



## ORIGINAL ARTICLE

### Estimation of Heritability on Pea (*Pisum sativum L.*)

Pallavi<sup>1</sup>, A. Singh<sup>2\*</sup> K. K. Pandey<sup>3</sup>

<sup>1</sup>National Beareau of Plant Genetic Resources, New Delhi- 110012

<sup>2</sup>Extension Scientist, Uttarakhand University of Horticulture and Forestry, Bharsar, Pauri Garhwal, Uttarakhand

<sup>3</sup>Department Of Agricultural Statistics, V.C.S.G. College of Horticulture, Uttarakhand University of Horticulture and Forestry, Bharsar, Pauri Garhwal, Uttarakhand.

E-mail : palankar.chahal19@gmail.com

#### ABSTRACT

A field experiment was conducted at Vegetable Research Centre of G.B.P.U.A. & T., Pantnagar, during 2010 and 11 on mollisols (sandy loam in texture having 7.62 pH) of Uttarakhand. For the study of heritability, the trail on vegetable pea (*Pisum Sativum L.*) was conducted. On the basis of recorded data, Genotypic Variance ( $\sigma^2_g$ ), Phenotypic Variance ( $\sigma^2_p$ ) and Environmental Variance ( $\sigma^2_e$ ) calculated for calculation of the heritability and genetic advance was calculated by the suitable methodology with the help of SPSS and SPAR. The total 10 characters was taken under study Viz. days of first flowering, nodes to first flowering, number of primary branches per plant etc. The results reveals that heritability (broad sense) Ranges between 99.97% to 22.50% highest heritability was recorded for days of flowering as 99.97% and lowest in number of seed per pod (22.50%). The genetic advance was recorded in percent of mean.

KEY WORDS: Heritability, Genetic variance, phenotypic variance, Environmental variance and Pea.

Received 22/10/2013 Accepted 29/11/2013

©2013 Society of Education, India

#### INTRODUCTION

Pea (*Pisum sativum L.*)  $2n = 2x = 14$  one the most important annual herbaceous legume crop of India, belongs to the Family Leguminosae (Fabaceae). It is largely confined to cooler temperate zone between the tropic of cancer and Mediterranean Region. Being a cool season crop, it is most extensively grown in the temperate region throughout the world. In tropics and subtropics, its cultivation is restricted to cooler altitude and winter season. In India, pea is cultivated over an area of 36.5 million ha with an annual production of 302.06 million mt.[2]. Statistics exhibits that it covered an area of 12.4 thousand hectares with an annual production of 71 thousand mt with a productivity of 6.6 tons per hectares in the state [2]. Green Peas are eaten cooked as a vegetable, and are marketed fresh, canned or frozen while ripe dried peas are used as whole, split or made into flour.

Peas are rich in health benefiting phyto-nutrients, minerals, vitamins and anti-oxidants. They are relatively low in calories when compared with beans, and cowpeas. Fresh pea pods are excellent source of folic acid, ascorbic acid (vitamin C) vitamin K. They also contain phytosterols especially  $\beta$ -sitosterol. Fresh green peas also contain adequate amounts of anti-oxidants flavonoids such as carotenes, lutein and zeaxanthin as well as vitamin-A. In addition to folates, peas are also good in many other essential B-complex vitamins such as pantothenic acid, niacin, thiamine, and pyridoxine. Furthermore, they are rich source of many minerals such as calcium, iron, copper, zinc and manganese.

Lack of sufficient genetic variability for economically important character is one of the reasons attributed for in significant progress in crop improvement. The natural selection over years operated towards increasing the potentiality for survival and wider adoption at the cost of yield traits. Futher the ones contributing for higher yield seems to be scattered in the natural population. A great extent of variability has been observed in different agronomic characters of Pea with respect to plant height, days to flowering, pod length, and seed weight etc.

In the present study, an attempt was made to study the heritability on different, characters of pea. In order to evaluate and compare the performance of fifty genotypes of Pea with respect to plant growth characters, maturity and yield.

## MATERIAL AND METHODS

The present study was undertaken during the period of October, 2010 to February 2011 for estimation of genetic advance and heritability for various characters in Pea. Ten parents and their forty F<sub>2</sub> progenies in Pea were evaluated for genetic advance & Heritability during the year 2010-11 at Vegetable Research Centre (VRC), G. B. Pant University of Agriculture and Technology, Pantnagar, U. S. Nagar (Uttarakhand). Genetic advance and heritability was worked out to understand the relative importance of one character over other influencing pod yield. The details of materials used and procedures followed during the investigation have been described below:

### Experimental Site

Vegetable Research Centre, Pantnagar is situated in the foot hills of Shivalik range of Himalayas in the narrow belt called Tarai. Geographically, it is situated at an altitude of 243.84 m above mean sea level and between 29.3°N latitude and 79.3° E longitude.

The details of the experimental plan are given below:

Design of experiment	Randomized Completely Block Design
Number of genotypes	50
Row to row distance	30 cm
Plant to plant distance	10 cm
Number of replications	3

The observations were recorded on 10 quantitative characters. Five randomly selected plants were tagged in each row and used for recording the observations of characters which are given below:

### Quantitative characters

1. Days to first flowering.
2. Node of first flowering.
3. Number of primary branches per plant.
4. Plant height (cm).
5. Number of pods per plant.
6. Pod length (cm).
7. Pod weight (g).
8. Number of seeds per pods.
9. 100-seed weight (g).
10. Green pod yield per hectare.

The mean values of each genotypes in each replication for all the traits were subjected to statistical analysis as per Randomized Completely Block Design.

Mean was calculated as the arithmetic mean of values for each character as given below:

$$\bar{X} = \frac{\sum X_i}{n}$$

Where;

$$\bar{X} = \text{Mean}$$

X<sub>i</sub> = Value of i<sup>th</sup> plant for a character

n = Number of plants

Variance was estimated as the mean squared deviation as given below:

$$V = \frac{1}{n-1} \sum (X_i - \bar{X})^2$$

Genotypic variance

$$\sigma_g^2 = \frac{MSg - MSe}{r}$$

Phenotypic variance

$$(\sigma^2_p) = \sigma^2_g + \sigma^2_e$$

Environmental variance

$$(\sigma^2_e) = MSe$$

Where;

The significance of differences among genotype mean was tested by 'F' test.

If, F calculated ≥ F tabulated

Then Variance is significant. Wherever the 'F'-test was found to be significant, Critical Difference (C.D.) was calculated for particular character.

C.D. (0.05) =  $SE_d \times 't'$  at 5% level of significance

Where,

't' = table value of 't' at error degree of freedom and 5% level of significance.

$SE_d$  = Standard error of difference between two treatment means.

Standard Error of Difference:

$$SE_d = \sqrt{2 \times EMS / r}$$

Where,

MSE = Mean Square Error

r = number of replications

The character showing significant differences among genotypes were further subjected to analysis on the following Parameters [1].

- Heritability
- Genetic advance
- Genetic advance as per cent of population mean

#### **Heritability Estimation**

Heritability in broad sense was calculated for each character by following formulae given by [5].

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

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'.

The genotypic and phenotypic variance was obtained from the expectation of mean squares of analysis of variance of RCBD.

For the calculation of genetic advance and heritability, SPSS-12 and SPAR 1.2(Statistical Software) was used.

## **RESULTS AND DISCUSSION**

The estimates of heritability (broad sense) and expected genetic advance as per cent of mean for all the 10 characters are given.

### **Heritability**

Range of heritability estimates in broad sense varied from 99.97% to 22.50%. Highest heritability 99.97% was recorded for days of flowering. Heritability estimates were moderate for node of first flower (78.27%), followed by 100-seed weight (68.25%), plant height (65.84%), number of primary branches per plant (53.50%) and low in number of pods per plant (30.86%) and number of seeds per pod showed low (22.50%).

The broad sense heritability, the proportion of genotypic variance to the phenotypic variance, is an important parameter in breeding and genetics, because knowledge of numerical magnitude of heritability is of special importance for planning in breeding programmes and for the examination of experimental results.

The heritable variation with heritability (broad sense) estimates would give reliable indication of the expected improvement through selection [5].

It is evident that days to flowering (99.97%) had high heritability, while node to first flower (78.27%), 100-seed weight (68.84%), plant height (65.84%) and number of primary branches per plant (53.50%) had moderate value of heritability, but number of seeds per pod (22.50%) had lowest heritability value among all the characters. Similar to this investigation, [6] observed high heritability for 100-seed weight and plant height. High heritability was also found for plant height at maturity by [9].

[8] reported moderately high genetic advance and heritability for plant height, 100-seed weight and pod length. [7] also indicated that seed yield and 100-seed weight are all heritable traits.

High heritability coupled with high genetic advance and low heritability along with low genetic advance might be due to additive and non-additive genetic components, respectively. In present investigation, high genetic advance coupled with high heritability was observed for plant height and 100-seed weight.

It indicated that in the present investigation the genotypic variation for these traits was probably due to high additive gene effects and thus early generation selection for highly heritable characters is expected to give better results. [10] also reported the additive gene effect for pods per plant, 100-seed weight, plant height and yield per plant.

[11] found same result on pea for different genetic character for Bangladesh. [13] reported that genetic diversity among varieties & wild species of pea on the basis of morphological, physiological characters and molecular marker.

Similar result was found by [4] Reported molecular diversity of different (16) Agro-ecological region of India on various pulse crop. [12] Reported same result on pea for Meerut District of Uttar Pradesh on 48 field pea crosses.

## REFERENCES

1. Allard, R. W. 1960. Principles of plant breeding. Wiley and Sons Publisher, New York. pp. 138-142.
2. Anonymous. 2011. Indian Horticulture Database 2011, National Horticulture, Board, Gurgaon. 195p.
3. Burtan, G. W. and Devane, E. W. 1953. Estimating heritability in tall Fescue (*Festuca arundinaceae*) from replicated clonal varietal trial. *Agron. J.*, 4:78-81.
4. Dube S. C., Tripathi A., Upadhyay B. K. (2012). Molecular diversity analysis of *Rhizoctonia Solani* isolates infecting various pulse crops in India different agro-ecological region of india. *Folia Microbial*, 57:513-24.
5. Johnson, H. W.; Robinson, H. R. and Comstolk, R. E. 1963. Estimation of genetic and Environmental Variability in Soyabean. *Agron. J.*, 47: 314-318.
6. Joshi, B. D. and Thomas, T. A. 1987. Genetic resources in temperate grain legumes. In: *Plant Genetic Resources in Indian perspective* (Paroda, R.S.; Arora, R.K. and Chandel, K. P. S. eds.) Proc. Natl. Plant Genet. Resources, NBPGR, New Delhi, pp. 255-167.
7. Lenka, D.; Nandi, A.; Tripathy, and Dhal, A. 1998. Genetic studies in spreading type Pea mutants: variability and performance. *ACIAR-Food- Legume Newsletter*. No-27 pp. 8-9.
8. Nandi, A., Tripathi, P., Singh, D. N., Lenka, D. and Senapati, N. 1995. Genetic variability and performance of Field Pea. *Leg. Res.* 18: 121 – 124.
9. Narsinghani, V. G. and Saxena, A. K. 1991. Character association in Pea. *Veg. Sci.*, 18.18: 106-108.
10. Raffi, S. A. and Nath, U.K. 2004. Variability, heritability and genetic advance and relationships of yield and yield contributing characters in Pea (*Pisum sativum L.*). *J. Bio. Sci.*, 4.2: 157-159.
11. Siddika A., Aminul Islam A. K. M., Golam Rasul M., Abdul Khaleque Mian M., Ahmed J (2013). Genetic Variability in Advanced generations of Vegetables Pea (*Pisum Sativum L.*). *International Journal of Plant Breeding* : 4, pp. 27-31.
12. Singh M., Malik S., Kumar M., K.V.Singh, Kumar S., Devi P., Kumar V., (2012). Studies of Variability, heritability and genetic advance in field pea (*Pisum SativumL.*). *Progressive Agriculture*,12(1):219-222.
13. Taran B., Zhang C., Warkentin T., Tullu A., Vandenberg A. (2005). Genetic diversity Among Varieties and Wild species accession of pea (*Pisum Sativum L.*) Based on Molecular Marker, morphological and physiological Characters. *Genome*, 48(2):257-272.

## Citation of This Article

Pallavi, A. Singh K. K. Pandey. Estimation of Heritability on Pea (*Pisum sativum L.*). *Adv. Biores.* Vol 4[4] December 2013: 89-92