

Genetic variability, heritability and genetic advance in chilli (*Capsicum annuum* L.)

V.P. SINGH¹ AND SUJIT K. YADAV^{2*}

¹Department of Botany, R.M.P. (P.G.) College, Gurukul Narsan, HARDIWAR (UTTARAKHAND)

²G.B. Pant University of Agriculture and Technology, Horticulture Research and Extension Centre, Dhakrani, DEHRADUN, (UTTARAKHAND) INDIA

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SUMMARY

Thirty six genotypes (8 parents of diverse origin and their 28 F₁s excluding reciprocals) were studied to estimate their genetic variability, heritability and genetic advance. Most of the characters were observed with wide range of variability. In the present investigation high to moderate heritability with high to moderate genetic advance were observed for number of seeds per fruit, ascorbic acid content, number of fruits per plant, fresh fruit weight per plant, fresh fruit yield (q/ha), seed weight per plant and seed yield (q/ha) showing dominancy of additive gene effects which suggested excellent chance of effective selection for improvement of these traits and high heritability coupled with medium genetic advance for stem diameter and total soluble solids and suggesting good chances of effective selection for these traits. While other traits showed non additive type of gene action.

Key words : Genetic variability, Heritability and Chilli.

Chilli is a small shrub of solaneous family. Chilli (*Capsicum annuum* L.) a new world genus has rich diversity. Although this is an important vegetable and condiment crop in India, its yield potential has not been fully exploited. Due to lack of high yielding varieties its production and productivity per unit area is very low. The main objective of any breeding programme has been to improve yield which is a complex character controlled polygenically and influenced greatly by environmental factors. Therefore, the selection of superior genotypes based on yield alone is not effective; attention has to be given towards the component characters contributing to yield in positive direction. Before starting any breeding programme, the extent of variability in any crop is of prime importance for its improvement. Therefore, the present investigation was undertaken at G.B. Pant Univ. of Ag. and Tech., Horticulture Research and Extn. Centre, Dhakrani (Distt.- Dehradun) Uttarakhand during the years 2005 to 2006.

MATERIAL AND METHODS

The present experiment was laid out in Randomized Block Design with two replications during 2005-2006. Thirty six genotypes (8 parents *viz.* PC-4, LCA-333, LCA-206, KA-2, Ajeet-6, Phule Mukta, JCA-283, LCA-357 and their 28 F₁s excluding reciprocals) were planted in the experimental field of at G.B. Pant Univeersity of Agriculture and Tech., Horticulture Research and Extension Centre, Dhakrani, Dehradun (Uttarakhand). Both plant and row spacing were maintained at 45 cm

apart. Each treatment within each replication was grown in a single row of 12 plants each.

Ten plants were randomly taken in each treatment within each replication for recording the observations on 20 quantitative characters *viz.* plant height (cm), stem diameter (cm), number of primary branches/plant, days of first picking, fruit body length (cm), peduncle length (cm), fruit length (cm), fruit thickness (cm), number of fruits/plant, fresh fruit yield/plant (g), fresh fruit yield (q/ha), dry fruit yield/plant, dry fruit yield (q/ha), number of seeds/fruit, seed weight/fruit (g), 1000-seed weight (g), seed yield (q/ha), seed germination (%), total soluble solids (%) and ascorbic acid content in mg/100g fresh fruit weight. The mean values were analyzed to determine genetic variability, heritability and genetic advance. Genotypic and phenotypic coefficients of variation were calculated by the formula suggested by Burton (1952). Heritability (in narrow sense), and genetic advance were calculated as per method given by Crumpaker and Allard (1962) and Johnson *et al.* (1955), respectively.

RESULTS AND DISCUSSION

The effective selection for the success of plant breeding programme depends upon the existence of genetic variability present in the breeding material. Larger is the variability greater the scope of selection and improvement. The phenotypic variance is consists of genotypic and environmental variability and therefore, it does not necessarily ensure effective selection because it may sometimes be largely due to environmental

* Author for correspondence.