



P-ISSN: 2349-8528

E-ISSN: 2321-4902

IJCS 2019; 7(5): 1975-1978

© 2019 IJCS

Received: 01-07-2019

Accepted: 03-08-2019

Ban SJCollege of Agriculture, Latur,
Maharashtra, India**Jagtap VS**College of Agriculture, Latur,
Maharashtra, India**Ghatul ID**College of Agriculture, Latur,
Maharashtra, India**Genetic variability studies in pea (*Pisum sativum* L.)****Ban SJ, Jagtap VS, Ghorpade SB and Ghatul ID****Abstract**

The present investigation was carried out to estimate phenotypic and genotypic coefficient of variation, heritability (broad sense) and genetic advance per cent of mean for 14 quantitative traits in 21 different genotypes of pea during Rabi 2017-18 at Instructional-Cum-Research Farm, Department of Horticulture, College of Agriculture Latur, Vasanttrao Nike Marathwada Krishi Vidyapeeth (M.S.). Significant differences among the genotypes were observed for all the characters under study. The PCV and GCV values were high for number of primary branches per plant, green pod yield per hectare, green pod yield per plot, green pod yield per plant, pod length, number of seeds per green pod and number of pods per cluster. High heritability and high genetic advance were observed for characters like plant height, number of primary branches per plant, days to initiation of first flowering, days to 50% flowering, days to first picking, number of pickings, number of clusters per plant, number of pods per cluster, pod length, number of seeds per green pod, green pod yield per plant, green pod yield per plot and green pod yield per hectare.

Keywords: GCV, PCV, heritability, genetic advance**Introduction**

Pea (*Pisum sativum* L.) belongs to family 'Leguminaceae' it grown in India as a winter vegetable in the plains of north and as a summer vegetable in the hills of India. It is one of the most important vegetable as well as pulse crop in India.

Pea is a very common nutritious vegetable grown throughout the world. It contains more proteins, carbohydrates, vitamins and minerals like calcium and phosphorus. The nutritive value of green pea (per 100 g of edible portion) is protein 6.2 g, fat 0.4 g, carbohydrate 16.9 g, iron 1.2 mg, phosphorus 102 mg, vitamin C 27 mg, vitamin B₁ 0.28 mg, vitamin B₂ 0.11 mg, vitamin B₃ 2.8 mg. (Duke 1981, Hulse 1994)^[4, 7]. It is an excellent food for human consumption taken either as a vegetable or in soup. Large production of peas is processed (canned, dehydrated or frozen) for consumption in off season. Being a proteinous vegetable it forms a valuable dish in the vegetarian diet. It ranks third in the world production amongst the grain legumes.

The extent of variability existed in the germplasm, which offers a better opportunity to select desirable genotype. The subsequent study of variability and inter-relations among the different characters helps to proceed further for effective selection. The basic information which have a plant breeder for producing new hybrids, the extent of variability should be required in a particular crop species. Larger variability ensures better chances of producing new derived varieties. The collection of germplasm from different sources provides raw material to the plant breeder. An access to wide variety of these resources constitutes an essential component of successful crop improvement programmes.

Materials and Methods

An experiment was carried out at Instructional-Cum-Research Farm, Department of Horticulture, College of Agriculture Latur during the year 2017-18 to evaluate twenty one diverse genotypes of pea. The experiment was laid out in Randomized Block Design (RBD) with two replications. Observations were recorded from five randomly selected plants of each genotype in each replication for fourteen characters viz., Plant height (cm), Number of primary branches/plant, Days to first flowering, Days to 50% flowering, Days to first picking, Number of pickings, Number of clusters per plant, Number of pods per cluster, Pod length, Number of seeds per pod, Crop duration, Green pod yield per plot, Green pod yield per hectare, Green pod yield per plant. The data generated was averaged and subjected to analyze the variability. Genotypic and phenotypic coefficients of variation were estimated by the formulae as

Correspondence**Ban SJ**College of Agriculture, Latur,
Maharashtra, India

suggested by Burton and DeVane (1953)^[3]. PCV and GCV values were categorized as low (0-10%), moderate (10.1-20%) and high (>20) values as indicated by Sivasubramanian and Menon (1973)^[17].

Heritability in broad sense was calculated by the formula as suggested by Allard (1960)^[2]. Heritability was classified as suggested Robinson *et al.* (1949)^[14] into low (0-30%), moderate (30.1-60%) and high (>60%). The Genetic advance (GA) resulting from selection of five per cent superior individuals was worked out as suggested by Allard (1960)^[2]. The GAM% was categorized into low (0–10%), moderate (10.1–20%) and high (>20%) as suggested by Johnson *et al.* (1955)^[8].

Results and Discussion

The analysis of variance indicated significantly higher amount of variability among the genotypes for all the characters studied *viz.*, plant height, primary branches per plant, days to initiation of first flowering, days to 50% flowering, days to first picking, number of pickings, number of clusters per plant, number of pods per cluster, pod length, number of seeds per pod, crop duration, green pod yield per plant, green pod yield per plot and green pod yield per hectare are given in Table 1 indicating the presence of genetic variability in the existing material. Similar findings reported by Kaur *et al.*, (2007)^[10], Nawab *et al.*, (2008)^[12], Pal and Singh (2013)^[13], Selvi *et al.*, (2014)^[15], Tambolkar *et al.*, (2016)^[19], Gudadinni *et al.*, (2017)^[5], Sharma *et al.*, (2017)^[16], Srinivas *et al.*, (2017)^[18] and Thouseem *et al.*, (2018)^[21].

In the present findings, phenotypic coefficient of variation were higher than the corresponding genotypic coefficient of variation for all the characters studied, (Table 2) However, the differences was narrow which implied less environmental influences. In other words it seems that genetic factors were predominantly responsible for expression of those attributes and selection could be made effectively on the basis of phenotypic performance Similar finding h reported by Thouseem *et al.*, (2018)^[21], Gudadinni *et al.*, (2017)^[5], Sharma *et al.*, (2017)^[16], Srinivas *et al.*, (2017)^[18] and Selvi *et al.*, (2014)^[15].

The phenotypic coefficient of variation ranged from 11.74% for days to 50% flowering to 78.44% for number of primary branches per plant. The phenotypic coefficient of variations was highest for characters *viz.*, number of primary branches per plant (78.44%), number of green pod yield per hectare (34.08%), green pod yield per plot (34.04%), green pod yield per plant (29.95%), pod length (28.42%), number of seeds per green pod (22.73%) and number of pods per cluster (21.09%) are given in Table 2. It indicates that these characters would respond to selection. Similar finding reported by Thouseem *et al.*, (2018), Gudadinni *et al.*, (2017)^[5], Sharma *et al.*, (2017)^[16], Tambolkar *et al.*, (2016)^[19], Thakur *et al.*, (2016)^[20], Kumar *et al.*, (2015)^[11] and Selvi *et al.*, (2014)^[15].

The rest of the characters such as number of clusters per plant (19.40%), plant height (19.15%), number of pickings (17.28%), days to first picking (14.71%), days to first flowering (13.61%), crop duration (12.33%) and days to 50% flowering (11.74%) exhibited moderate phenotypic coefficient of variation. Similar finding reported by Kaur *et al.*, (2018)^[9], Thouseem *et al.*, (2018)^[21], Gudadinni *et al.*,

(2017)^[5], Srinivas *et al.*, (2017)^[18], Tambolkar *et al.*, (2016)^[19], Ahmad *et al.*, (2014)^[1] and Pal and Singh (2013)^[13].

The genotypic coefficient of variation varied from 8.28% for crop duration to 77.96% for of number of primary branches per plant. The genotypic coefficient of variation was highest for characters *viz.*, number of primary branches per plant (77.96%), green pod yield per hectare (32.26%), green pod yield per plot (32.22%), green pod yield per plant (28.77%), pod length (28.26%), number of seeds per green pod (22.39%) and number of pods per cluster (20.47%). The high values of GCV suggested greater phenotypic genotypic variability among the genotypes and responsiveness of the attributes for making further improvement by selection. Similar finding reported by Thouseem *et al.*, (2018)^[21], Gudadinni *et al.*, (2017)^[5], Sharma *et al.*, (2017)^[16], Tambolkar *et al.*, (2016)^[19], Thakur *et al.*, (2016)^[20], Kumar *et al.*, (2015)^[11] and Selvi *et al.*, (2014)^[15].

The moderate genotypic coefficient of variation were recorded in the characters, such as number of clusters per plant (19.03%), plant height (17.76%), number of pickings (15.71%), days to first picking (14.20%), days to first flowering (13.14%) and days to 50% flowering (11.46%). This indicated the moderate variability influenced by environment. Similar finding reported by Kaur *et al.*, (2018)^[9], Thouseem *et al.*, (2018)^[21], Gudadinni *et al.*, (2017)^[5], Srinivas *et al.*, (2017)^[18], Ahmad *et al.*, (2014)^[1] and Pal and Singh (2013)^[13].

The low genotypic coefficient of variation was noted only in crop duration (8.28%) character, which indicated the major influence of environment. Similar finding reported by Tambolkar *et al.*, (2016)^[19].

Heritability however indicates only the effectiveness with which selection of a genotype can be based on phenotypic performance, but fails to indicate the genetic progress. Heritability estimates along with genetic advance are more effective and reliable in predicting the improvement through selection (Johnson *et al.*, 1955)^[8].

High heritability coupled with high genetic advance were observed for plant height (86.1, 33.95), number of primary branches per plant (98.8, 159.62), days to initiation of first flowering (93.3, 26.11), days to 50% flowering (95.2, 23.03), days to first picking (93.2, 28.24), number of pickings (82.7, 29.42), number of clusters per plant (96.3, 38.47), number of pods per cluster (94.2, 40.93), pod length (98.9, 57.90), number of seeds per green pod (97.1, 45.47), green pod yield per plant (92.3, 56.93), green pod yield per plot (89.6, 62.81) and green pod yield per hectare (89.6, 62.91) (Tables 2). The results suggested the importance of additive gene action for the inheritance of these characters and improvement could be brought about by phenotypic selection. Similar finding reported by Gupta *et al.*, (2018)^[6], Thouseem *et al.*, (2018)^[21], Gudadinni *et al.*, (2017)^[5], Sharma *et al.*, (2017)^[16], Tambolkar *et al.*, (2016)^[19], Pal and Singh (2013)^[13] and Ahmad *et al.*, (2014)^[1].

Moderate heritability coupled with moderate genetic advance was observed for crop duration (45.1, 11.46). The result suggested the importance of additive gene action for the inheritance of this character and improvement could be brought about by phenotypic selection. Similar finding reported by Tambolkar *et al.*, (2016)^[19].

Table 1: Analysis of variance for different characters studied in the genotypes of pea.

S. No.	Characters	Mean sum of squares		
		Replication	Treatments	Error
1	Plant Height (cm)	9.315	302.034**	22.588
2	Number of primary branches/plant	0.000	9.836**	0.060
3	Days to initiation of first flowering	5.357	77.081**	2.757
4	Days to 50% flowering	2.881	76.229**	1.881
5	Days to first picking	9.524	112.529**	7.524
6	Number of pickings	0.095	2.057**	0.195
7	Number of clusters/plant	0.275	3.635**	0.069
8	Number of pods per cluster	0.004	0.329**	0.010
9	Pod length (cm)	0.005	8.361**	0.046
10	Number of seeds/green pod	0.004	4.748**	0.070
11	Crop duration (days)	120.024	252.164**	95.374
12	Green pod yield/plant (g)	0.457	139.489**	5.616
13	Green pod yield/plot (kg)	0.001	0.508**	0.028
14	Green pod yield/ha (q)	1.907	719.822**	39.396

** significant @1%

Table 2: Mean, range and different genetic parameters in pea.

S. No	Genetic parameters	Mean	Range	GV	PV	GCV	PCV	Heritability (h ²)	GA 5%	GA as % of mean
1	Plant height (cm)	66.54	48.42-96.27	139.72	162.31	17.76	19.15	86.1	22.59	33.95
2	Number of primary branches /plant	2.84	1.00-11.00	4.89	4.95	77.96	78.44	98.8	4.53	159.62
3	Days to initiation of first flowering	46.40	33.00-54.00	37.16	39.92	13.14	13.62	93.3	12.12	26.11
4	Days to 50% flowering	53.21	39.00-60.50	37.17	39.06	11.46	11.74	95.2	12.25	23.03
5	Days to first picking	71.29	48.00-86.00	102.50	110.03	14.20	14.72	93.2	20.13	28.24
6	No. of pickings	6.14	4.00-8.00	0.93	1.13	15.71	17.28	82.7	1.81	29.42
7	No. of clusters/plant	7.01	5.30-9.00	1.78	1.85	19.04	19.40	96.3	2.70	38.47
8	No. of pods per cluster	1.95	1.10-2.70	0.16	0.17	20.47	21.09	94.2	0.80	40.93
9	Pod length (cm)	7.21	3.77-10.09	4.16	4.20	28.26	28.42	98.9	4.18	57.90
10	No. of seeds/ green pod	6.83	4.60-9.60	2.34	2.41	22.40	22.73	97.1	3.11	45.47
11	Crop duration	106.93	88.50-125.0	78.40	173.77	8.28	12.33	45.1	12.25	11.46
12	Green pod yield/ plant	28.44	17.20-46.03	66.94	72.55	28.77	29.95	92.3	16.19	56.93
13	Green pod yield/ plot	1.52	0.86-2.54	0.24	0.27	32.22	34.04	89.6	0.96	62.81
14	Green pod yield/ ha	57.17	32.36-95.70	340.21	379.61	32.26	34.08	89.6	35.97	62.91

References

- Ahmad HB, Rauf S, Rafiq M, Mohsin AU, Iqbal A. Estimation of genetic variability in pea (*Pisum sativum* L.). J Glob. Innov. Agric. Soc. Sci. 2014; 2(2):62-64.
- Allard RW. Principles of plant breeding. John Wiley and Sons, New York. 1960, 485.
- Burton TW, DeVane EW. Estimating heritability in tall fescue (*Festuca arundinacea*) from replicated clonal material. Proejtunniens. 1953; 9(22):12-15.
- Duke JA. Hand book of legumes of world economic importance. Plenum Press, New York, 1981, 199-265.
- Gudadinni P, Bahadur V, Ligade P, Topno SE, Prasad VM. Study on genetic variability, heritability and genetic advance in garden pea (*Pisum sativum* var. *Hortense* L.). Int. J Curr. Microbiol. App. Sci. 2017; 6(8):2384-2391.
- Gupta A, Singh MK, Rout S. Assessment of genetic variability, heritability and genetic advance in pea (*Pisum sativum* L.). J Pharmacognosy. Phytochemistry. 2018; 7(3):545-546.
- Hulse JH. Nature, composition and utilization of food legumes, 1994, 77-97.
- Johnson. Genetic advance analysis in pea (*Pisum sativum* L.). Madras. Agric. J. 1955; 6(7):387-390.
- Kaur G, Chamroy T, Kumar S, Savita. Studies on genetic variability in pea (*Pisum sativum* L.) under organic cultivation. Int. J Chemical. Studies. 2018; 6(4):2291-2294.
- Kaur H, Singh M, Brar PS. Genetic variability in pea (*Pisum sativum* L.). J Res. Punjab. agric. Univ. 2007; 44(4):301-303.
- Kumar R, Kumar M, Dogra RK, Bharat NK. Variability and character association studies in garden pea (*Pisum sativum* var. *Hortense* L.). Legume Res. 2015; 38(2):164-168.
- Nawab NN, Subhani GM, Mahmood K, Shakil Q, Saeed A. Genetic variability, correlation and path analysis studies in garden pea (*Pisum sativum* L.). J Agric. Res. 2008; 46(4):333-340.
- Pal AK, Singh S. Assessment and genetic variability in garden pea (*Pisum sativum* L. var. *Hortense*). Int. J Agric. Sci. 2013; 9(1):293-296.
- Robinson HF, Comstock RE, Harvey PH. Estimates of heritability and the degree of dominance in corn. Agronomy. J. 1949; 41(8):353-359.
- Selvi BS, Rajangam J, Muthuselvi R. Genetic variability and heritability studies for quantitative traits in pea (*Pisum sativum* L.). Plant. Archives. 2014; 14(2):955-959.
- Sharma PP, Vyas M, Meghawal DR. Estimation of genetic variability, heritability and correlation analysis in field pea (*Pisum sativum* L.) genotypes. J Plant. Development. Sci. 2017; 9(1):53-56.
- Sivasubramanian S, Menon M. Heterosis and inbreeding depression in rice. Madras Agric. J. 1973; 60:1139-1144.
- Srinivas J, Kale VS, Nagre PK. Studies on genetic variability, heritability and genetic advance in cowpea [*Vigna unguiculata* (L.) Walp]. Int. J Curr. Microbiol. App. Sci. 2017; 6(6):3314-3318.
- Tambolkar BB, Chavan NH, Vidhate SB. Variability studies in pea (*Pisum sativum* L.) with respect of growth,

- yield and yield attributes parameters Int. J Tropical. Agric. 2016; 34(6):1765-1769.
20. Thakur S, Thakur R, Mehta DK. Genetic variability and association studies for green pod yield and component horticultural traits in garden pea under high hill dry temperate conditions of Tabo valley of Spiti district of Himachal Pradesh. Int. J Sci. Env. Tech. 2016 5(4):1987-1992.
21. Thouseem N, Thomas B, Elizabeth N. Genetic parameters in seed yield components of cowpea (*Vigna unguiculata* L. Walp.). Int. J Curr. Microbiol. App. Sci. 2018; 7(2):2268-2274.