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Genetic Divergence for Grain Yield in Early and Mid- Early Duration of Rice Genotypes

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ABSTRACT

Genetic divergence of sixty three rice genotypes of rice was studied for thirteen quantitative characters of different duration groups *viz*., early and mid early duration. Genetic divergence was estimated using Mahalanobis's statistics (D^2) and principal component analysis. Cluster analysis revealed 63 genotypes were grouped into 8 clusters. The lines chosen from the same ecogeographic region were found scattered in different clusters which indicated that genetic diversity and geographic distribution were not necessarily related. The intercluster distances were higher than the intra-cluster distance reflecting wider genetic diversity among the genotypes of different groups. The highest inter-cluster distance was observed between cluster I & VIII where as the highest intra-cluster distance was found in the cluster VIII indicated that the highly divergent types existed in these clusters. Spikelets per panicle was found to be the maximum contributors towards the total divergence. The genotypes from these clusters may be used as potential donors for future hybridization programme to develop early rice variety with good grain yield.

Key words : Genetic divergence, Cluster analysis, Transgressive segregants

Genetic diversity is a powerful and biochemical tool for determination of genetic discrimination among the genotypes which is used to select appropriate plant genotype(s) for hybridization to develop high yielding potential variety (Bhatt, 1970). With the development of biometrical methods such as Multivariate analysis (Rao,1952) based on Mahalonobis's D^2 statistics and principal component analysis (PCA), it has become possible to quantify the magnitude of genetic diversity among the germplasm for their evaluation in respect of breeding programme. For the development of any genotype with desirable traits, it is necessary to include diverged parents in crossing programme. Arunachalam (1981) reported that more diverse the parents, greater the chances of obtaining heterotic F1's. Divergence analysis is a useful tool in quantifying the degree of divergence between biological population at genotypic level and to assess relative contribution of different components to the total divergence both at intra and inter-cluster levels (Murty and Arunachalam, 1966; Ram and Panwar, 1970). It also permits to select the genetically diverged parents which can produce new recombinants with desirable traits when they are crossed together. Joshi and Dhawan (1966) reported that genetic diversity was very much important
factor for any hybridization program aiming at genetic improvement of yield especially in self pollinated crops. They also inferred that Mahalanobis's D^2 statistics was a powerful tool for choosing parents for hybridization aiming at hybrid improvement. Hence, the present study was, undertaken to analyze the genetic divergence of 63 genotypes of rice, to identify diverged genotypes, which could be used as parents in developing heterotic rice hybrids.

MATERIAL AND METHODS

A total of 63 rice genotypes were included in the study obtained from DRR, Hyderabad. All the genotypes were grown at Department of genetics and plant breeding, Allahabad during *kharif* season 2011. Thirty-days old seedlings of each entry were transplanted in $10m^2$ plots in RBD design with

Table 1. Distribution of 63 genotypes of rice into different clusters.

CLUSTER NO	Name of genotypes included	No of genotypes
I	CRR 646-B-12-B, Rewa 862-1	2
II	VDN-94-10, Sahbhagidhan, CR 2995-5-3-2-1-1, CR 2903-7-5, RTN 62-6-7-1, CR 2994-5-3-2-1-1, Narendra 97, NDR 1107, RP 5124-11-6-2, RP 5219-9-6-7-3-2-1-1, HRI-172, US 314, KMP 148, JGL 17183	14
III	TM 07575, NDR-359, WGL-365, Lalat, AAIR-7	5
IV	Gontra Bidhan 3, CB 08-504, C1446-5-18-17-2-MLD2, CR2881-19-1, R 1570-2644-2-1547,NP 107-5, MITHILA, IR80655-30-3-2-1, NLR 40058, RH-1531, IR82019-54-1-2, AD 06084	12
V	CHR-10, CR 2928-21-5-3-1, CR 2926-15-3-4-2, CR 2929-57-4-2-3, PAU 3832-79-4-3-1, CR 2995-1-2-3-1-1, RP 5125-5-9-1, CR 2930-26-2-2-1, UPR 3426-3-1-1, CN 1561-70-19-35-9-MLD1, OR 2172-7, CN 1223-5-4-3-2, JGL 17196, CR 2881-19-1(A), AD 04022, OM 5240, MR258, R-RF-69	18
VI	CR 2927-42-2-3-2, CR 2649-7, UPR 3426-3-1-1, IR81366-124-1-2-2, PAU 3832-196-4-1-2	5
VII	RP 5210-Bio-FBRI-15-3-22, RP 5127-9-3, RP 5210-Bio-FBRI-15-3-22, NLR 40024, IR82571-544-2-3	5
VIII	RP 5128-9-6-7-3-2-1-1, OM 5629	2

three replications using one seedling per hill with a spacing of 20cm x 15cm. Cultural practices were followed to raise the crop as per the standard recommendations. Observations from five randomly selected plants from individual plot were recorded for plant height (cm), days to maturity, effective tillers/m^2, number of spikelets/panicle, flag leaf length(cm), flag leaf width(cm), biological yield per hill, harvest index, panicle length (cm), 1000-grain weight(g) and grain yield (t/ha). Means of these data over the replications were subjected to both univariate and multivariate analysis. Genetic divergence was studied following Mahalanobis's (1936) generalized distance (D^2) statistics. The varieties were grouped into a number of clusters by Tocher's method as described by Rao (1952).

RESULTS AND DISCUSSION

The analysis of variance revealed the presence of significant variability among red rice genotypes for all the characters studied. Based on relative magnitude of D2 estimates, 63 genotypes were grouped into eight clusters (Table 1). Among the different clusters, cluster V contained maximum 18 genotypes followed by cluster II and cluster IV contains 14, 12 respectively. Cluster III, VI and VII contained 5 genotypes each, cluster I and VIII contained 2 genotypes each. The pattern of group constellations raveled that significant variability existed among the genotypes. The clustering pattern of genotypes (Table 1) revealed that the genotypes of different states and different duration groups were clubbed together in one cluster (or) genotypes of same state and duration were distributed in different clusters. As observed from the clusters, the genotypes included in cluster V are different duration groups indicating that there was no parallelism between clustering pattern and duration of genotypes. Similar finding was also reported by Binodh A.K., Kalaiyarasi and Thiyagarajan (2010).

Therefore, the kind of genetic diversity found among the genotypes belonging to same geographic origin might be due to difference in adaptation, selection criteria, selection pressure and environmental conditions (Vivekananda and Subramanian 1993). A wide range of variation was observed in cluster means for all the characters studied (Table 2). The cluster VIII was characterized by maximum number of panicle number per plant, maximum number of tillers per

Table 2. Cluster mean value for 13 morphological characters in rice germplasm.

	Days to 50% Flowering	Plant Height (cm)	Flag Leaf Length (cm)	Flag Leaf Width (cm)	No of Tillers/ Hill	No of Panicles/ Hill	Panicle Length (cm)	No of Spikelets/ Panicle	Biological Yield/ Hill(gm)	Days to Maturity	Test Weight (gm)	Harvest Index(%)	Economic Yield/ Hill
1 Cluster	77.83	148.13	42.05	1.50	12.23	10.63	29.29	187.06	66.33	108.66	21.60	48.52	32.16
2 Cluster	86.09	109.68	34.10	1.35	11.74	9.72	26.21	146.56	54.85	116.92	23.60	43.93	23.38
3 Cluster	100.93	107.48	39.54	1.61	14.34	12.41	27.63	246.62	77.06	132.13	21.29	45.25	35.55
4 Cluster	92.97	104.83	34.38	1.36	9.85	8.79	26.28	215.10	63.80	123.50	21.82	44.83	28.13
5 Cluster	92.53	87.96	30.26	1.20	11.53	9.80	23.78	114.64	48.33	123.75	22.22	44.78	21.25
6 Cluster	104.86	97.02	32.42	1.22	9.62	8.14	24.90	156.96	53.93	135.40	26.59	45.52	24.73
7 Cluster	94.66	96.77	31.82	1.34	14.98	13.20	23.88	176.84	65.20	125.73	17.70	43.67	27.54
8 Cluster	79.83	89.63	26.50	1.16	17.13	15.93	22.73	98.40	51.50	110.50	22.75	44.50	23.16

plant. The cluster I had highest value for plant height, flag leaf length, panicle length, harvest index and less number for days to flowering. Cluster III had highest value for flag leaf width, number of spikelets per panicle, biological yield per hill and economic yield per hill. The cluster VI characterized by highest test weight. The selection and choice of percents mainly depends upon contribution of characters towards divergence (Nayak *et al.*, 2004). In the present study (Table 3) the number of spikelets per panicle (29.70 %) followed by number of tillers per plant (27.65 %) and plant height(23.55) had maximum contribution towards divergence. In addition, flag leaf width (8.19%) and test weight (4.20%) also contributed towards total divergence.

The genotypes were included in cluster VIII were more divergent than cluster I, II, III, IV,V,VI and VII. The tendency of genotypes from diverse geographic regions to group together in one cluster might be due to similarity in requirements and selection approaches under domestic cultivation was reported by Arunachalam and Ram (1967) and Mehetre *et al.* (1998). Among the eight clusters, inter cluster distance was highest between cluster I and VIII which has been reflected in the relatively high mean values for the most of the characters (Table 2). In the present investigation, hybridization among genotypes Rewa 862-1 from cluster I (for large panicle length, early maturity and high harvest index), TM 07575, AAIR-7(WYD-25) of cluster III (for more number of spikelets per panicle, economic yield), IR81366-124-1-2-2 from cluster VI (for maximum test weight), RP 5128-9-6-7-3-2-1-1, OM 5629 from cluster VIII (for more panicles per hill) are expected to give desirable recombinants in segregating generations, because they possessed desirable features as seen from their cluster means.

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Table 3. Per cent contribution of characters towards genetic divergence in rice germplasm.

S. No.	Characters	Contribution Per cent
1	Spikelets per panicle	29.70
2	Tillers per plant	27.65
3	Plant Height	23.55
4	Flag Leaf Width	8.18
5	Test Weight	4.20

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