Bulletin of Environment, Pharmacology and Life Sciences
Bull. Env. Pharmacol. Life Sci., Vol 6 Special issue [3] 2017: 546-549

Online ISSN 2277-1808
Journal's URL:http://www.bepls.com
CODEN: BEPLAD
Global Impact Factor 0.533
Universal Impact Factor 0.9804
NAAS Rating 4.95

FULL LENGTH ARTICLE **OPEN ACCESS**

Genetic Diversity For Grain Yield In Upland Rice Genotypes

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ABSTRACT
Genetic divergence of thirty one rice genotypes of rice was studied for thirteen quantitative characters . Genetic divergence was estimated using Mahalanobis's statistics (D2) and principal component analysis. Cluster analysis revealed 32 genotypes were grouped into 4 clusters. The lines chosen from the same eco geographic region were found scattered in different clusters which indicated that genetic diversity and geographic distribution were not necessarily related. The inter cluster 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 II & IV where as the highest intra-cluster distance was found in the cluster III 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

Received 28.07.2017 Revised 04.08.2017 Accepted 26.08. 2017

INTRODUCTION

Genetic diversity is a powerful tool for determination for 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 advanced biometrical methods such as Multivariate analysis (Rao, 1952) based on Mahalonobis's D2 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. 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 D2 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 32 genotypes of rice, to identify diverged genotypes, which could be used as parents in developing heterotic rice hybrids.

MATERIALS AND METHODS

A total of 32 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 season July 2012 to October 2012. entries was planted in RCB design with three replications using one seedling per hill with a spacing of 20cm x 15cm. Cultural practices were followed to raise the crop as per recommendation for transplanting irrigated rice. Observations from five randomly selected plants from individual plot were recorded for days to 50% flowering, plant height (cm), flag leaf length(cm),flag leaf width(cm), days to

maturity, no of tillers per hill, no of panicles per hill, panicle length (cm), number of spikelets/panicle, ,biological yield per hill, harvest index, 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 (D2) extended by Rao (1952).

RESULTS AND DISCUSSION

The analysis of variance revealed the presence of significant variability among genotypes for all the characters studied. Genetic divergence among genotypes is essential for an efficient and successful hybridization programme since the cross involving genetically diverse parents is likely to produce high heterotic effects and also more variability could be expected in the segregating generations. Genetic divergence analysis therefore, was attempted to identify suitable parents among 30 genotypes of groundnut belonging to different eco-geographical regions.

Mahalanobis's D2 statistic, a powerful tool for quantifying the degree of divergence and Tocher's method were utilized for grouping the genotypes into different clusters. The results obtained were discussed hereunder. Based on relative magnitude of D2 estimates, 32 genotypes were grouped into 10 clusters (Table 1). Among the different clusters, cluster I contained maximum 15 genotypes followed by cluster II contains 6 genotypes. Cluster IX contains 3 genotypes. Cluster 8 contains 2 genotypes. Cluster III,IV,V,VI,VII,X contains 1 genotype individually. The formation of largest cluster I comprising 10 genotypes might be due to free flow (or) exchange of breeding material from one place to another or/and the unidirectional selection practiced by breeders of different locations. six genotypes were not included with any other cluster as they maintained separate identity from all others. 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.

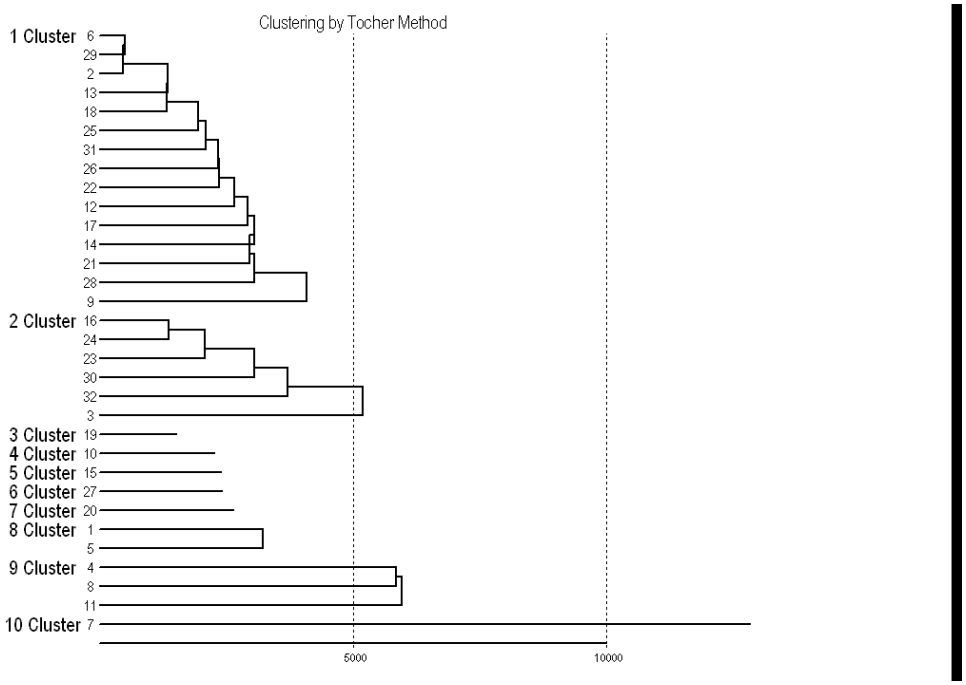
Therefore, the kind of genetic diversity found among the genotypes belonging to same geographic origin might be due to difference in adaptation, selection criteria, selection pressure and environmental conditions (Vivekananda and Subramanian 1993). A wide range of variation was observed in cluster means for all the characters studied (Table 2). The average intra and inter-cluster D2 values of various clusters are furnished in Tab. The maximum intra-cluster D2 (7.92) distances were recorded by cluster IX. While minimum distance (0.00) was noticed in clusters III,IV,V,VI,VII,X as they included single genotype each. Inter cluster average D2 values ranged from 3032.22 to 54246.43 . The maximum inter-cluster distance was observed between cluster II and IX (54246.43) followed by cluster II and X (53304.23), cluster VIII and X (42447.27), cluster IV and X (36571.93), indicating wide diversity among these genotypes (Table 4.6). Hence, genotypes from these clusters may be utilized as parents for hybridization which would result in high heterotic expression for yield components and wider segregation in filial generations. By using such genotypes as parents in hybridization programme,

The cluster VIII was characterized by maximum number of panicle number per plant, maximum number of tillers per 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 (54.44 %) harvesting index (16.53%), biological yield (14.72%),plant height(11.29%)fallowed by number of tillers per plant (27.65 %) and had maximum contribution towards divergence. In addition, flag leaf length (1.21%) and test weight(0.20%), no of tillers per panicle (0.20%)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

Mahlnbobis Euclidean^2 Cluster Distances										
	Group. 1	Group. 2	Group. 3	Group. 4	Group. 5	Group. 6	Group. 7	Group. 8	Group. 9	Group. 10
Group. 1	3032.22	7198.44	6484.77	5474.50	6322.89	7332.27	9618.29	9442.85	30437.71	33839.20
Group. 2	7198.44	4635.43	19005.97	12291.76	11192.48	19557.97	20966.49	14192.91	54246.43	53304.23
Group. 3	6484.77	19005.97	0.00	8335.08	6864.33	2410.21	3394.59	12358.57	13341.87	18710.25
Group. 4	5474.50	12291.76	8335.08	0.00	11309.42	7378.48	16182.14	6219.03	24977.11	36571.93

Group. 5	6322.89	11192.48	6864.33	11309.42	0.00	7175.94	4978.05	8439.14	29388.05	24015.27
Group. 6	7332.27	19557.97	2410.21	7378.48	7175.94	0.00	4617.94	12771.25	13462.85	12823.78
Group. 7	9618.29	20966.49	3394.59	16182.14	4978.05	4617.94	0.00	14808.45	17569.25	17058.02
Group. 8	9442.85	14192.91	12358.57	6219.03	8439.14	12771.25	14808.45	3223.16	29900.52	42447.27
Group. 9	30437.71	54246.43	13341.87	24977.11	29388.05	13462.85	17569.25	29900.52	7915.31	20557.24



Cluster Means							
	Char. 1	**Char. 2**	**Char. 3**	**Char. 4**	**Char. 5**	**Char. 6**	**Char. 7**
Group. 1	80.60	115.77	33.92	1.40	8.24	6.93	22.97
Group. 2	79.50	119.42	32.75	2.00	8.87	8.04	21.74
Group. 3	81.00	116.00	32.53	1.20	4.47	3.67	25.30
Group. 4	83.00	115.27	40.15	1.63	9.73	8.50	26.60
Group. 5	74.00	135.60	38.19	1.30	7.37	6.67	27.50
Group. 6	84.00	126.51	37.65	1.40	8.23	6.70	20.56
Group. 7	80.00	120.00	33.70	1.30	8.33	6.00	21.00
Group. 8	78.00	115.85	36.44	1.42	7.38	6.13	24.97
Group. 9	82.00	110.22	37.52	1.49	10.52	10.08	24.45
Group. 10	80.00	158.00	33.56	1.67	6.60	6.20	24.29
	Char. 8	Char. 9	Char. 10	Char. 11	Char. 12	Char. 13	
Group. 1	105.60	150.31	22.87	47.50	24.28	11.88	
Group. 2	104.83	124.05	25.09	46.46	23.65	11.51	
Group. 3	106.00	176.70	21.08	43.87	27.40	7.36	
Group. 4	108.00	155.20	36.00	59.39	26.55	18.37	
Group. 5	99.00	147.47	32.27	31.41	24.36	10.00	
Group. 6	109.00	172.40	28.20	49.52	22.55	14.35	
Group. 7	105.00	170.23	25.47	22.00	20.51	7.90	
Group. 8	103.00	139.72	57.60	27.82	23.70	15.70	
Group. 9	107.00	210.60	34.05	41.01	23.31	14.20	
Group. 10	105.00	194.30	21.53	56.46	20.38	15.33	Group. 10

Source	Times Ranked 1st	Contribution %
1 days to 50% flowering	0	0.00 %
2 PLANT HEIGHT IN	56	11.29 %

3 FLAG LEAF LENGTH IN	6	1.21 %
4 FLAG LEAF WIDTH IN C	0	0.00 %
5 no of tillers per	1	0.20 %
6 no of panicle per hi	0	0.00 %
7 panicle length	0	0.00 %
8 days to maturity	4	0.81 %
9 no of spikelets per	270	54.44 %
10 biological yield	73	14.72 %
11 harvest index %	82	16.53 %
12 test weight in g	1	0.20 %
13.seed yield per plant	3	0.60%

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 II and IX which has been reflected in the relatively high mean values for the most of the characters (Table 2). Hence, genotypes 4 and 16 may be selected for crossing with other parents for more effective crossing programme, and to achieve desired segregants for tall plant stature with good grain yield.

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CITATION OF THIS ARTICLE