

Study of genetic variability and correlation in mungbean

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SUMMARY

In order to access the genetic variability, seventy seven diverse genotypes of mungbean [*Vigna radiata* (L.) Wilczek] were evaluated for ten characters viz., days to 1st flowering, days to 50% flowering, days to maturity, plant height (cm), primary branches per plant, secondary branches per plant, seed per pod, pod per plant, seed yield per plant (g) and 100 seed weight (g). High heritability coupled with high expected genetic advance observed for 100 seed weight, pod per plant, secondary branches per plant, plant height and primary branches per plant revealed the preponderance of additive gene effects in the expression of these traits. Seed yield per plant exhibited positive and significant association with days to 50% flowering followed by days to maturity, secondary branches per plant and days to 1st flowering at genotypic and phenotypic levels. Based on these findings it is suggested that selection may be an effective tool for the genetic improvement in mungbean.

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Key words : Genetic variability, Heritability, Genetic advance, Correlation, Mungbean

Mungbean is the major pulse crop of India, yet limited success has been achieved so far in augmenting its yield. The information on the nature and magnitude of variation in the available gene pool and knowledge of association among different economic traits is important for any crop improvement programme. Heritability and genetic advance of yield and its components is prerequisite for the improvement through selection. Similarly studies on association of different traits help to identify the real components of yield and provide an effective basis for selection. Therefore, an attempt was made to gather information on extent of variability, heritability, genetic advance and interrelationship between seed yield and component traits in genotypes of mungbean.

MATERIALS AND METHODS

The experimental material for the present study was consisted of seventy seven diverse genotypes of mungbean procured from the germplasm stock maintained at the IIPR, Kanpur, were grown during the *Kharif* season of 2009 at Regional Research Station, Saini, Kaushambi of Chandra Shekhar Azad University of Agriculture and Technology, Kanpur. The material was planted in a Randomized Block Design with three replications. Each genotype was grown in three rows of 3 meter length with

row to row and plant to plant spacing of 30 and 10 cm, respectively. The observations on the ten characters were recorded on five randomly selected plants in each of the three replications/blocks for days to 1st flowering, days to 50% flowering, days to maturity, plant height (cm), primary branches per plant, secondary branches per plant, seed per pod, pod per plant, seed yield per plant (g) and 100 seed weight (g). The mean value of data were subjected to statistical analysis to obtain analysis of variance using Panse and Sukhatme (1985), genotypic and phenotypic coefficients of variation as suggested by Burton and Devance (1953), heritability in broad sense by Hanson *et al.* (1956) and expected genetic advance and correlation coefficient by Johnson *et al.* (1955).

RESULTS AND DISCUSSION

The existence of genetic variability present in the breeding programme is responsible for the effective selection. Larger is the variability, greater the scope of selection and improvement. The main objective of any breeding programme is to study the genetic variability in the material under study and utilization of suitable breeding procedure with the help of selection in the desired direction. The results revealed the presence of wide range of variability among the genotypes of mungbean. The estimates of mean, range, genotypic and phenotypic coefficients of variation, heritability and expected genetic advance to all the characters are presented in Table 1.

The treatment mean squares were significant for all

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