Electronic Journal of Plant Breeding, 9(4): 1335-1341 (Dec 2018) DOI: 10.5958/0975-928X.2018.00166.7
ISSN 0975-928X

Research Article

Genetic diversity studies in rice (*Oryza sativa* L.)

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(Received: 18 Jul 2018; Revised: 10 Sep 2018; Accepted: 10 Sep 2018)

Abstract

Thirty-seven elite germplasm lines being maintained at Regional Agricultural Research Station, Maruteru were evaluated for their genetic diversity with regard to grain yield, yield components and quality traits. The genotypes were classified into 18 clusters, based on Mahalanobis D^2 statistics. Geographical and genetic diversity were observed to be unrelated, as genotypes from diverse geographical regions were placed in the same cluster, while, genotypes from the same centre were grouped into different clusters. Results on inter-cluster distances revealed maximum diversity between genotypes of clusters XVI and XVII. Intra-cluster distance was maximum for cluster XVIII, indicating the existence of variability within the cluster. A perusal of the results on cluster means revealed greater yield for cluster XII indicating the desirability of genotypes from the cluster for improvement of grain yield. Further milling percentage, days to 50 per cent flowering, number of grains panicle^{-1}, 1000-seed weight and head rice recovery percentage, together accounted for 89.79 per cent of the total genetic divergence, indicating their importance as selection criteria in the choice of parents for hybridization programmes.

Key words

D^2 analysis, genetic divergence, rice.

Introduction

Rice is an important staple food of almost half of the world's population and is referred to as "Global Grain". 'Rice is Life' was the theme of International year of rice 2004 denoting its overwhelming importance as an item of food and commerce. Rice is widely grown in tropical and subtropical regions with wide range of ecosystems under varying temperature and water regimes in more than 114 countries. Among the rice growing countries in the world, India has the largest area under rice cultivation and ranks second in production next to China. However, to meet the food demands of the growing population and to achieve food security in the country, the present production levels need to be increased by 2 million tonnes every year, which is possible through heterosis breeding and other innovative breeding approaches (Padmavathi, 2012). Development of new high yielding and quality rice varieties, superior to the existing varieties, mainly depends on the amount of genetic variability present in the population. Genetic divergence study is therefore important for choice of parents in hybridization programme. Information on genetic diversity in terms of nature and degree of divergence for grain yield, yield components and quality characters would help the plant breeder in selection of right type of parents for hybridization programmes and designing of effective breeding strategies aimed at development of high yielding varieties with good grain quality. Mahalanobis D^2 statistics is a valuable tool in quantifying the degree of divergence. It helps the breeder to estimate the genetic divergence in the population for use in plant breeding programmes. In this context, the present study was undertaken to classify and understand the nature and magnitude of genetic diversity among the pre-release elite rice genotypes of different rice research stations using Mahalanobis D^2 statistics.

Material and Methods

Experimental material for present investigation comprised 37 elite rice genotypes obtained from Regional Agricultural Research Station, Maruteru, West Godavari district of Andhra Pradesh. The sowing was undertaken in nursery during *kharif* 2017 and transplanting of the seedlings was effected 25 days after sowing. The normal, healthy and vigorous seedlings of each genotype were transplanted in a six-row plot of 4.5-metre length, with a spacing of 20 x 15 cm and the crop was raised following recommended package of practices. Data were recorded on five randomly selected plants in each replication for the characters, namely, plant height, ear bearing tillers plant^{-1}, panicle length, number of grains panicle^{-1} and grain yield plant^{-1} for all the genotypes.

However, days to 50 per cent flowering was recorded on plot basis, while observations on 1000-seed weight, L/B ratio, hulling percentage, milling percentage and head rice recovery percentage were obtained from a random grain sample drawn from each genotype in each replication. The data obtained were subjected to standard statistical procedures. Genetic divergence analysis was done following the D^2 statistics proposed by Mahalanobis (1936) and described by Rao (1952).

Results and Discussion

The analysis of variance (ANOVA) of 37 genotypes of rice for grain yield, yield attributes and quality traits is presented in Table 1. The results revealed significant differences among the genotypes studied for all the characters, except hulling percentage and milling percentage indicating the existence of significant variability for grain yield, yield components and most of the quality traits studied.

The results on genetic divergence of the genotypes studied for grain yield, yield components and quality characters are presented in Tables 2-5. A perusal of the results on grouping of the 37 genotypes studied in the present investigation (Table 2) revealed that the genotypes were grouped into 18 clusters based on relative magnitude of D^2 values such that the genotypes belonging to same cluster had an average smaller D^2 value than those belonging to different clusters. Among the clusters, cluster I was the largest comprising 14 genotypes, representing collections from different centres of the Andhra Pradesh and Chhattisgarh, namely, Maruteru, Nellore and Raipur, while cluster IV had five genotypes from Maruteru. The cluster XIII had two genotypes from Maruteru, while cluster XVIII had two genotypes, one from Utukur and other from Nellore. The clusters II, (Bapatla), III (Bapatla), V (Nellore), VI (Maruteru), VII (Nellore), VIII (Maruteru), IX (Maruteru), X (Maruteru), XI (Maruteru), XII (Jangamaheswarapuram), XIV (Maruteru), XV (Bapatla), XVI (Bapatla) and XVII (Maruteru) were solitary or monogenotypic with zero intra-cluster D^2 values. These results are in broad agreement with the findings of Ashok *et al.* (2017). Further, the mode of distribution of genotypes from different geographical regions into various clusters was at random indicating no relation of geographic and genetic diversity. Genotypes chosen from the same eco-geographical region were observed to be present in different clusters as well as in same cluster, while varieties from diverse geographical regions were included in the same cluster. The findings are in conformity with the reports of Chandramohan *et al.* (2016). Genotypes from Maruteru were observed to be distributed over 10 clusters (cluster I, IV, VI, VIII, IX, X, XI, XIII, XIV and XVII), while genotypes from diverse geographical regions of different centres were placed in the same cluster (cluster I and XVIII). Similar results were reported earlier by Ashok *et al.* (2017).

An analysis of inter- and intra-cluster distances (Table 3) revealed maximum inter-cluster distance between cluster XVI and XVII (642.95), followed by cluster VI and XVII (576.98) indicating that genotypes from these clusters were highly divergent meriting due consideration in selection of parents for hybridization. The greater the distance between two clusters, the wider would be the genetic diversity between genotypes of the clusters. Therefore, hybridization between the genotype (BPT 2782) of cluster XVI and the genotype of cluster XVII (MTU 2284-103-1-9) is expected to result the greater variability and transgressive segregents. Minimum inter-cluster distance was observed between cluster II and III (21.12), indicating their close relationship and similarity with regard to the characters studied for most of the genotypes in the two clusters. Further, intra-cluster distance was observed to be minimum for cluster I (37.23) and maximum for cluster XVIII (48.45), while it was zero for the monogenotypic clusters (cluster II, III, V to XII and XIV to XVII). The genotypes included in cluster XVIII exhibiting maximum intra-cluster distance, are inferred to be more divergent than those in other clusters.

The cluster mean values for grain yield, yield components and quality characters are presented in Table 4. A perusal of these results revealed considerable differences between the clusters for all characters under study. Cluster mean for days to 50 per cent flowering was highest in cluster XV (123 days) and lowest in cluster V and VII (98 days), while for plant height, it was highest in cluster XII (137.20 cm) and lowest in XIV (106.20 cm). However, ear bearing tillers plant^{-1} was highest in cluster XIII (11.70) and lowest in VIII (6.00), while panicle length was highest in cluster IX (31.32 cm) and lowest in cluster V (20.27 cm). Similarly, number of grains panicle^{-1} was highest in cluster IX (306.20) and lowest in cluster V (138.70). Further, grain yield plant^{-1} was highest in cluster XII (18.40 g) and lowest in cluster XI (9.70 g), while1000-seed weight was highest in cluster XVI (23.40 g) and lowest in cluster III (14.24 g). L/B ratio was highest in cluster VI (3.10) and lowest in cluster XIV (2.11), while hulling percentage was highest in cluster IX (81.98%) and lowest in XIV (77.12%). However, milling percentage was highest in cluster XVI (74.29%) and lowest in XVII (61.22%), while head rice recovery percentage was highest in cluster XVI (70.86%)

and lowest in XVII (48.69%). Selection of genotypes from clusters with high mean for the respective traits is suggested for utilization in hybridization programmes aimed at improvement of the respective traits. A perusal of these results also revealed that there was no cluster with all the desirable traits, which ruled out the possibility of direct selection of genotypes for immediate use. Therefore, judicious combination of all the targeted traits requires hybridization between the selected genotypes from divergent clusters.

Information on the relative contribution of various plant characters towards divergence was reported to aid the breeder in choice of parents for hybridization and effective selection (Ashok *et al.*, 2017). In the present study milling percentage contributed maximum (31.08%), followed by days to 50 per cent flowering (17.87%), number of grains panicle^{-1} (16.37%), 1000-seed weight (13.21%) and head rice recovery percentage (11.26%) towards the total divergence (Table 5). Contribution of remaining characters to the total divergence was however, relatively low. Therefore, milling percentage, days to 50 per cent flowering, number of grains panicle^{-1}, 1000-seed weight and head rice recovery percentage contributing to 89.79 per cent of the total divergence need to be stressed in selection of parents for hybridization. Similar results have been reported earlier by Chandramohan *et al.* (2016) for days to 50 per cent flowering; Bharathi *et al.* (2016) for number of grains panicle^{-1}; Saraswathi *et al.* (2012) for 1000-seed weight and Ashok *et al.* (2017) for head rice recovery percentage.

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Electronic Journal of Plant Breeding, 9(4): 1335-1341 (Dec 2018) DOI: 10.5958/0975-928X.2018.00166.7
ISSN 0975-928X

Table 1. Analysis of variance for 37 genotypes for grain yield, yield attributes and quality characters in rice (*Oryza sativa* L.)

Source of variation	d.f.	Days to 50 % flowering	Plant height (cm)	Ear bearing tillers plant^{-1}	Panicle length (cm)	Number of grains panicle^{-1}	Grain yield plant^{-1} (g)	1000-seed weight (g)	L/B ratio	Hulling (%)	Milling (%)	HRR (%)
Replications	1	5.96	108.49	0.62	50.09	22.11	1.00	8.97	0.04	0.02	0.10	0.94
Genotypes	36	68.98**	163.87**	2.54**	10.49**	3785.59**	13.70**	11.83**	0.09**	3.86	14.88	44.94**
Error	36	4.93	91.78	0.76	5.54	327.16	3.47	1.37	0.03	18.91	17.12	18.16
CD (0.05)		4.50	8.64	1.77	4.77	36.68	3.78	2.38	0.34	-	-	8.64
CV (%)		2.05	8.38	10.60	9.04	8.33	13.95	6.09	6.83	5.43	5.91	6.71

*,**Significant at 5 and 1 per cent levels, respectively

Table 2. Distribution of the 37 genotypes into different clusters

Cluster No.	Number of Genotypes	Genotypes included in cluster	Source
I	14	MTU 2386-25-2-1, RM 168-28-1-1-1, HR M5, MTU 2336-70-46-25-44, RM 146-36-1-1-1, MTU 2336-62-25-39-16, MTU 1238, MTU 2347-158-3-1-1, MTU 2284-103-1-7, NLR 3083, HR L4, RP6112-MS-128-5-2-3-1-4-5, MTU 2404-25-2, MTU 2411-74-1-1-1	Maruteru, Nellore, Raipur
II	1	BPT 2798	Bapatla
III	1	BPT 5204	Bapatla
IV	5	MTU 2247-55-2, MTU 1061, MTU 2049-5-2-1, MTU 2244-128-18, MTU 2331-19-1-1-2	Maruteru
V	1	NLR 3445	Nellore
VI	1	MTU 2201-34-3-1	Maruteru
VII	1	NLR 5815-10-1-1-1	Nellore
VIII	1	RM 138-80-3-1-1-1	Maruteru
IX	1	MTU 2345-98-3	Maruteru
X	1	MTU 2331-216-1-1	Maruteru
XI	1	MTU 2347-87-1-1-1	Maruteru
XII	1	JMP 16	Jangamaheswarapuram
XIII	2	MTU II 388-44-1-1-3-1-1, MTU 2337-216-1-1	Maruteru
XIV	1	MTU 2067-9-1-1-2	Maruteru
XV	1	BPT 2659	Bapatla
XVI	1	BPT 2782	Bapatla
XVII	1	MTU 2284-103-1-9	Maruteru
XVIII	2	UTR 51, NLR 5813-7-1-1-1	Utukur, Nellore

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Table 3. Average intra and inter-cluster distances for the 37 genotypes

Cluster No.	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV	XV	XVI	XVII	XVIII
I	37.23	49.59	77.09	69.51	54.59	53.99	71.64	51.74	74.30	74.31	91.17	66.41	215.75	69.36	157.03	77.14	442.72	99.73
II		0.00	21.12	96.33	49.19	76.80	110.64	47.20	52.39	91.89	67.65	36.66	249.93	69.72	228.53	102.60	472.08	61.81
III			0.00	120.97	116.08	99.08	174.66	57.81	34.53	76.74	34.97	53.51	282.62	101.65	270.05	111.54	538.00	116.65
IV				42.43	102.54	73.22	144.35	78.37	133.47	108.82	155.45	81.36	238.14	116.24	90.04	74.42	464.22	178.71
V					0.00	89.21	40.04	88.56	117.32	156.16	164.85	75.58	254.99	79.02	212.08	91.84	462.59	78.99
VI						0.00	121.99	63.33	93.30	124.06	94.81	75.46	314.18	160.56	186.52	47.15	576.98	155.64
VII							0.00	109.77	120.26	126.73	178.77	118.07	168.90	62.84	209.83	132.30	337.74	101.30
VIII								0.00	30.71	85.70	89.16	48.52	213.43	64.55	218.31	85.77	421.44	82.41
IX									0.00	74.41	43.73	48.60	231.51	81.35	290.74	91.91	456.07	106.04
X										0.00	59.19	101.21	118.95	59.59	136.64	160.51	317.18	149.83
XI											0.00	77.84	272.16	143.60	284.06	132.03	532.24	147.57
XII												0.00	211.92	89.29	195.08	69.40	404.31	95.86
XIII													38.31	103.63	185.68	355.85	76.16	226.20
XIV														0.00	170.18	168.85	250.21	76.55
XV															0.00	204.30	358.45	312.98
XVI																0.00	642.95	213.03
XVII																	0.00	366.55
XVIII																		48.45

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Table 4. Cluster means for grain yield, yield components and quality components for the 37 genotypes

Cluster No.	Days to 50 % flowering	Plant height (cm)	Ear bearing tillers plant^{-1}	Panicle length (cm)	Number of grains panicle^{-1}	Grain yield plant^{-1} (g)	1000-seed weight (g)	L/B Ratio	Hulling (%)	Milling (%)	HRR (%)
I	107	125.05	8.26	25.48	197.48	11.79	19.31	2.52	79.48	70.12	64.54
II	106	114.90	7.20	22.51	184.90	12.31	14.57	2.54	80.51	71.93	65.16
III	111	108.90	8.70	25.21	277.70	15.80	**14.24**	2.48	78.13	70.42	64.92
IV	113	115.82	9.38	26.69	217.26	16.09	21.76	2.29	80.28	71.85	64.40
V	**98**	117.60	9.50	**20.27**	**138.70**	15.18	19.37	2.50	78.77	69.45	63.70
VI	110	130.80	8.60	27.41	226.30	14.88	21.33	**3.10**	81.85	73.34	67.50
VII	**98**	116.00	7.40	24.63	164.60	13.21	21.50	2.69	81.59	69.99	65.50
VIII	108	111.10	**6.00**	28.75	255.10	13.29	18.90	2.34	80.50	71.12	60.05
IX	106	109.80	6.40	**31.32**	**306.20**	13.13	17.47	2.50	**81.98**	72.81	65.74
X	117	116.50	10.50	28.01	275.10	17.21	21.60	2.50	78.50	67.65	63.82
XI	111	135.40	7.70	23.77	206.60	**9.70**	14.57	2.71	78.42	68.36	60.24
XII	105	**137.20**	9.90	28.71	261.80	**18.40**	18.35	2.33	81.90	72.39	64.78
XIII	111	111.65	**11.70**	26.43	265.65	15.83	20.94	2.25	79.88	68.15	61.80
XIV	107	**106.20**	6.20	26.74	202.83	12.56	16.60	**2.11**	**77.12**	65.84	58.82
XV	**123**	131.50	8.90	27.01	185.50	17.23	22.26	2.27	81.54	69.85	66.83
XVI	107	126.00	8.40	31.30	241.60	16.70	**23.40**	2.46	81.77	**74.29**	**70.86**
XVII	109	109.20	6.60	27.92	261.80	16.03	19.27	2.29	79.69	**61.22**	**48.69**
XVIII	99	121.25	9.45	24.07	179.25	11.98	15.51	2.51	79.90	69.35	56.54

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ISSN 0975-928X

Table 5. Relative contribution of characters studied towards genetic divergence in rice

S. No.	Source	Times ranked first	Contribution %
1	Days to 50 per cent flowering	119	17.87%
2	Plant height	1	0.15%
3	Ear bearing tillers plant^{-1}	5	0.75%
4	Panicle length	3	0.45%
5	Number of grains panicle^{-1}	109	16.37%
7	Grain yield plant^{-1}	22	3.30%
6	1000-seed weight	88	13.21%
8	L/B Ratio	37	5.56%
9	Hulling (%)	0	0.00%
10	Milling (%)	207	31.08%
11	HRR (%)	75	11.26%