A study on D² analysis in rice

V. ARIVOLI, K. SARAVANAN AND M. PRAKASH

SUMMARY
Twenty three genotypes of rice were grouped into eleven clusters. It revealed the presence of morphological differences between the genotypes. The clusters V vs IX and IV vs IX were divergent clusters. Hence, genotypes in the clusters IX, IV and V could be crossed among themselves to produce wider segregation among the progenies. The cluster III showed high mean for grain yield per plant. Cluster X showed low mean for earliness. The characters *viz.,* total number of grains per panicle, number of filled grain per panicle and plant height contributed maximum towards total genetic divergence. Hence, selection may be practiced for these characters.

Key words : Rice, D² analysis, Genetic diversity

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 centers (Khush and Virk, 2000). The greater the genetic diversity in the germplasm, the more would be the breeding potential and scope for improvement. Crosses between genetically diverse parents are likely to produce high heterotic effects and also produce a wide spectrum of 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. The experiment was conducted at plant breeding Farm, Department of Agricultural Botany, Annamalai University during Navarai 2006. Each entry was sown with a spacing of 20 x 20. Fourteen quantitative and qualitative characters *viz.,* days to 50 per cent flowering, plant height, number of tillers per plant, number of panicles per plant, panicle length, number of grains per panicle, 1000 grain weight, grain yield per plant, grain length, grain breadth, grain LIB ratio, kemel length, kernel breadth and kemel L/B ratio were observed for five randomly chosen plants per replication per entry. The data were subjected to Mahalonobis's

Correspondence to:
V. ANBANANDAN, Department of Agricultural Botany, Faculty of Agriculture, Annamalai University, ANNAMALAINAGAR (T.N.) INDIA
Authors' affiliations:
K. SARAVANAN AND T. SABESEAN, Department of Agricultural Botany, Faculty of Agriculture, Annamalai University, ANNAMALAINAGAR (T.N.) INDIA

(1936) D² analysis and the genotypes were grouped by Tocher's method as suggested by Rao (1952).

RESULTS AND DISCUSSION

The analysis of variance revealed a significant difference among the twenty three genotypes for all the characters indicating the existence of high genetic variability among the genotypes. for all the traits. Particulars of the genotypes used for the present study are presented in Table 1. The twenty three genotypes

Table 1 : Particulars of genotypes used		
Genotype	Name of genotype	Origin
G_1	ADT 36	TRRI, Aduthurai
G_2	ADT 37	TRRI, Aduthurai
G_3	ADT 39	TRRI, Aduthurai
G_4	ADT 40	TRRI, Aduthurai
G_5	ADT 41	TRRI, Aduthurai
G_6	ADT 42	TRRI, Aduthurai
G_7	ADT 43	TRRI, Aduthurai
G_8	ADT 45	TRRI, Aduthurai
G_9	ADT 47	TRRI, Aduthurai
G_{10}	ADT 48	TRRI, Aduthurai
G_{11}	CO 43	TNAU, Coimbatore
G_{12}	CO 45	TNAU, Coimbatore
G_{13}	CO 46	TNAU, Coimbatore
G_{14}	CO 47	TNAU, Coimbatore
G_{15}	IR36	IRRI, Manila, Philippines
G_{16}	IR64	IRRI, Manila, Philippines
G_{17}	CR 1009	CRRI,Cuttack
G_{18}	White ponni	PBS, Coimbatore
G_{19}	BPT 5204	Bapatla
G_{20}	ASD 19	Ambasamuthiram
G_{21}	TKM9	Thirurkuppam
G_{22}	Pusa basmathi	Pusa, New Delhi
G_{23}	ADT 38	TRRI, Aduthurai