

## Genetic diversity analysis in mungbean [*Vigna radiata* (L.) Wilczek]

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### SUMMARY

Seventy seven genotypes of mungbean were evaluated for ten different characters and mean values were worked for genetic diversity by Mahalanobis  $D^2$  statistic. The results of multivariate analysis ( $D^2$ ) indicated the presence of considerable genetic divergence among these genotypes. The genotypes were grouped into 9 clusters. Cluster III had maximum intra-cluster distance while inter-cluster distance was highest between clusters VIII and IX. cluster means indicated that none of the cluster was superior for all the characters studied. Therefore, hybridization between genotypes belonging to different clusters is suggested for development of superior genotypes.

**Key Words :** Divergence, mungbean

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Mungbean [*Vigna radiata* (L.) Wilczek] is one of widely grown short duration grain legume in India fitting well in also cropping systems. It is grown as *Kharif* (both as sole and intercrop) and summer crop. In any improvement programme, genetic diversity plays an important role and has been emphasized again and again by many workers (Joshi and Dawan, 1966, Murthy and Arunachalam, 1966). Genetic divergence has been used as an indirect parameter of moderate effectiveness in selecting parental lines. More the diverse parents, greater are the chance of increased spectrum of variability, providing ample scope for selection of desired plant. Therefore, an effort was made to estimate the nature and magnitude of genetic diversity in a set of 77 genotypes of mungbean.

### MATERIALS AND METHODS

The experimental material for the present study was consisted of seventy seven diverse to genotypes of mungbean procured from the germplasm stock maintained at the IIPR, Kanpur, were grown during the *Kharif* season of 2009 at regional research Centre, Saini 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 first flowering, days to 50 per cent flowering, days to maturity, plant height (cm), primary branches per plant, secondary branches per plant, seeds per pod, pods per plant, seed yield per plant (g) and 100 seed weight (g). the replicated data were subjected to genetic divergence analysis using Mahalanobis's  $D^2$ - statistic (Mahalanobis, 1936) as suggested by Rao (1952). All the genotypes were grouped into respective cluster on the basis of  $D^2$  values following Tocher's method.

### RESULTS AND DISCUSSION

The analysis of variance revealed highly significant variation among the genotypes for all the traits studied. These differences could be used in distinguishing genotypes on the basis of their morphology. Mahalanobis  $D^2$  statistic was computed for all the ten characters in order to assess the genetic diversity present among the genotypes under study. in all, nine clusters were formed (Table 1). Cluster I was the biggest cluster having 15 genotypes which was followed by

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