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Genetic divergence among maintainers and restorer lines of rice

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ABSTRACT

Genetic divergence was worked out in 86 rice genotypes obtained from IRRI, DRR and other hybrid rice breeding centres at Directorate of Rice Research, Andhra Pradesh, India during wet season, 2008. Based on thirteen important yield attributes, the genotypes were grouped into ten clusters. Cluster IV was the largest with 21 genotypes from different centres, while the clusters V and X had 3 genotypes each. Cluster IV included 14 genotypes from IRRI, Philippines; 3 genotypes from DRR, Hyderabad; one each from PAU, Kapurthala; IARI, New Delhi; NDUAT, Faizabad and RARS, Maruteru. There was no relationship between geographical distribution and genetic diversity. Characters like plant height, 1000-seed weight, days to 50% flowering and number of filled grains per panicle had contributed more to the total divergence. These characters could, therefore, form the basis for selection of parents showing good mean performance from distinctly placed clusters to obtain heterotic combinations.

Key words : *rice, genetic divergence, maintainer lines, restorers*

Among the limited available options to increase production and productivity of rice, hybrid rice technology is the most feasible and readily adoptable. For selection of most suitable and genetically divergent parents for successful breeding programme, it is necessary to study the genetic diversity of germplasm lines. Diversity of parents is very much emphasized in crossing programmes because the cross between the genotypes with maximum genetic divergence are likely to yield desirable recombinations. Accumulation of genetic variability is more in the populations from diversified environments as compared to populations from a similar ecological regions.

The characters responsible for discrimination between populations can narrow down the problem of selecting divergent parents for breeding programme. In three line hybrid rice breeding programme especially, to realize potential sizable heterosis restorer and CMS divergence is a major factor. Hence, an attempt has been made to study the genetic divergence in rice genotypes (maintainers and restorers) obtained from different research centres.

MATERIALS AND METHODS

The experimental material consisted of 86 genotypes and one check variety IR 64) from advanced breeding lines developed at Crop Improvement division, Directorate of Rice Research, Hyderabad and International Rice Research Institute, Manila, Philippines (Table 1). All the 86 genotypes were grown in randomized block design with three replications at research farm, Directorate of Rice Research, Hyderabad during wet season, 2008. Thirty days old seedlings were transplanted in a two row plot with a row length of 3.6 m with 24 hills in each row. The spacing adopted was 20 x 15 cm at the rate of one seedling hill^{-1}. The recommended package of practices was followed for raising a healthy crop. The observations were recorded on five randomly selected plants per replication for each entry on 13 quantitative

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Table 1. Maintainer and elite restorer rice lines used in genetic diversity analysis.

S. No	Genotype	Source
Maintainer lines		
1	IR 58025B	IRRI, Philippines
2	IR 6888B	IRRI, Philippines
3	IR 68897B	IRRI, Philippines
4	APMS 6B	RARS, Maruteru
5	CRMS 32B	CRRI, Cuttack
6	PMS 10B	PAU, Kapurthala
7	PMS 17B	PAU, Kapurthala
8	DRR 2B	DRR, Hyderabad
9	DRR 6B	DRR, Hyderabad
10	DRR 8B	DRR, Hyderabad
11	DRR 10B	DRR, Hyderabad
12	DRR11B	DRR, Hyderabad
13	DRR13B	DRR, Hyderabad
14	DRR14B	DRR, Hyderabad
15	DRR15B	DRR, Hyderabad
16	PUSA 5B	IARI, New Delhi
17	IR 68229B	IRRI, Philippines
18	IR 80151B	IRRI, Philippines
19	IR 80155B	IRRI, Philippines
20	IR 79156B	IRRI, Philippines
Restorer Lines		
21	IR 40	IRRI, Philippines
22	IR 41	IRRI, Philippines
23	IR 42	IRRI, Philippines
24	IR 43	IRRI, Philippines
25	IR 44	IRRI, Philippines
26	IR 45	IRRI, Philippines
27	IR 46	IRRI, Philippines
28	IR 47	IRRI, Philippines
29	IR 48	IRRI, Philippines
30	IR 49	IRRI, Philippines
31	IR 50	IRRI, Philippines
32	IR 51	IRRI, Philippines
33	IR 52	IRRI, Philippines
34	IR 53	IRRI, Philippines
35	IR 54	IRRI, Philippines
36	IR 55	IRRI, Philippines
37	IR 56	IRRI, Philippines
38	IR 57	IRRI, Philippines
39	IR 58	IRRI, Philippines
40	IR 59	IRRI, Philippines
41	IR 60	IRRI, Philippines
42	IR 10198	IRRI, Philippines
43	IR 29723	IRRI, Philippines

S. No	Genotype	Source
Restorer Lines		
44	IR 40750	IRRI, Philippines
45	KMR 3	UAS, Mandya
46	NDR 3026	NDUAT,Faizabad
47	DR 714-1R	DRR, Hyderabad
48	BR 827-35	IRRI, Philippines
49	IR 24	IRRI, Philippines
50	IR 72	IRRI, Philippines
51	IR 66	IRRI, Philippines
52	C 20 R	TNAU,Coimbatore
53	MTU 9992	RARS ,Maruteru
54	619-2	DRR, Hyderabad
55	EPLT 109	DRR, Hyderabad
56	EPLT 104	DRR, Hyderabad
57	BCW 56	DRR, Hyderabad
58	RWC 15	DRR, Hyderabad
59	1005	DRR, Hyderabad
60	1096	DRR, Hyderabad
61	1190-2	DRR, Hyderabad
62	611-1	DRR, Hyderabad
63	PNR 3156	DRR, Hyderabad
64	GQ 37-1	DRR, Hyderabad
65	UPRI 92-133	GBPUAT,Pantnagar
66	SG 27-277	DRR, Hyderabad
67	IR 55178	IRRI, Philippines
68	TCNP 7444	DRR, Hyderabad
69	GQ 70	DRR, Hyderabad
70	SG 27-2	DRR, Hyderabad
71	SC5 9-3	DRR, Hyderabad
72	3699-2	DRR, Hyderabad
73	118	DRR, Hyderabad
74	IBL 57	DRR, Hyderabad
75	SG 27-77	DRR, Hyderabad
76	SG 27-175	DRR, Hyderabad
77	SG 17-118-3	DRR, Hyderabad
78	612-1	DRR, Hyderabad
79	GQ 25	DRR, Hyderabad
80	GQ 120	DRR, Hyderabad
81	124	DRR, Hyderabad
82	SC5 2-2-1	DRR, Hyderabad
83	TCP 8021	DRR, Hyderabad
84	SG 27-177	DRR, Hyderabad
85	517	DRR, Hyderabad
86	IR 64	IRRI, Philippines

characters. The mean values were subjected to analysis of variance and then to Mahalanobis[1] D^2 statistic to measure genetic divergence as suggested by Rao, (1952). The genotypes were grouped into various clusters following Toucher's method described by Rao, (1952).

RESULTS AND DISCUSSION

The analysis of variance revealed significant differences among the 86 genotypes for all the 13 traits, indicating the existence of genetic variability (Table 2). On the basis of relative magnitude of D^2 statistics, the 86 genotypes were grouped into ten clusters (Table 3). The maximum number of genotypes were included in the cluster IV (21 genotypes), whereas the clusters V and X had 3 genotypes each. Cluster IV included the genotypes from all the sources *i.e.,* IR 46, IR 66, IR 72, IR58, IR 48, IR 59, IR 47, IR 49, IR 54, IR 57, IR 55178, IR 64, IR 24 and IR 79156B from IRRI, Philippines; IR 40750, DRR 2B and DRR 11B from DRR, Hyderabad; PMS 10B from PAU, Kapurthala; PUSA 5B from IARI, New Delhi; NDR 3025 from NDUAT, Faizabad and MTU 9992 from RARS, Maruteru. Thus the pattern of distribution of genotypes from different geographical regions into different clusters was random, indicating that there is no correlation between clustering pattern and eco-geographical distribution of the genotypes. De and Rao (1987) reported that geographical diversity is not necessarily related to genetic diversity. Tendency of genotypes occurring in clusters across the geographical boundaries demonstrates that the geographical isolation is not the only factor causing genetic diversity in rice. Similarly, the forces other than geographical origin such as genetic drift, natural and artificial selection, exchange of breeding material might have played an important role in the diversity of genotypes. Variation in the environment could also be responsible for this diversity. Similar conclusions have been drawn by several workers *viz*, Bose and Pradhan (2005), Chand *et al*. (2005) and Chaturvedi and Maurya (2005) in rice.

Table 2. Analysis of variance for grain yield and yield attributes in rice.

Character	Mean Sum of Squares		
	Replications (d.f=2)	Treatments (d.f=85)	Error (d.f=170)
Days to 50% Flowering	13.14	193.10 **	6.11
Plant Height	120.75	554.84 **	14.02
Flag Leaf Length	3.76	33.63 **	6.77
Flag Leaf Width	0.09	0.20 **	0.01
Culm Length	94.04	451.57 **	11.14
Panicle Length	1.84	17.85 **	2.08
Productive tillers plant^{-1}	1.22	9.28 **	1.42
Panicle Weight	0.03	0.56 **	0.09
Filled grains panicle^{-1}	386.28	3405.18 **	178.87
Spikelet fertility %	6.72	30.06 **	12.38
1000 Seed Weight	0.56	30.40 **	1.04
Grain yield plant^{-1}	1.75	30.50 **	6.47
Productivity day^{-1}(kg ha^{-1})	2.81	153.92 **	28.09

*and ** significant at P=0.05 and 0.01 levels, respectively.

Table 3. Distribution of 86 rice genotypes in different clusters

Cluster No.	No. of genotypes	Genotypes
I	13	IR 40, IR 41, IR 42, IR 80155, IR 53, DR 714-1R, IR 45, UPRI 92-133, RWC 15, DRR 6B, IR 50, IR 10198, IR 44, SG 26-120
II	12	IR43, DRR 8B, DRR 10B, DRR 13B, CRMS 32B, GQ 25, DRR 14B, GQ 70, APMS 6B, IBL 57, GQ 120,1005
III	5	PMS 17B, DRR 15B, IR 68888B, IR68229B, IR 80151B
IV	21	IR 46, IR 66, IR 72, IR58, IR 40750, IR 48, DRR 11B,PMS 10B, DRR 2B, IR 59, MTU 9992, IR 47, IR 49, IR 54, IR 79156B, PUSA 5B, IR 57, NDR 3026, IR 55178, IR 64, IR 24
V	3	IR 58025B, IR 68897B, SC52-2-1
VI	7	IR 51, IR55, IR 52 , IR60 ,1190-2, IR 29723, BR827-35
VII	3	IR56, SG27-177, SG27-277
VIII	6	KMR3, 3699-2, 1096, SG27-2, BCW56, 612-1
IX	13	C20R, GQ 37-1, 619-2, 517, 611-1, PNR 3156, SG27-175, TCP 8021, SG27-77, 124, SG17-118-3, EPLT 104, SC5 9-3
X	3	EPLT 109, EPLT118, TCNP 7444

The intra and inter cluster divergence among the material studied was of varying magnitude (Table 4). Intra cluster D values ranged from 5.95 to 8.14. The

shortest intra cluster distance was shown by cluster X indicating the genotypes fall in this cluster *viz.,* EPLT 109, 118 and TCPN 7444 resembles one another and appeared to have evolved from a common genotype, while the maximum intra cluster distance of 8.14 was found in the cluster VII.

flag leaf width, number of filled grains panicle^{-1} and panicle weight; cluster I for early flowering, dwarfness, spikelet fertility percentage and productivity per day; cluster III for shortest culm length, productive tillers plant^{-1} and grain yield plant^{-1}; cluster VII for panicle length becomes obvious. These results indicate none

Table 4. Average intra (Diagonal) and inter cluster D^2 and D values of 86 genotypes in rice

	1 cluster	2 cluster	3 cluster	4 cluster	5 cluster	6 cluster	7 cluster	8 cluster	9 cluster	10cluster
1 cluster	57.97 (7.61)	167.38 (12.94)	115.32 (10.74)	97.02 (9.85)	153.77 (12.40)	176.48 (13.28)	313.01 (17.69)	281.78 (16.79)	181.71 (13.48)	321.34 (17.93)
2 cluster		58.78 (7.67)	90.18 (9.50)	106.32 (10.31)	99.56 (9.98)	143.31 (11.97)	131.02 (11.45)	156.06 (12.49)	111.31 (10.55)	171.83 (13.11)
3 cluster			40.82 (6.39)	83.07 (9.11)	146.35 (12.10)	150.65 (12.27)	219.78 (14.82)	235.11 (15.33)	169.17 (13.01)	279.23 (16.71)
4 cluster				43.47 (6.59)	85.962 (9.27)	67.06 (8.19)	190.91 (13.82)	139.72 (11.82)	101.73 (10.09)	203.36 (14.26)
5 cluster					36.34 (6.03)	105.81 (10.29)	178.84 (13.37)	137.86 (11.74)	104.68 (10.23)	122.20 (11.05)
6 cluster						44.74 (6.69)	153.11 (12.37)	83.07 (9.11)	82.54 (9.09)	168.37 (12.98)
7 cluster							66.31 (8.14)	100.82 (10.04)	101.15 (10.06)	162.23 (12.74)
8 cluster								48.29 (6.95)	75.60 (8.70)	160.09 (12.65)
9 cluster									57.97 (7.61)	125.32 (11.19)
10 cluster										35.42 (5.95)

The maximum inter cluster distance was observed between cluster I and cluster X followed by cluster I and cluster VII, indicating more genetic diversity between these two groups, while the lowest inter cluster distance was noticed between cluster IV and cluster VI suggesting close genetic relationship and similarity for most of the traits between genotypes of these two groups. The crosses involving genotypes from these clusters would give wider and desirable recombinants. Chand *et al*. (2005) and Chaturvedi and Maurya (2005) also recommended that the parents should be selected from two clusters having wider inter cluster distance to realize much variability and high heterotic effect.

Considerable differences in the cluster means were observed for almost all the characters (Table 5). The maximum cluster mean values were observed in the cluster VIII for flag leaf length; Cluster X for

of the clusters containing the genotypes with all the desirable characters for direct selection and exploitation. The characters contributing maximum to the divergence need greater emphasis for deciding on the clusters for purpose of further selection and choice of parents for hybridization. The highest contribution towards genetic diversity was obtained for plant height (29.90%) (Table 6). The other traits with descending consideration were 1000-seed weight, days to 50% flowering and number of filled grains panicle^{-1}. In contrast, the trait panicle length did not contribute towards total diversity. These results are in conformity with the earlier findings Madhavilatha *et al*. (2005) and Mundhe *et al*. (2006).

From the foregoing discussion, it is concluded that plant height, 1000 seed weight, days to 50% flowering and number of filled grains panicle^{-1} are the important traits contributing towards divergence and

Table 5. Cluster means from 86 genotypes of rice for yield attributes

Cluster Number	Days to 50% flowering	Plant height (cm)	Flag leaf length (cm)	Flag leaf width (cm)	Culm length (cm)	Panicle length (cm)	Productive tillers plant^{-1}	Panicle weight (cm)	Filled grains panicle^{-1}	Spikelet fertility %	1000seed weight (g)	Grain yield plant^{-1} (g)	Produ-ctivity day^{-1} (kg ha^{-1})
1 cluster	90.56	87.72	22.99	1.25	68.23	19.48	10.77	2.48	91.50	85.64	21.98	20.73	46.42
2 cluster	106.39	93.06	25.34	1.51	74.49	18.58	9.81	2.86	136.16	81.99	15.85	20.11	40.74
3 cluster	106.93	83.545	23.65	1.35	64.79	18.75	11.17	2.35	80.15	82.39	17.44	24.71	43.96
4 cluster	105.84	95.30	22.94	1.28	75.10	20.20	10.94	2.81	101.47	84.04	22.29	21.79	42.79
5 cluster	105.33	93.01	23.21	1.28	73.24	19.77	9.66	2.88	189.33	79.47	20.81	19.69	44.30
6 cluster	111.76	109.73	24.32	1.33	87.35	22.38	9.06	3.25	107.77	85.13	23.82	21.84	41.65
7 cluster	111.56	122.84	27.43	1.60	96.90	25.94	7.96	3.07	145.44	84.18	14.62	19.18	35.99
8 cluster	112.22	121.13	21.74	1.28	100.17	20.97	8.57	3.17	137.46	82.54	20.77	19.18	37.02
9 cluster	103.54	114.98	26.28	1.54	93.7	21.3	8.42	2.97	131.70	82.67	20.28	19.07	39.29
10 cluster	110.55	110.71	27.40	2.29	88.54	22.17	6.40	3.26	200.70	78.84	20.95	18.09	34.88

Table 6. Contribution of different characters towards genetic divergence in 86 genotypes of rice.

Cluster number	Times Ranked 1st	Contribution %
Days to 50% Flowering	752	20.57
Plant Height (cm)	1093	29.90
Flag Leaf Length (cm)	64	1.75
Flag Leaf Width (cm)	203	5.55
Culm Length (cm)	99	2.71
Panicle Length (cm)	0	0.00
Productive tillers plant^{-1}	27	0.74
Panicle Weight (g)	56	1.53
Filled grains panicle^{-1}	400	10.94
Spikelet fertility %	18	0.49
1000 Seed Weight (g)	837	22.90
Grain yield Plant^{-1} (g)	59	1.61
Productivity day^{-1} (kg ha^{-1})	47	1.29

for discriminating the genotypes. Based on the inter cluster distances, the genotypes IR 45 and SG 26-120 from cluster I, CRMS 32B, GQ 25, GQ 70, APMS 6B, IBL 57, GQ 120 and 1005 from cluster II, IR 79156B and PUSA 5B from cluster IV, IR 58025B and SC52-2-1 from cluster V, IR 55, IR60 and BR827-35S from cluster VI, SG27-77 from cluster VII, KMR3, 1096 and 612-1 from cluster VIII, GQ 37-1, 619-2, 517, 611-1, 124 and SC5 9-3 from cluster IX, EPLT 109 and 118 from cluster X were selected for hybridization programme as they are expected to produce high heterotic crosses. The five CMS lines *viz.*, IR 58025A, IR 79156A, APMS 6A, PUSA 5A, CRMS 32A and twenty three restorer parents *viz*., 1096, 1005, 619-2,612-1, 611-1, GQ-25, GQ-37-1, GQ-70, GQ-120, KMR-3, IBL-57, BR827-35, EPLT-109, SC_5 2-2-1, SC_5 9-3, SG27-77, SG26-120, 118, 124, 517, IR 43, IR55 and IR60 are may be used as female lines and male parents, respectively for hybridization.

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