



Research Paper

Article history :

Received : 01.02.2013

Revised : 21.04.2013

Accepted : 16.05.2013

Genetic variability and character association in field pea (*Pisum sativum* L.) genotypes

■ P. BASAIWALA¹, N.K. RASTOGI AND M. PARIKH¹

Members of the Research Forum

Associated Authors:

¹Department of Genetics and Plant Breeding, Indira Gandhi Krishi Vishwavidyalaya, RAIRPUR (C.G.) INDIA

Author for correspondence :

N.K. RASTOGI

Department of Genetics and Plant Breeding, Indira Gandhi Krishi Vishwavidyalaya, RAIRPUR (C.G.) INDIA

Email : [nitrastogi1966@gmail.com](mailto:nitinrastogi1966@gmail.com)

ABSTRACT : Genotypic and phenotypic coefficients of variation, heritability, expected genetic advance, correlation and path analysis for yield and yield contributing traits were estimated using thirty two genotypes of field pea. Moderate to high PCV and GCV were recorded for pod bearing length, plant height, seed yield plant⁻¹, pods plant⁻¹, harvest index, seeds pod⁻¹ and hundred seed weight. High heritability coupled with high genetic advance was observed for plant height, pod bearing length, pods plant⁻¹, harvest index and seed yield plant⁻¹. Correlations were estimated to estimate the strength of association between yield and ten other characters. Seed yield plant⁻¹ was positive and significantly correlated with plant height, pod bearing length, pods plant⁻¹, seed setting %, seeds pod⁻¹ and harvest index. Plant height, pods plant⁻¹ and seed setting % had positive direct effect and exhibited significant positive correlation with seed yield, indicating a true relationship of these traits with seed yield. Hence, direct selection for these traits would be rewarding for yield improvement in field pea.

KEY WORDS : Genetic variability, Correlation, Path analysis, Field pea

HOW TO CITE THIS ARTICLE : Basaiwala, P., Rastogi, N.K. and Parikh, M. (2013). Genetic variability and character association in field pea (*Pisum sativum* L.) genotypes, *Asian J. Hort.*, 8(1) : 288-291.

Pulses occupy an important position in the agrarian economy of our country. They own a strategic position in intensive as well as subsistence agriculture, as they are an excellent source of dietary protein for millions of people, nutritious feed for livestock, and a mini-nitrogen plant having profound ameliorative effect on soil.

Among the major pulse crops grown in India, field pea (*Pisum sativum* L.) belonging to family Leguminosae is cultivated for green pod seeds as vegetable and for dry seeds. In India, pea is grown in an area of 0.59 million ha with production of 0.80 million tons and productivity of only 1355.9 kg/ha (Food & Agriculture Organization, 2008). The major field pea producing states are UP, MP, Bihar, Assam and Orissa which together account for about 95% of the total area and production of pea in India. Productivity of this crop has remained stagnant and area is shrinking due to the unavailability of genotypes with high yield potential and adaptability to different ecological zones. To increase the production of this crop there is a need to operate field pea breeding programme in an efficient manner.

Genetic variability is an essential prerequisite for crop

improvement programme for obtaining high yielding varieties. On the other hand, yield being complex character is associated with some yield contributing characters.

The understanding of association of characters is of prime importance in developing an efficient breeding programme. The correlation studies provide information about association between any two characters. The path coefficient analysis provides the partitioning of correlation coefficients into direct and indirect effects giving the relative importance of each of the causal factors. The present study was undertaken in order to find out the genetic variability, inter-relationship among different characters and the direct and indirect contribution of these characters towards yield.

RESEARCH METHODS

Thirty two genotypes of field pea were grown in randomized complete block design with three replications during *Rabi* 2009-10 at the field experimentation center in Deptt. of Genetics and Plant Breeding, IGKV, Raipur (CG). Each genotype was sown in 3 rows 4 m long and 40 cm apart keeping plant to plant distance of 10 cm and plot to plot 80 cm.