maximum green pod yield per hectare (92.60 q) followed by genotype Arkel (79.37 q). The range noted for crop duration was 89.00 to 125.00 days, with the average crop duration 112.23 days. The Mudkhed Local was found maximum crop duration (125.00 days) followed by Aurangabad Local (121.00 days).

Genotypic and phenotypic coefficients of variation for different characters are presented in Table 2. The maximum genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were observed for number of leaves per plant (46.24, 46.99), leaf area per plant dsm⁻¹ (41.16, 42.60), and number cluster per plant (38.53, 39.88) respectively. While, days to 50% flowering (17.41, 19.72), days to first picking (17.13, 20.63), number picking (14.34, 17.50) exhibited moderate

Sr. No.	Characters	Range	Grand mean	GCV (%)	PCV (%)	Heritability (%)	GA
1	Plant height (cm)	43.08 - 96.88	55.42	23.94	25.13	90.8	26.05
2	Number of branches/ plant	4.00 - 9.10	6.06	28.02	29.86	88.1	3.28
3	Number of leaves/plant	101.80 - 281.80	160.26	37.11	38.30	93.8	118.73
4	Leaf area/plant (dsm ⁻¹)	19.24 - 68.71	31.95	41.16	42.60	93.3	26.18
5	Days to initiation of first flowering	28.00 - 53.50	41.56	21.35	22.80	87.7	17.12
6	Days to 50% flowering	34.00 - 42.50	48.56	17.41	19.72	77.9	15.38
7	Days to first picking	45.00 - 86.00	68.10	17.13	20.63	68.9	19.95
8	Number of picking	4.50 - 8.00	6.23	14.34	17.50	67.2	1.51
9	Number of cluster/plant	11.70 - 37.50	18.95	38.53	39.88	93.3	14.54
10	Number of pod in cluster	1.00 - 2.00	1.93	12.17	14.43	71.1	0.40
11	Pod length (cm)	3.92 - 8.02	6.36	22.96	25.70	79.8	2.69
12	Number of seed/green pod	3.76 - 8.06	6.05	20.48	22.71	81.2	2.30
13	Green pod yield/plant (g)	16.36 - 45.53	27.34	28.53	30.64	91.4	1.26
14	Green pod yield/plot (kg)	1.10 - 3.50	1.97	32.44	33.93	93.8	34.05
15	Green pod yield/ha (q)	29.10 - 92.60	52.21	32.67	33.72	86.7	14.97
16	Crop duration (days)	89.00 - 125.50	112.23	7.57	10.38	53.1	12.77

 Table 2

 Estimation of genetic parameters-range, mean, GCV, PCV, heritability and Genetic advance

GCV and PCV respectively. The crop duration (7.57, 10.38) exhibited lowest for GCV and PCV respectively. Similar result was reported by Muhammad and Muhammad (2002) and Shinde *et al.* (2009).

Heritability in broad sense estimates were highest for number of leaves per plant (93.8%), leaf area per plant dsm⁻¹ (93.3%), number cluster per plant (93.3%), green pod yield per plant (91.4%), plant height (90.8%), number of branches per plant (88.1%), days to initiation of first flowering (87.7%), green pod yield per hectare (86.7%), number of seed per green pod (81.2%), pod length (79.8), days to 50% flowering (77.9%), number of pod in cluster (71.1%), days to first picking (68.9%) and number of picking (67.2%). The estimates of heritability were moderate for crop duration days (53%) respectively. Similar results were recorded by Singh *et al.* (2003), Dayal Prasad Babu and Suresh (2007), Javaid *et al.* (2002) and Shinde *et al.* (2009).

Genetic advance over mean was estimated for different character and results are presented in Table 2. The high expected genetic advance were observed for the characters viz., number of leaves per plant

(118.73%), green pod vield per plant (34.05%), leaf area per plant dsm⁻¹(26.18%) and plant height (26.05%).Similar result was recorded Javaid et al. (2002)and Dayal Prasad Babu and Suresh(2007). However, moderate expected genetic advance were observed for days to first picking (19.95%), days to initiation of fist flowering (17.12%), days to 50 % flowering (15.38), green pod vield per hectare (14.97%), number cluster per plant (14.54%) and crop duration days (12.77%). Low value of expected genetic advance were observed for the number of branches per plant (3.28%), pod length (2.69%), number of seed per green pod (2.30%), number of picking (1.51%), green pod yield per plot (1.26%) and number of pod in cluster (0.40%). Similar result was observed by Kaur et al. (2007), Choudhary et al. (2013), Sardhana et al. (2007).

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