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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

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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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Table A: Particulars of genotypes used

Genotypes	Name of genotypes
G_1	AUR 13
G_2	AUR 14
G_3	BPT 5204
G_4	AUR 10
G_5	AUR 9
G_6	AUR 8
G_7	AUR 7
G_8	AUR 6
G_9	AUR 5
G_{10}	AUR 1
G_{11}	AUR 12
G_{12}	AUR 11
G_{13}	AUR 3
G_{14}	JEERAGA SAMBA
G_{15}	IR 42
G_{16}	IR 36
G_{17}	CO 43
G_{18}	KURNOOL SONA
G_{19}	AUR 4
G_{20}	ADT 43
G_{21}	ADT 49
G_{22}	PY 5
G_{23}	IR-55408-01

based on the relative magnitude of D^2 values. The maximum number of genotypes were included in cluster III (9 genotypes) followed by cluster I (5 genotypes) and cluster VI (3 genotypes) (Table 2).

The clustering pattern, revealed that the genotypes from different sources clustered together showing that there was no association between ecogeographical distribution of genotypes and genetic divergence. Similar finding were also reported by Maurya and Singh (1977) and De *et al*. (1992). This indicated that, in general, selection have been rewards the same goal in different centres of origin of these genotypes and yet, there is sufficient genetic variability distinctly differentiates them into seven clusters. Hence, the chosen genotypes used in the present study could be considered as a valid material.

Genetic drift and selection in different environments may cause greater diversity than geographical diversity (Murthy and Arunachalam, 1966; Singh *et al*., 1988). During the past 30 years, the genetic diversity among the improved India rice has narrowed down due to massive international exchange of germplasm (Khush and Aquino, 1994). The genotypes from the same centre of origin were also distributed in different clusters. This kind of genetic diversity may be due to differential adoption to varied agro-ecosystems (Senapati and

Table 1: Analysis of variance for 14 characters in rice

Sources	df	MSS											
		Days to 50 per cent flowering	Plant height	Number of tillers per plant	Number of productive tillers per plant	Panicle length	Number of grains per plant	Thousand grain weight	Grain length	Grain breadth	Grain L/B ratio	Kernel length	Kernel breadth	Kernel L/B ratio	Grain yield per plant
Replication	1	3.14	91.85	68.17	36.54	2.17	5.57	0.03	0.02	0.00	0.01	0.00	0.17	0.33	16.32
Genotypes	22	19.48**	829.15**	49.67**	44.12**	32.72**	5909.76**	17.00**	0.61**	0.10**	0.95**	0.61**	0.12**	0.49**	36.29**
Error	22	2.08	86.80	7.35	4.36	2.21	211.83	0.01	0.01	0.01	0.08	0.02	0.02	0.40	1.11

Table 2: Composition of D^2 clusters for 23 rice genotypes

Cluster	Number of genotypes	Name of genotypes
I	5	AUR 13, AUR 14, BPT 5204, AUR 5, KURNAOOL SONA.
II	2	AUR 7, AUR 6.
III	9	AUR 10, AUR 9, AUR 8, AUR 1, AUR 12, AUR 11, AUR 3, JEERAGA SAMBA, CO 43.
IV	2	AUR 4, PY 5.
V	2	IR 42, IR 36.
VI	2	ADT 39, IR-55408-01.
VII	1	ADT 43.

Sarkar, 2005).

Average intra and inter cluster distance among 23 genotypes revealed that the genetic diversity between the genotypes in cluster I exhibited a maximum intra cluster distance of 34.31 (Table 3). It indicated that the genotypes within this cluster were more diverse. While cluster II showed intra cluster distance of 11.30.

The inter cluster distance ranged from 11.30 to 194.91 as exhibited by clusters. Inter cluster distance, indicated greater divergence, between cluster V and cluster VII (194.91). It was followed by cluster IV and cluster V (181.90). Hence, the genotype of cluster V could be used in hybridization with the genotypes of cluster VI and VII respectively to achieve greater variability in segregating generations. The minimum distance was between cluster II and cluster VII (21.69) indicated close relationship among the genotypes included (Table 3).

Genotypes belonging to clusters separated by high genetic distance may be used in hybridization programme to obtain a wide spectrum of variation among the segregants (Bhatt, 1970). Therefore, selection of divergent genotypes from the clusters namely VI, IV and VII would produce a broad spectrum of variability for different traits studied, which may enable further selection and improvement of grain yield and yield parameters. The hybrids developed from the selected

Table 3: Average inter and intra cluster D^2 and D value for 23 rice genotypes

Cluster	I	II	III	IV	V	VI	VII
I	1177.18 (34.31)	973.79 (31.20)	1853.36 (43.05)	6079.82 (77.97)	12367.54 (111.20)	1430.58 (37.82)	8024.74 (89.58)
II		122.81 (11.30)	1416.69 (37.63)	5664.04 (75.26)	12412.69 (111.41)	1468.99 (38.32)	7677.64 (87.62)
III			1020.67 (31.94)	2655.07 (51.27)	19216.54 (138.62)	823.47 (28.69)	3954.69 (62.88)
IV				438.26 (20.93)	33089.25 (181.90)	2738.06 (52.32)	470.62 (21.69)
V					438.92 (20.95)	17947.60 (133.96)	37990.51 (194.91)
VI						550.90 (23.45)	4207.82 (64.86)
VII							0.00 (0.00)

Table 4: Cluster means of 23 rice genotypes for 14 characters

Cluster	Days to 50 per cent flowering	Plant height	Number of tillers per plant	Number of productive tillers per plant	Panicle length	Number of grains per plant	Thousand grain weight	Grain length	Grain breadth	Grain L/B ratio	Kernel length	Kernel breadth	Kernel L/B ratio	Grain yield per plant
I	85.10	68.60	14.60	11.40	21.00	140.40	18.48	5.97	1.85	3.38	5.85	2.26	2.66	18.20
II	84.50	78.50	13.00	10.25	19.25	74.00	18.12	6.62	1.62	4.10	6.50	2.00	3.25	14.90
III	82.38	78.16	15.38	12.61	22.55	135.55	19.87	6.45	1.64	3.97	6.38	2.11	3.08	17.47
IV	88.25	105.25	22.50	19.75	22.25	171.00	22.40	6.95	1.60	4.37	6.85	2.00	3.42	22.70
V	84.25	113.25	20.00	16.25	27.75	207.25	11.50	5.92	1.82	3.27	5.82	2.32	2.60	23.10
VI	84.50	115.50	24.25	21.00	30.00	204.75	19.67	6.32	1.57	4.12	6.20	1.90	3.35	25.95
VII	89.00	85.00	14.00	10.50	28.50	105.00	23.45	5.90	1.70	3.50	5.80	2.05	2.85	13.30
G.mean	84.30	85.06	16.73	13.71	23.26	145.26	19.05	6.32	1.69	3.82	6.23	3.00	3.00	18.90

Table 5: Percentage contribution of characters for genetic diversity

Sr. No.	Characters	Contribution of each character (%)
1.	Days to 50 per cent flowering	3.14
2.	Plant height	1.15
3.	Number of tillers per plant	5.90
4.	Number of productive tillers per plant	12.12
5.	Panicle length	8.12
6.	Number of grains per plant	13.56
7.	Thousand grain weight	2.16
8.	Grain length	0.39
9.	Grain breadth	1.17
10.	Grain L/B ratio	2.56
11.	Kernel length	2.37
12.	Kernel breadth	1.42
13.	Kernel L/B ratio	1.55
14.	Grain yield per plant	44.39

genotypes within the limit of compatibility of these clusters may produce high magnitude of heterosis of segregant which would be rewarding in a rice breeding programme.

The cluster mean values showed a wide range of variation for all the traits under study (Table 4). Cluster VI was characterized with high mean value for plant height, number of tillers per plant, number of productive tillers per plant, panicle length, number of grains per plant, kernel L/B ratio and grain yield per plant. Cluster III exhibited earliness for flowering. Cluster V had low mean for thousand grain weight. The single genotypic clusters were quite different from the other clusters by either highest or lowest value for a particular character. The monogenotypic cluster VII had high mean for days to 50 per cent flowering, grain length, kernel length and grain yield per plant formed a separate cluster. Similar results were reported by Sardana *et al*. (1997), Manonmani and Khan (2004). Cluster V had low mean for thousand grain weight, grain L/B ratio and kernel L/B ratio.

Higher cluster values were recorded for each trait in different cluster. This indicated that none of the clusters contained genotypes with all the desirable characters which could be directly selected and utilized. In such context recombination breeding between genotypes of different clusters may be employed as suggested by Singh *et al*. (1996). The relative contribution of individual characters towards the expression of genetic diversity estimated over character wise D^2 value revealed that with 44.39 per cent contribution grain yield per plant with 13.56 per cent number of grains per plant were the major forces of discrimination among the genotypes tested (Table 5). The characters *viz*., days to 50 per cent flowering (3.14 per cent), number of tillers per plant (5.90 per cent), number of productive tillers per plant (12.12 per cent) and panicle length (8.12 per cent) also contributed towards the genetic divergence. Similar finding were made by Manonmani and Khan (2004) and Kotaiah *et al*. (1987).

Often the traits that contribute more to divergence has little to do with a complex character such a yield (Manonmani and Khan, 2004). Merely the presence of high amount of genetic diversity in population may not be adequate to effect improvement over best existing cluster. Singh *et al*. (1988) opined that while considering the genetic diversity among the parents to be included in hybridization programme, their yield potential should not be ignored. It is necessary to carefully analyse the selection of a particular cluster from which genotypes are to chosen in a crossing programme as well as selection of a particular genotypes from the selected cluster. While selecting genotypes from distant clusters, their mean values for different traits should also be given importance to generate promising breeding material (Pradhan and Mani, 2005). In the present study the cluster mean the different traits indicated considerable difference between the clusters for all the traits studied.

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