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RESEARCH ARTICLE

Assessment of Character Contribution to the Divergence in Rice (*Oryza sativa* L.) Germplasm

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Sixty-five rice accessions were evaluated for eleven characters to study genetic diversity. Result indicated presence of considerable genetic divergence among the accessions and their pattern of distribution into various clusters was random and independent of geographical origin. Cluster I, III and II contain 28, 19 and 12 accessions, respectively, while clusters IV, V, VI, VII, VIII and IX were monogenotypic. The highest intra cluster distance was observed for cluster III (7.72) followed by cluster II (4.85). Cluster VII had highest mean value for filled grains per panicle (210.06), total grains per panicle (251.33), spikelet fertility per cent (89.19) and grain yield per plant (30.81 g) and cluster VIII for days to 50 per cent flowering (155.33), days to maturity (180.33) and plant height (177.21 cm). Days to flowering had maximum contribution (47.74 %) to the total divergence followed by days to maturity (13.7 %) and plant height (13.65 %). The accessions falling in different clusters with high mean grain yield and high mean for component characters can be utilized for hybridization programme to obtain elite segregants.

Key Words: Character contribution, Clustering, D^2 analysis, Genetic divergence, *Oryza sativa*

Introduction

Genetic diversity is a pre-requisite for any crop improvement breeding programme as it helps in estimating and establishing the genetic relationship in the collection of accessions, identifying diverse parental combinations to create segregating progenies with maximum genetic variability and superior recombinations (Thompson *et al.*, 1998; Islam *et al.*, 2012; Ramadan *et al.*, 2015). Parents identified on the basis of divergence would be more promising for breeding program (Kwon *et al.*, 2002). Thus, accurate assessment of the levels and patterns of genetic diversity can be invaluable in crop breeding for diverse applications including introgression of desirable genes from diverse accessions into the available genetic base and for widening the narrow genetic base of the developed varieties (Roy, 2013). The D^2 technique based on multivariate analysis developed by Mahalanobis (1936) had been found to be a potent tool in quantifying the degree of divergence in accessions and provides a measurement of relative contribution of different components on diversity both in inter and intra-cluster level and genotypes drawn from widely divergent clusters are likely to produce heterotic combinations and wide variability in segregating generation. Thus, the present investigation was intended to characterize the rice accessions on the basis of D^2 analysis (Mahalanobis, 1936).

Materials and Methods

Experimental Material and Site

The present investigation analysed 65 rice genotypes listed in Table 1, received from DBT Networking Project, Institute of Agricultural Sciences, Banaras Hindu University. The plants were raised in Randomized Block Design with three replications during the kharif season 2015 at Agricultural Research Farm, Institute of Agricultural Sciences, Banaras Hindu University. The 21 days old seedlings were used for transplanting at row to row 20 cm spacing and plant to plant was 15 cm, respectively.

Traits Observed

Observations were recorded on randomly selected plants from each entry for eleven quantitative traits viz., days to 50 per cent flowering (DF), days to maturity (DM), number of effective tillers per plant (ET), plant height

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Table 1. Genotypes used under study

S. No.	Genotype	S. No.	Genotype	S. No.	Genotype
1	OR 1946-2-1	2	IR 83142-76	3	Vandana
4	IR 82635-B-B-47-1	5	IR 82589-B-B-7-2	6	IR 82635-B-B-23-1
7	CRR 660-2	8	CRR 428-237-1-3-1	9	Rewa 1208-15
10	IR 83399-B-B-52-1	11	PAU 3832-79-4-3-1	12	IR 83182-6-4
13	IR 78755-190-B-1-3	14	IR 82635-B-B-25-4	15	RP 5345-9-6-3
16	RRF-48	17	IR 55423-01	18	CB 10-504
19	GK 5022	20	Anjali	21	IR 10L-105
22	B 11576F-MR-18-2	23	CR 3631-1-3	24	BAU 411-05
25	IR 82921-B-B-1	26	BD 104	27	IR 77298-14-1-2-13
28	CR 422-63-51-B-2-1-1-1-B	29	IR 1718-59-1-2-3	30	IR 82635-B-B-145-1
31	NDR 1140	32	CR 3633-1-2	33	IR 368B-TB-25-MP-2
34	UPLRI – 7	35	IR 87694-28-7-2-1	36	RP 5330-63-5-2-1-B
37	MGD 1206	38	IR83867-B-B-250-CRA-1-1	39	IR 83926-B-B-71-4
40	IR 60080-46A	41	BD 108	42	BVS 1
43	BVD 111	44	BVD 203	45	BAU 389-02
46	BAU/IRRI 497	47	LC -1	48	LC -2
49	LC -3	50	LC -4	51	LC -5
52	LC – 6	53	LC – 7	54	LC – 8
55	LC – 9	56	LC – 10	57	LC – 11
58	LC – 12	59	LC – 13	60	LC – 14
61	LC – 15	62	LC – 16	63	LC – 17
64	LC – 18	65	LC – 19		

(PH), panicle length (PL), panicle weight (PW), filled grains per panicle (FG), total grains per panicle (TG), spikelet fertility percent (SFP), test weight (TW) and grain yield per plant (GY).

Statistical Analysis

Analysis of variance was carried out by the method of Panse and Sukhatme (1967) for each of the sixty-five genotypes. Genetic divergence was estimated by Mahalanobis' D^2 statistics (1936). After arranging the D^2 values of all combinations of one genotype with the others in ascending order of magnitudes, the genotypes were grouped into a number of clusters by Tocher's method described by Rao (1952). Each character was ranked on the basis of values in all the combination of genotype for estimation of contribution of individual characters towards divergence.

Results and Discussion

Analysis of variance revealed that the genotypes differed significantly for all the characters under study and might be of diverse origin (Table 2). These findings were in accordance with the findings of Paikhomba *et al.* (2014) and Islam *et al.* (2016).

Cluster Distances and Composition

D^2 analysis revealed the presence of considerable diversity in the set of sixty-five accessions under study. The accessions were observed to be distributed in nine different clusters. Clustering pattern indicated that twenty-eight out of 65 accessions belong to the same cluster i.e. cluster I (Table 3). On the other hand, 19 accessions belong to cluster III and 12 belong to cluster II. Rest other clusters i.e. cluster IV, V, VI, VII, VIII and IX consists of one accessions each for which the intra-cluster distance was observed to be zero. Intra-cluster and inter-cluster distances i.e. $\sqrt{D^2}$-values have been presented in Table 4. Cluster III showed the maximum intra-cluster distance i.e. 7.72 followed by cluster II (4.85) and I (4.48). Genotypes included in the same cluster indicated their close relationship among themselves as compared to genotypes in other clusters. The maximum inter-cluster distance was observed between cluster II and VIII (23.33) indicating that the hybridization between the most diverse genotypes would yield desirable segregants with the accumulation of favorable genes in the segregating generations. The next two diverse clusters were cluster VII and VIII (22.61) and cluster V and VIII (19.75). The clustering pattern indicated wide diversity between different groups of genotypes. The inter-cluster distances were higher than the intra-cluster distances which indicate the existence of substantial diversity among the parents (Kumar *et*

Table 2. Analysis of variance (ANOVA) for eleven quantitative traits in sixty-five rice genotypes

Source of variation	df	Mean Sum of Squares										
		DF	DM	ET	PH	PL	PW	FG	TG	SFP	TW	GY
Replication	2	1.00	10.23	7.45	114.74	0.51	0.07	5.17	15.32	25.18	7.34	1.65
Treatment	64	994.01**	960.59**	12.90**	2060.52**	23.77**	2.48	3692.41**	4949.83**	181.33**	44.57**	95.23**
Error	128	4.99	4.19	2.55	88.75	0.72	0.11	244.88	157.38	40.46	3.01	8.36

**Significant at $p< 0.01$.

(DF) days to 50 per cent flowering, (DM) days to maturity, (ET) number of effective tillers per plant, (PH) plant height, (PL) panicle length, (PW) panicle weight, (FG) filled grains per panicle, (TG) total grains per panicle, (SFP) spikelet fertility percent, (TW) test weight and (GY) grain yield per plant.

Table 3. Grouping of sixty-five rice genotypes into nine clusters (by Tocher method)

Clusters	Germplasm	Number
I	IR 55423-01, LC – 18, LC – 13, IR 1718-59-1-2-3, LC – 16, BVS 1, BAU 389-02, BVD 203, LC – 11, LC – 17, LC – 7, LC – 6, LC – 14, Vandana, OR 1946-2-1, LC – 19, LC – 3, LC – 4, IR 368B-TB-25-MP-2, LC – 2, CR 422-63-51-B-2-1-1-1-B, IR 10L-105, CR 3633-1-2, LC – 9, CB 10-504, R RF-48, IR 83867-B-B-250-CRA-1-1, LC – 5	28
II	BAU 411-05, LC – 12, IR 82635-B-B-25-4, IR 60080-46A, MGD 1206, CRR 660-2, IR 78755-190-B-1-3, CRR 428-237-1-3-1, RP 5345-9-6-3, RP 5330-63-5-2-1-B, BD 104, IR 83926-B-B-71-4	12
III	IR 82589-B-B-7-2, IR 87694-28-7-2-1, IR 77298-14-1-2-13, IR 83399-B-B-52-1, IR 83182-6-4, UPLRI – 7, BD 108, IR 82635-B-B-47-1, IR 83142-76, Rewa 1208-15, BVD 111, BAU/IRRI 497, LC – 1, CR 3631-1-3, LC – 15, B 11576F-MR-18-2, LC – 8, IR 82635-B-B-145-1, PAU 3832-79-4-3-1	19
IV	GK 5022	1
V	NDR 1140	1
VI	Anjali	1
VII	IR 82921-B-B-1	1
VIII	IR 82635-B-B-23-1	1
IX	LC – 10	1

Table 4. Average Intra- and Inter-cluster √D2 values among nine clusters (by Tocher's method)

Clusters	I	II	III	IV	V	VI	VII	VIII	IX
I	4.48	7.43	11.84	7.17	7.65	6.94	8.31	18.86	7.96
II		4.85	16.09	11.48	9.86	11.14	9.11	23.33	12.59
III			7.72	10.18	11.44	10.85	14.89	11.13	11.13
IV				0	8.56	9.63	8.12	16.26	8.25
V					0	9.32	6.95	19.75	12.64
VI						0	11.56	16.92	6.21
VII							0	22.61	12.97
VIII								0	15.23
IX									0

(Figure in diagonal indicate intra-cluster √D2 value)

al., 2014). Similar results of inter and intra cluster distances in rice were reported by Senapati and Sarkar (2005), Kuchanur *et al.* (2009), Roy (2013) and Singh *et al.* (2015).

Cluster Mean for Different Characters under Study

A perusal of cluster means indicated that there existed considerable differences in the mean values of different traits (Table 5). Cluster VII exhibited highest mean value for filled grains per panicle (210.06), grains per panicle (251.33), spikelet fertility per cent (89.19) and grain yield per plant (30.81), while cluster VIII had highest mean value for days to 50 per cent flowering (155.33), days to maturity (180.33) and plant height (177.21) likewise cluster IX had highest mean value for panicle length (33.38) and test weight (29.72). Cluster II and IV had highest mean value for number of tillers

Table 5. Cluster mean values for different eleven characters

Cluster	DF	DM	ET	PH	PL	PW	FG	TG	SFP	TW	GY
I	97.86	132.56	8.94	112.79	26.48	3.22	128.61	160.87	79.54	23.10	22.65
II	85.91	117.00	**11.57**	104.97	22.78	2.21	89.30	106.41	82.60	22.68	20.22
III	128.63	160.42	9.93	133.79	24.94	2.96	139.28	168.91	82.66	19.39	22.65
IV	111.66	140.66	7.46	125.45	27.25	**5.76**	198.00	220.73	82.74	28.67	32.36
V	103.33	137.00	9.80	98.11	23.41	3.00	199.86	226.13	85.73	14.88	22.25
VI	107.33	138.33	9.60	123.09	31.49	2.45	137.80	177.06	77.68	16.17	16.86
VII	95.00	122.33	8.20	142.71	24.94	5.41	**210.06**	**251.33**	**89.19**	22.13	**30.81**
VIII	**155.33**	**180.33**	10.33	**177.21**	25.47	2.78	80.73	80.73	72.00	24.89	16.23
IX	109.33	142.33	8.06	155.487	**33.38**	4.32	142.86	142.86	89.06	**29.72**	28.63

*Bold numbers are highest mean value

(DF) days to 50 per cent flowering, (DM) days to maturity, (ET) number of effective tillers per plant, (PH) plant height, (PL) panicle length, (PW) panicle weight, (FG) filled grains per panicle, (TG) total grains per panicle, (SFP) spikelet fertility percent, (TW) test weight and (GY) grain yield per plant.

(11.57) and panicle weight (5.76), respectively. Thus, the genotypes in cluster VII, VIII and IX seem to be quite promising for these mentioned traits. Similar findings were observed by Singh *et al.* (2011) and Chouhan *et al.* (2014) for days to maturity, plant height, total number of tiller per plant and test weight. It has been observed that distribution of highest and lowest mean values for different traits under study in distinct cluster suggested that the traits contributing to the total divergence.

Contribution of Different Traits towards Total Genetic Divergence

The perusal of the comparison of contribution of different characters towards genetic diversity was estimated based on ranking method (Fig. 1) and it was observed that days to 50 per cent flowering contributed maximum (47.74%). The second largest contributor was days to maturity (13.7%) followed by panicle length (13.65%) and panicle weight (6.59%). The character like test weight, spikelet fertility, total grain per panicle and filled grain per panicle was found to be least contributing traits. Similar results were reported by Khare *et al.* (2014).

Conclusion

A wide range of variation was evident among 65 rice germplasms evaluated. The sixty-five rice accessions were grouped into nine clusters which were in concordance with the clustering pattern obtained by Mahalanobis D^2 statistics. The parents for hybridization program should be selected based on the magnitude of genetic distance, contribution of different characters' towards the total divergence and magnitude of cluster

Fig. 1. Percentage contribution of each character towards total genetic divergence in 65 germplasm

means for different characters performance having maximum heterosis. A higher heterosis could be produced from the crosses between genetically distant parents. Therefore, crosses between the genotypes of clusters II and VIII, VII and VIII, V and VIII would give high manifestation of heterosis and is expected to be effective in accumulation of favorable genes in segregating generations.

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