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Studies On Genetic Variability, Heritability And Genetic Advance In Mungbean (*Vigna Radiata* L. Wilczek)

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ABSTRACT

Studies on genetic variability, heritability and genetic advance for ten characters were estimated in mungbean by using the nineteen diverse genotypes. Significant variability was observed for number of clusters per plant, number of productive branches per plant, number of productive pods per plant, biological yield per plant and seed yield per plant. High estimates of heritability and genetic advance were observed for 100 seed weight. While, number of clusters per plant and number of productive pods per plant exhibited moderate heritability and high genetic advance. Based on these findings it is suggested that selection may be an effective tool for the genetic improvement in mungbean.

Key words: Genetic variability, heritability, genetic advance, mungbean

INTRODUCTION

Development of high yielding varieties of crops requires information on the nature and magnitude of genetic variability present in the available stocks. Although mungbean [Vigna radiata (L.) Wilezek] is one of the major pulse crops of India, yet limited success has been achieved so far in augmenting its yield. Inadequate information on nature and magnitude of genetic variability may be one possible reason for low yield. Yield, being the most important and complex character, is governed by many physiological processes within the plant and is also influenced by the environmental factors. Consequently, a rational approach towards improvement of yield necessitates the selection of desirable components of yield and suitable genotypes. Therefore, an attempt was made to gather information on extent of variability, heritability and genetic advance for seed yield and component traits in 19 genotypes of mungbean.

MATERIALS AND METHODS

The experimental material consisting of nineteen diverse genotypes of mungbean was grown during the spring season at research farm of CSK Himachal Pradesh Krishi Vishvavidyalaya, Research Station, Berthin (H. P.) . The material was planted in a randomized block design with three replications. Each plot consisted of three rows of 2.5 meter length with row to row and plant to plant spacing of 30 and 10 cm. respectively. Observations were recorded on five competitive plants in each plot for eight

¹Present Address : C.C.R.P.G. College, Muzaffarnagar (U.P.) *Author for correspondence characters viz. plant height, number of clusters per plant, number of productive branches per plant, number of productive pods per plant, number of seeds per pod, 100 seed weight, biological yield per plant and seed yield per plant . Days to 50% flowering and days to 80% maturity were recorded on plot basis. The mean value of data were subjected to statistical analysis to obtain analysis of variance Panse and Sukhatme, (1985), genotypic and phenotypic coefficients of variation (GCV and PCV)as suggested by Burton and Devance, (1953), heritability in broad sense Hanson *et al*, (1956) and expected genetic advance Lush, 1949 and Johnson *et al*, (1955).

RESULTS AND DISCUSSION

Analysis of variance (Table-1) revealed that there is significant variability for most of the characters under study. High variability was observed for the productive pods per plant (18.36 to 49.67), biological yield per plant (25.95 to 56.36), productive branches per plant (1.97 to 3.87), seed yield per plant (3.51 to 7.99) and number of clusters per plant (9.87 to 17.93) whereas, two characters i.e. plant height (51.83 to 70.67) and 100 - seed weight (2.50 to 3.74) were found to have moderate magnitude of variability. A very low magnitude of variability was obtained for remaining three characters i.e. days to 50 % flowering (50.00 to 56.33), days to 80 % maturity and number of seed per pod (9.37 to 11.03).

An estimate of heritable fraction of variability is of paramount importance in any crop improvement programme. In the present study high heritability (Table 1)

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