

## RESEARCH ARTICLE

# Studies on genetic variability, heritability and genetic advance for quantitative characters in field pea

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### SUMMARY

The fifty genotypes of field pea were studied out during *Rabi* 2015-2016 and 2016-17 at Oilseed Research Farm, Kalyanpur of Chandra Shekhar Azad University of Agriculture and Technology, Kanpur (U.P.). The experiment was laid in a Randomized Complete Block Design with three replications for days to 50% flowering, days to maturity, plant height, number of primary branches, number of nodes per plant, pod length, number of seed per pod, 100 seed weight, number of pod per plant and seed yield per plant. Analysis of variance showed significant differences among all the genotypes under study. The phenotypic co-efficient of variation was higher than genotypic co-efficient of variation for all the characters indicating the effect of environment on these characters. Studies of variation indicated that considerable amount of variation in plant height, number of pod per plant, number of nodes per plant, pod length and number of 100-seed weight which could be utilized for breeding for improvement. All traits showed high heritability except number of primary branches per plant (13%) and number of seeds per pod (18%). The higher genetic advance showed in plant height.

**Key Words :** Genetic variation, Heritability, Genetic advance

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**F**ield pea (*Pisum sativum* var. *arvense* L.), is an important pulse crop of India. It is a diploid species with  $2n = 2x = 14$  chromosome belongs to Leguminosae family. Peas originated in south west Asia.

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Two types of peas are generally cultivated all over the world. One is the garden pea and second is field pea. Field pea (*Pisum sativum* var. *arvense*) is the fourth leading legume in terms of consumption in the world. This is an important *Rabi* pulse crop of India and was among the first crop cultivated by man. This crop is highly productive, grown for food and forage. Field pea is extensively used as dry, whole or split pulse (Dal). This crop plays an important role in nourishment because of a rich source of proteins, carbohydrates and vitamins for human nutrition.

Field pea is an annual, cool season pulse grain and can be of the indeterminate (climbing) type or determinate

(bush or dwarf) type (Zohary and Hopf, 2002). The majority of pea plants exhibit an indeterminate growth habit (Cousin, 1997). Most cultivars of pea produce white or reddish-purple flowers, which are self pollinated. Each flower produces a pod containing four to nine seeds (Zohary and Hopf, 2002). Indeterminate cultivars mature in 90 -100 days while determinate types have a shorter maturity time, usually 80 - 90 days in western Canada and northern USA. The average yield of field pea is 2000 kg ha<sup>-1</sup> (Saskatchewan Pulse Growers, 2006), however, pea seed yield is subject to wide variation.

Field pea is potentially the highest yielder. The major pea growing countries are Russia, China, France, Australia, USA and India. In India it is grown in Uttar Pradesh, Madhya Pradesh, Bihar, Assam, Orissa and Rajasthan which together share as much as 94.5% of the total area and contribute 94.9% of the total production of this crop. In India pea is grown over an area of 0.364 million hectares with the production of about 3.02 million tonnes. Uttar Pradesh alone produces about 75% of total pea produced in India. In Madhya Pradesh pea is grown over an area of 52.03 thousand hectare with production of about 497.43 thousand metric tonnes, the productivity of pea is about 956 kg per hectare (Anonymous, 2013).

The major production constraints in field pea have been found such as lack of improved high yielding varieties, non-availability of irrigation and use of poor quality seeds. To improve the genetic contents of any crops, genetic variability is a prerequisite for crop improvement programme. The extent of genetic variability and its exploitation for selection of desirable types is the prime objective of any crop improvement breeding programme. To improve the effectiveness of selection, total variability has to be partitioned into heritable and non- heritable components. Genotypic, phenotypic and environmental co-efficients of variation, estimates of heritability and expected genetic advance are the genetic parameters which help to predict genetic gain besides indicating the type of gene action which considerable help in improving the efficiency of selection programme.

## **MATERIAL AND METHODS**

The experimental materials of the study comprised of 50 genotype of field pea from Indian origin. These varieties/lines were procured from germplasm lines available in Legume Section, Department of Genetics and Plant Breeding, Chandra Shekhar Azad University of Agriculture and Technology, Kanpur. A field

experiment was conducted during *Rabi* season 2015-16 and 2016-17 at the Oilseed Research Farm, Kalyanpur, CSAUA&T, Kanpur. All the genotypes were sown in Randomized Complete Block Design with three replications. Each genotype was sown in four lines in 3.0 m long and 3.0 m broad plots and spaced at 75 cm between row to row and 30 cm plant to plant distance, respectively. Genetic variability parameter *viz.*, mean, variance, phenotypic co-efficient of variation (PCV) and genotypic co-efficient of variation (GCV) (Burton and De Vane, 1953), heritability (h<sup>2</sup>) (Hanson *et al.*, 1956) and genetic advance (GA) (Johnson *et al.*, 1955) among characters were calculated by following the standard procedures with the help of MSTATC, Statistica 2 and Genres software's.

## **RESULTS AND DISCUSSION**

Field pea (*Pisum sativum* L.) is autogamous crop having low out crossing ranging from zero to four per cent. The study of variance and other genetic parameters greatly help in formulating a suitable breeding programme for improvement of the crop. Knowledge about magnitude and nature of variability present in population is a pre-requisite for any crop improvement programme. Variability is a result of its genotype and genotype x environment interactions. Only heritable component of variation is of prime importance from breeding point of view. So it is necessary to divide total variability into its heritable and non heritable component of variation. Present study revealed highly significant difference among the tested genotype in respect of all characters. This indicated that these genotypes can be utilized for future field pea breeding programme. Widest range of mean of the genotype was observed in days to maturity followed by plant height, days to flower initiation and seed yield per plant. While lowest range of variability were observed for primary branches per plant followed by number of seeds per pod, pod length and number of pods per plant. It is clear from the result that the genotypes were more variable for plant height, days to maturity, seed yield per plant and days to flower initiation. This indicated that emphasis should be given for these characters while adopting selection for crop improvement.

The findings were quite similar to as reported by Tyagi and Srivastava (2002); Mehta *et al.* (2005); Singh and Singh (2006); Kumar *et al.* (2007) and Kumar (2008) for plant height, Tyagi and Srivastava (2002); Singh *et*

al. (2003); Singh and Singh (2006); Chadha *et al.* (2008) and Kumar (2008) for pods per plant, Tyagi and Srivastava (2002) for biological yield per plant, Singh and Mir (2005); Singh and Singh (2006); Kumar *et al.* (2007) and Kumar (2008) for seed yield per plant, Kumar (2008) for days to 50 per cent flowering and days to maturity .

Phenotypic and genotypic co-efficient of variation was maximum for plant height followed by pod length, number of pods per plant (Table 1). Minimum phenotypic and genotypic co-efficient of variation was recorded for days to 50% flowering, days to maturity followed by seed yield per plant. Moderate GCV obtained for plant height followed by pod length, number of nodes per plant, 100-seed weight and the finding of Sardana *et al.* (2007); Nawab *et al.* (2008) and Lal *et al.* (2011) for 100 seed

weight, Mehta *et al.* (2005) and Sardana *et al.* (2007) for pod length, Mehta *et al.* (2005) and Lal *et al.* (2011) for number of seeds per pod was similar to the present findings. Moderate PCV was observed for number of pods per plant, number of nodes per plant, number of seed per pod. The findings are agreement with the result of Ramesh *et al.* (2002); Tyagi and Srivastava (2002); Sharma *et al.* (2003); Singh and Mir (2005); Gupta *et al.* (2006); Choudhary *et al.* (2010); Singh *et al.* (2012) and Kumar *et al.* (2013) for number of effective pods per plant, Ramesh *et al.* (2002); Choudhary *et al.* (2010) and Singh *et al.* (2012) for plant height, Tyagi and Srivastava (2002); Sharma *et al.* (2003); Singh and Mir (2005); Kumar (2008); Singh *et al.* (2012) and Kumar *et al.* (2013) for seed yield per plant.

**Table 1 : Analysis of variance (ANOVA) for ten characters in fifty field pea genotypes**

Source of variance	d.f	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of primary branches per plant	Number of nodes per plant	Pod length (cm)	Number of seeds per pod	100 seed weight (g)	Number of pod per plant	Seed yield per plant (g)
Replication	2	2.98	0.42	0.08	0.18	5.62	0.88	0.05	0.04	0.04	4.38
Treatment	49	3.45**	119.22**	3458.55**	0.44	15.31**	2.12**	0.51*	5.58**	15.19**	13.14**
Error	98	1.04	1.36	3.04	0.30	6.17	1.11	0.30	0.02	4.86	2.54

\* and \*\* indicate significance of values at P=0.05 and 0.01, respectively

**Table 2 : Phenotypic and genotypic co-efficient of variation among fifty genotypes for ten characters in field pea**

Sr. No.	Character	PCV	GCV
1.	Days to 50% flowering	4.61	4.38
2.	Days to maturity	5.29	5.20
3.	Plant height(cm)	36.55	36.49
4.	Number of primary branches per plant	14.48	5.36
5.	Number of nodes per plant	16.44	9.45
6.	Pod length(cm)	19.53	9.38
7.	Seed per pod	12.29	5.34
8.	100 seed weight(g)	8.54	8.49
9.	Pod per plant	16.25	10.46
10.	Seed yield per plant(g)	8.06	6.14

**Table 3 : Heritability (h<sup>2</sup>) %, genetic advance and genetic advance per cent over mean among fifty genotypes for ten characters in field pea**

Sr. No.	Character	Heritability per cent (h <sup>2</sup> ) %	Genetic advance at 5%	Genetic advance per cent over mean 5%
1.	Days to 50% flowering	90	6.13	8.58
2.	Days to maturity	96	12.69	10.54
3.	Plant height(cm)	99	69.82	75.08
4.	Number of primary branches per plant	13	0.16	4.08
5.	Number of nodes per plant	33	2.06	11.19
6.	Pod length (cm)	23	0.57	9.29
7.	Number of seeds per pod	18	0.23	4.77
8.	100 seed weight(g)	98	2.78	17.38
9.	Number of pod per plant	41	2.46	13.88
10.	Seed yield per plant(g)	58	2.95	9.64

In the present findings phenotypic co-efficient of variation were higher than the corresponding genotypic co-efficient of variation for all the characters studied, 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. The finding of Mahanta *et al.* (2001) and Chadha *et al.* (2008) were similar to the present findings. The GCV and PCV values indicated that lot of variability exists among the genotypic and phenotypic level and better chances of improvement is possible by selection.

A great amount of genetic advance under selection can be achieved when the characters under selection are highly heritable and stable. Therefore, the characters with high heritable values are of much importance for plant breeder than those which are of low heritable. Thus, heritability in broad sense and genetic advance in per cent of mean as direct selection parameter provide index of transmissibility of traits which expression about the effectiveness of selection in improving the character.

The genetic advance which predicts the advancement in the succeeding generation of selection is a very potential method for handling the breeding material and affecting the gain through careful selection. In the present study on high heritability were observed for almost all the characters. Among them plant height, 100-seed weight, days to maturity and days to 50% flowering showed high heritability and they were having corresponding high genetic gain (Table 3). This indicates that the additive part of total variation was acting on those characters.

Similar results were confirmatory with that Singh and Singh (2006); Sardana *et al.* (2007); Choudhary *et al.* (2010) and Lal *et al.* (2011) for plant height, Sureja and Sharma (2000); Singh and Singh (2006); Sardana *et al.* (2007); Choudhary *et al.* (2010); Lal *et al.* (2011) and Singh *et al.* (2012) for number of effective pods per plant, Singh and Singh (2006); and Singh *et al.* (2012) for seed yield per plant, Sardana *et al.* (2007) and Lal *et al.* (2011) for 100-seed weight, Tyagi and Srivastava (2002) and Lal *et al.* (2011) for number of seeds per pod, Singh and Singh (2006) and Singh and Mir (2005) for days to 50 per cent flowering and days to maturity, Singh and Singh (2006) and Sardana *et al.* (2007) for pod length.

High values of broad sense heritability for the above

characters expressed that they were less influenced by environmental conditions. It reflected that the phenotypes were the true representative of their genotypes and selection based on phenotypic performance would be reliable.

The improvement in yield could be effected through these yield contributing components and selection efficiency decides success of any crop breeding programme. Selection for trait which is contributing to yield is an important aspect. To know the relationship between the characters, correlation studies are essential for crop improvement.

### Conclusion :

Studies on variability, heritability and genetic advance showed that plant height, days to maturity, 100-seed weight and days to 50% flowering are having considerable importance to breeder for selection. Studies of variation indicated that considerable amount of variation in plant height, number of pod per plant number of nodes per plant pod length and number of 100-seed weight which could be utilized for breeding for improvement. All traits showed high heritability except number of primary branches per plant (13%) and number of seeds per pod (18%). The higher genetic advance showed in plant height (69.82) and low in number of primary branches per plant (0.16).

### REFERENCES

- Anonymous (2013). Annual report of NHB, Gurgaon, Haryana
- Burton, G.W. and Devane, E.H. (1953). Estimating heritability in tall Fescue. *Agron. J.*, **45** : 478-481.
- Chadha, Sanjay, Sharma, Rajeev and Chaudhary, D.R. Vidyasagar (2008). Genetic variability studies in summer pea under cold desert areas of North-Western Himalayas. *Agric. Sci. Digest*, **28**(1): 10-13.
- Choudhary, Harshawardhan, Verma, M.K. and Sofi, A.A. (2010). Genetic variability, heritability and genetic advance for yield components in garden pea. *Pantnagar J. Res.*, **8**(2): 195-197.
- Cousin, R. (1997). Peas (*Pisum sativum* L.). *Field Crops Res.*, **53**: 111-130.
- Gupta, A.J., Singh, Y.V. and Verma, T.S. (2006). Genetic variability and heritability in garden pea (*Pisum sativum* L.). *Indian J. Hort.*, **63**(3): 332-334.
- Hanson, C.H., Robinson, H.F. and Comstock, R.E. (1956). Bimetric studies of yield in segregating population

- of Korean Lespedeza. *Agron. J.*, **48**(2): 268-272.
- Johnson, H.W., Robinson, H.F. and Comstock, R.E. (1955). Estimates of genetics and environment variability in soybean. *Agron. J.*, **47**(1): 314-318.
- Kumar, Bhupendra (2008). Variability, heritability and genetic advance in pea (*Pisum sativum* L.). *Internat. J. Plant Sci.*, **3**(1): 211-212.
- Kumar, Brijendra, Adesh Kumar, Singh, A.K. and Lavanya, G.R. (2013). Selection strategy for seed yield and maturity in field pea (*Pisum sativum* arvense). *African J. Agric. Res.*, **8**(44): 5411-5415.
- Kumar, Rakesh, Ram Dhari, Kumar, Ram and Malik, B.P.S. (2007). Assessment of morphological variability and genetic diversity in pea germplasm (*Pisum sativum* L.). *National J. Plant Improve.*, **9**(1): 5-8.
- Lal, G.M., Meena, M.L., Kunj, Chandra and Singh, C.M. (2011). Assessment of genetic variability and interrelation between yield and its contributing components in field pea (*Pisum sativum* L.). *Environ. & Ecol.*, **29**(3A): 1235-1239
- Mahanta, I.C., Senapati, N., Samal, K.M. and Dhal, A. (2001). Genetic variability performance character association and co-heritability in field pea (*Pisum sativum* L.). *Legume Res.*, **24**(2): 92-96.
- Mehta, Seema, Kohli, U.K., Mehta, Devinder and Kumar, Dharminder (2005). Genetic variability studies in pea (*Pisum sativum* L.). *Haryana J. Hort. Sci.*, **34** (1/2): 140-141.
- Nawab, N.N., Subhani, G.M., Khalid Mahmood Qamar and Shakil Akhtar Saeed (2008). Genetic variability, correlation and path analysis studies in garden pea (*Pisum sativum* L.). *J. Agric. Res. (Lahore)*, **46**(4): 333-340.
- Ramesh, C., Tewatia, A.S. and Dahiya, M.S. (2002). Genetic variability and heritability studies in garden peas (*Pisum sativum* L.). *Haryana J. Hort. Sci.*, **31**(3/4): 250-252.
- Sardana, S., Mahajan, R.K., Gautam, N.K. and Ram, B. (2007). Genetic variability in pea (*Pisum sativum* L.) germplasm for utilization. *SABRAO J. Hort.*, **39** (1) : 31-41.
- Saskatchewan Pulse Growers (2006). Pulse Manual. Chapter 6: Field Pea.
- Sharma, A.K., Singh, S.P. and Sharma, M.K. (2003). Genetic variability, heritability and character association in pea (*Pisum sativum* L.). *Crop Res. (Hisar)*, **26**(1): 135-139.
- Singh, A., Singh, Shalini and Babu, J.D.P. (2012). Heritability, character association and path analysis studies in early segregating population of field pea (*Pisum sativum* L. var. arvense). *Internat. J. Plant Breeding & Genetics*, **5** (1) : : 86-92.
- Singh, A.K. and Mir, M.S. (2005). Genetic variability, heritability and genetic advance in pea (*Pisum sativum* L.) under cold arid region of Ladakh. *Environ. & Ecol.*, **23S** (Special 3): 445-449.
- Singh, A.K. and Singh, R.R. (2006). Genetic variability, genetics divergence and heritability studies in garden pea (*Pisum sativum* L.). *Indian J. Hort.*, **57**(3):
- Singh, G., Singh, M., Singh, V. and Singh, B. (2003). Genetic variability, heritability and genetic advance in pea (*Pisum sativum* L.). *Prog. Agric.*, **3**(1/2): 70-73.
- Sureja, A.K. and Sharma, R.R. (2000). Genetic variability and heritability studies in garden pea (*Pisum sativum* L.). *Indian J. Hort.*, **57** (3): 243 - 247.
- Tyagi, M.K. and Srivastava, C.P. (2002). Genetic variability and correlations among yield and yield characters over two environments in pea. *Indian J. Agric. Res.*, **36**(1): 53-56.
- Zohary, D. and Hopf, M. (2002). *Domestication of Plants in the old world: The origin and spread of cultivated plants in West Asia, Europe and the Nile Valley*. Third Edition. Oxford University Press Inc. New York

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