

## Variability and genetic divergence in rice bean

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Genetic variability and divergence studies conducted on 50 genotypes of Rice bean revealed significant differences for all the twelve characters studied. High genotypic and phenotypic coefficient of variation were noticed for harvest index, number of root nodules per plant, seed yield per plant and pods per plant. Whereas number of branches per plant exhibited moderate GCV and PCV values. High heritability coupled with high genetic advance were also observed for the above characters indicating additive gene action and emphasized the effectiveness of selection for the improvement of these traits. Substantial amount of genetic diversity was observed among 50 genotypes studied. All the 50 genotypes were grouped into 22 clusters by using Mahalanobis D2 statistics. In general the inter cluster distances were higher than intra cluster distances. Maximum inter cluster distance was observed between cluster XI and XVIII. Maximum intra cluster distance was observed between cluster IX followed by cluster IV.

**Key words :** Rice bean, Genetic divergence, Clusters

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### INTRODUCTION

The importance of the genetic diversity in hybridization programme has long been utilized by the breeders. It is commonly found that the level of heterosis exhibited by a hybrid is a function of genetic divergence between the parents (Moll *et al.*, 1974). Exploration of genetic variability in the available germplasm is a prerequisite for any successful breeding programme. Greater the genetic diversity in the material, more is the chances of getting the desired type. Hence, the present investigation was carried out to estimate the extent of genetic variability and genetic divergence in rice bean.

### RESEARCH METHODOLOGY

Fifty genotypes of rice bean collected from Officer In-charge, Regional Research Station, Umam (Meghalaya) were evaluated in randomized block design with the three replications in the experimental plot of Botany farm, Agriculture College, Pune -5 during the *Kharif* season of 2006. Each replication was further divided into plots equal to the number of entries in the trial. Each plot was 4.5 m long. Each entry was represented by the row of 4.5m length spaced at 45 cm between the rows and 15 cm between the plants within the row. Observations were recorded on five randomly selected plants from each treatment in each replication

on twelve important quantitative traits namely days to 50% flowering, days to maturity, plant height at harvest, number of branches per plant, number of pods per plant, pod length, number of seeds per pod, 100 seed weight, seed yield per plant, harvest index, number of root nodules per plant, shattering percentage etc.

The analysis of variance was carried out as suggested by Panse and Sukhatme (1985). The genotypic and phenotypic coefficient of variance was estimated as per the formula suggested by Burton (1952). Heritability in broad sense was estimated as per the formula given by Burton (1952) and genetic advance were calculated as per the procedure given by Johnson *et al.* (1955). The genetic divergence among the genotypes was calculated using the method given by Mahalanobis (1936).

### RESULTS AND ANALYSIS

The analysis of variance revealed highly significant differences among 50 genotypes for all the twelve characters. This indicates existence of significant amount of variability among the genotypes for the characters studied.

The parameters of genetic variability are mean, range, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability and genetic advance. The highest GCV and PCV were recorded for the trait harvest index (24.67 and 30.60)