Research Paper

Genetic divergence analysis in rice

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Abstract : Twenty three genotypes of rice were grouped in to seven clusters. It revealed the presence of morphological difference between the genotypes. The clusters V *vs* VII and IV *vs* V were divergent clusters. Hence, genotypes in the clusters V, VI and VII could be crossed among themselves to produce wider segregation among the progenies. The cluster VI showed high mean for grain yield per plant, plant height, number of tillers per plant number of productive tiller per plant, panicle length, number of grains per plant and kernel L/B ratio. Cluster III showed low mean for earliness. The character viz., number of grains per panicle, thousand grain weight and plant height contributed maximum towards total genetic divergence. Hence, selection may be practiced for these characters.

Key Words : D^2, Inter and intra cluster anlaysis, Rice

INTRODUCTION

Rice (*Oryza sativa* L.) is the most important cereal crop cultivated widely in many parts of the world. South and South East Asia form the primary centre of genetic diversity of the cultivated rice (Abrol and Gadgil, 1999). At present about fifty thousand accessions of rice germplasms are being maintained at various rice research centres (Khush and Virk, 2000). Genetic diversity in conventionally assessed by morphological traits. However, such traits are affected by environment, phenology or development stage of the plant and the types of plant material. The greater the genetic diversity in the germplasm, the more would be the breeding potential and scope for improvement the D^2 technique is based on multivariate analysis developed by Mahalonobis (1936) has been found to be a potent tool in quantifying the degree of divergence in germplasm. This analysis provides a measurement of relatives contribution of different components on diversity both of intra and inter cluster level and genotypes drawn from widely divergent clusters are likely to produce heterotic combinations and wide variability in segregating generations. Hence, to assess the genetic diversity among rice genotypes, the present study was taken up.

MATERIALS AND METHODS

Twenty three genotypes were evaluated in randomized block design replicated twice (Table A). The experiment was conducted at plant breeding farm, department of Genetics and Plant Breeding, Annamalai University during navarai 2011. Each entry was sown with a spacing at 20 x 20 cm. Fourteen quantitative characters namely days to 50 per cent flowering, plant height, number of tillers per plant, number of productive tiller per plant, panicle length, number of grains per plant, thousand grain weight, grain length, grain breath, grain L/B ratio, kernel length, kernel breath, kernel L/B ratio, grain yield per plant were observed for five randomly chosen plants per replication per entry. The data were subjected to Mahalonobis's (1936) D^2 analysis and the genotypes were grouped by Tochers methods as suggested by Rao (1952).

RESULTS AND DISCUSSION

The analysis of variance showed significant difference among the twenty three genotypes for all the fourteen characters indicating the existence of high genetic variability among the genotypes for all the traits (Table 1). The twenty three genotypes were grouped into seven different clusters

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