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Research Article

Genetic diversity analysis of rice germplasm lines for yield attributing traits

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Abstract

Genetic divergence is an efficient tool for the selection of parents used in hybridization programme. In the present study, fifty three rice genotypes consisting of high yielding rice varieties/ cultures and IRRI germplasm lines were raised at Rice Research Station, Tirur during Sornavari, 2009 to identify diverse genotypes. They were evaluated for eight yield and yield attributing characters using D^2 analysis, to study the diversity pattern among the genotypes. Based on the analysis, the genotypes were grouped into 11 clusters. Maximum number of 16 and 15 genotypes were grouped under cluster XI and I respectively, while clusters II, IV, V, VI, VIII, IX and X had only two genotypes each and clusters III and VII consisting of 3 and 5 genotypes respectively. Maximum inter cluster D^2 value was observed between cluster I and X (32.96) followed by cluster I and IV (32.90). The greater the distance between the two clusters indicates wider the genetic diversity between genotypes. Hence, the genotypes in cluster I *viz*., ADT 39, ADT 43, ADT (R) 45. ASD 16, ASD 18 ASD 20, BL 17, BL 18, BL 24 CB 64110, JGL 17198, JGL 17204, JGL 17196, JGL 17187 and IR 36 had wider diversity with varieties TKM 11, TKM (R) 12 in cluster X and with IRRI germplasm lines IR 81396-B-B-164-4, IR 79913-B--362-B-3 in cluster IV and these lines may be utilized in further breeding programme for the exploitation of hybrid vigour. The intra cluster distance was maximum in cluster VII (24.62) followed by cluster XI (22.15) indicates hybridization involving genotypes within the same clusters may result in good cross combinations. Among the eight traits studied, maximum contribution was made by grain yield (50.87%) followed by days to 50 per cent flowering (15.02%), total grains per panicle (10.52%) and plant height (10.23%). Hence, grain yield, days to 50% flowering, total grains per panicle and plant height together contribute 86.62% towards total divergence. Therefore, these characters may be given importance during hybridization programme.

Keywords:

Rice, genetic diversity, yield

Introduction

Rice is one of the most important food crop and a primary food source for more than one third of world's population (Singh and Singh, 2008). In order to meet the food requirement of growing population, development of high yielding varieties is essential. The success of any breeding programme depends on the selection of parents for hybridization. The parents involved in the development of varieties should be divergent. The germplasm provides immense scope for wide variability.

Genetic divergence is an efficient tool for an effective choice of parents for hybridization programme. Such study also selects the genetically divergent parents to obtain desirable combinations In the segregating generations. Information on nature and degree of genetic divergence would help the plant breeder in choosing the right parents for the breeding programme (Vivekananda and Subramaniam, 1993). Keeping this in view, the present study was focused to assess the genetic diversity 53 promising rice genotypes using Mahalanobis D^2 statistics.

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Materials and Methods

Fifty three rice genotypes consisting of high yielding rice varieties/ cultures and IRRI germplasm lines were raised at Rice Research Station, Tirur during Sornavari, 2009 (May-August) to identify diverse genotypes. The experiment was laid out in Randomized Block Design with three replications. The genotypes were raised in plot of 6 rows with each row of 5 metre length. Row to row and plant to plant spacing was maintained at 20 x 15 cm. The recommended agronomic practices were followed. They were evaluated for eight yield and yield attributing characters viz., days to 50% flowering, plant height, number of productive tillers, panicle length, total grains per panicle, filled grains per panicle, spikelet fertility percentage and grain yield. Ten random plants / replication/ genotype were tagged for recording observations. The genetic

distance between the genotypes was worked out using Mahalanobis D^2 analysis (1936) and grouping of varieties into clusters was done following the Tochers method as detailed by Rao, 1952.

Results and discussion

Analysis of variance showed significant differences for all the eight characters studied among the genotypes. Based on D2 value, 53 genotypes were grouped into 11 clusters (Table 1). Maximum number of genotypes (16 genotypes) was grouped in cluster XI. Cluster I consists of 15 genotypes followed by cluster VII with five genotypes. Cluster III had three genotypes, while the remaining clusters were represented by two genotypes each. The overall composition of the clustering pattern showed that genotypes collected from the same geographic origin were distributed in different clusters. Similar findings of non- correspondence of geographic origin with genetic diversity were also reported by Shanmugasundaram *et al*., (2000) and Nayak *et al*., (2004)

The intra and inter cluster distance are presented in Table 2. Inter cluster distance was higher than intra cluster distance indicating wider genetic diversity among the genotypes. The maximum inter cluster distance was observed between cluster I and X (32.96) followed by between cluster I and IV (32.90) and between cluster I and VIII indicating wider genetic diversity among the genotypes between these groups (Subudhi *et al*., 2009). The hybrids developed from the selected members of these clusters would produce highly variable population in the segregating generations. The minimum inter cluster distance was found between cluster V and VI (7.67) followed by between cluster II and VI (11.43). These genotypes in these clusters are genetically very close and hence, hybridization among the varieties will not give fruitful result.

The maximum intra cluster distance was observed in cluster VII (24.62) followed by cluster XI (22.15) and cluster I (20.08). Hence, selection within these clusters may be exercised based on the highest areas for the desirable traits, which would be made use of in improvement through intervarietal hybridization (Joshi *et al*., 2008).

A perusal of results of cluster means (Table 3) revealed that cluster I with fifteen genotypes exhibited highest mean value for total grains per panicle (167.00), filled grains per panicle (153.56), spikelet fertility (91.65) and grain yield (4.91) and lowest mean value for plant height(83.64). Cluster II and III had genotypes with long panicles. Cluster IV was characterized by maximum panicle length (25.78) but with minimum total grains (83.33),filled grains (74.33) and grain yield (3.38), while the cluster VII had maximum number of productive tillers. Early flowering genotypes (77.83 days) viz., IR 82310-B-B-67-2 and IR 81413-B-B-75-3 were grouped in cluster VIII and tall genotypes (IR 81422-B-B-2004 and Vandana) with maximum height of 108.90 were grouped in cluster IX. The genotypes viz., TKM 11 and TKM (R) 12 in cluster X had long flowering duration.

None of the clusters contained genotypes with all the desirable traits which could be directly selected and utilized. All the minimum and maximum cluster mean values were distributed in relatively distant clusters. However the cluster I recorded desirable mean value for maximum number of productive traits viz., total grains per panicle, filled grains per panicle, spikelet fertility percentage and grain yield. Similar results were also reported by Bose and Pradhan (2005) while studying the divergence in deep water rice genotypes, thereby underlining the fact that the hybridization between genotypes of different clusters is necessary for the development of desirable genotypes. Based on the per se performance of the beat genotypes within the clusters, they may be directly selected or may be used as potential parents in hybridization programme.

The contribution of each trait to total divergence is presented in table 4. Among the traits studied, grain yield contributed maximum divergence (50.87%) followed by days to fifty percent flowering (15.02%), total grains per panicle (10.52%) and plant height (10.23%). The minimum percentage of contribution was observed in filled grains (0.65%) followed by productive tillers (2.39%), spikelet fertility percentage (4.50%) and panicle length (5.81%). The traits *viz.,* grain yield, days to fifty percent flowering, total grains per panicle and plant height contributed 86.64 per cent towards total divergence. Hence, these characters should be given importance during hybridization and selection in the segregating population.

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Table 1 Clustering pattern of 53 genotypes

Cluster	Number of genotypes	Name of genotypes
I	15	ADT 39, ADT 43, ADT (R) 45, ASD 16, ASD 18, ASD 20, BL 17, BL 18, BL 24,CB 64110, JGL 17198, JGL 17204, JGL 17196, JGL 17187, IR 36
II	2	IR 81449-B-B-109-1, APO
III	3	MDU 5, IR 823614-511-B, IR 82299-B-B-57-2
IV	2	IR 81396-B-B-164-4, IR 79913-B--362-B-3
V	2	IR71525-19-1-1,IR 72
VI	2	IR 84179-B-4, IR 827072-24-4-3
VII	5	PMK 2, PMK (R) 3, Rupali, IR 78875-190-B-1-3, IR 84179 B-403
VIII	2	IR 82310-B-B-67-2, IR 81413-B-B-75-3
IX	2	IR 81422-B-B-2004,Vandana
X	2	TKM 11, TKM (R) 12
XI	16	TKM 9, WGL 365, IR 81449-B-B-109-3, IR 82098-B-B-3-1, IR813699-B-B-165-1, IR 714371-54-1-1, UPLRI 7, IR 64, IR 81423-B-B-111-3, IR 81421-B-B-25-4, IR 81413-B-B-75-4, IR 78933-B-24-75-3, IR 82589-B-B-62-4, IR 92589-B-B-147-1, IR 825890-B-B-102-2, IR 82635B-B-58-4

Table 2 Intra and inter cluster average of yield traits in 53 rice genotypes

	I	II	III	IV	V	VI	VII	VIII	IX	X	XI
I	20.08	25.21	27.47	32.90	22.77	24.98	31.88	32.24	29.40	32.96	27.53
II		4.02	20.26	17.60	14.28	11.43	18.61	22.09	14.56	14.08	17.89
III			16.33	15.25	12.91	12.97	24.88	17.79	27.98	28.46	20.50
IV				5.34	16.57	12.28	21.11	12.98	26.67	24.84	20.10
V					5.40	7.67	22.19	15.32	21.53	23.50	17.41
VI						6.26	19.02	12.64	18.88	20.31	15.92
VII							24.62	23.37	21.53	21.40	23.59
VIII								7.93	26.09	27.85	20.96
IX									8.38	12.80	23.21
X										9.04	24.67
XI											22.15

Table 3 Cluster mean of different yield characters in 53 rice genotypes

Cluster	Days to fifty % flowering	Plant height	Productive tillers	Panicle length	Total grains per panicle	Filled grains per panicle	Spikelet fertility %	Plot yield (kg)
I	84.47	83.64	10.36	22.93	167.00	153.56	91.65	4.91
II	88.17	100.30	8.77	24.08	120.83	108.17	89.47	4.05
III	80.89	87.53	9.51	23.62	102.89	91.44	88.67	3.59
IV	80.33	98.15	9.25	25.78	83.33	74.33	89.21	3.38
V	85.00	89.53	10.77	21.85	106.00	95.33	89.94	3.94
VI	83.50	95.27	9.50	22.52	106.17	96.00	90.44	3.85
VII	83.27	105.33	11.27	23.26	129.67	116.27	89.60	3.94
VIII	77.83	96.00	9.92	20.93	88.33	80.33	90.57	3.50
IX	88.67	108.90	9.75	18.85	145.50	131.00	90.07	4.26
X	91.17	108.83	10.12	21.97	157.17	139.50	88.71	3.49
XI	83.13	95.84	9.35	23.07	116.15	104.08	89.01	4.05

Table 4 Percentage of contribution of each character towards total divergence

Character	No. of first rank	Contribution (%)
Days to fifty % flowering	207	15.02
Plant height	141	10.23
Productive tillers	33	2.39
Panicle length	80	5.81
Total grains	145	10.52
Filled grains	9	0.65
Spikelet fertility %	62	4.50
Plot yield	701	50.87
Total	1378	100