Genetic Diversity Analysis in Exotic Hybrid Rice Genotypes Grown During Wet Season in Bangladesh

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Abstract

Two experiments were conducted with 43 IRRI developed F_1 hybrid rice genotypes (HRDC) for ten agronomic characters in a randomized complete block design to study the genetic diversity through multivariate analysis in Gazipur and Pabna districts, respectively during wet season 2013. On the basis of D^2 values, the genotypes were grouped into five different clusters. During wet season, cluster III comprised maximum number of genotypes (15). The data obtained across locations showed that there are significant differences among HRDC genotypes for all growth parameters, yield and yield components. The highest yield (5.65 t ha^{-1}) was observed in HRDC 1341 because of produced heaviest panicle (4.28 g) and the lowest (2.48 t ha^{-1}) in HRDC 1311 because of obtained lowest fertility (49.9 %) and 1000-grain wt. (12.9 g), respectively. The maximum inter-cluster distances were observed between cluster I and V (11.63) and the minimum between cluster III and IV (2.35). The highest intra-cluster distance (1.73) was observed in cluster III and minimum in cluster I (0.00), since it consisted with one genotype. Difference in cluster means existed for almost all the characters studied. Among the characters, growth duration, spikelet panicle^{-1}, fertility (%) and 1000-grain wt contributed the most for divergence in the genotypes. The highest mean values for fertility percentage, panicle weight and 1000 grain wt. but early flowering and short maturing genotypes were grouped into Cluster II followed by Cluster III and IV indicating that the genotypes have genetic potentiality to contribute better for yield maximization of hybrid rice.

Keywords: Genetic diversity, cluster, F_1 hybrid rice genotypes, multivariate analysis

1. Introduction

Production of rice (*Oryza sativa* L.) in Bangladesh has to be increased by at least 60% to meet up food requirement of the increasing population by the year 2020 (Masum, 2009). To achieve this target, rice yield should increase to 5.5 t ha^{-1} compared to 2.8 t ha^{-1} at present (Bhuiyan, 2002). But there is a little scope to increase rice area. Moreover, the arable land is decreasing at the rate of 1% per annum (BBS,

2011). The yield ceiling of modern rice varieties has been plateaued (Bhuiyan, 2002). Julfiquar *et al.* (2002) reported that hybrid rice is an alternative to break the present yield ceiling of semi-dwarf modern varieties in Bangladesh. Efforts aimed at breaking the yield barrier in rice have been amply demonstrated by Lanceras *et al.* (2004), Degenkolbe *et al.* (2009); Akhter *et al.* (2003) and Chen *et al.* (2009). It has been proved practically in China that hybrid rice has more than 20% yield advantage over improved inbred

varieties (Tiwari *et al*., 2011). In Bangladesh, hybrid rice gains positive response in dry season and a few varieties have been cultivated in wet season (Moinul and Biswas, 2011). The national average yield of rice in Bangladesh during the wet season is very low at around 2.29 t ha^{-1} (BBS, 2012), whereas it is 3.8 t ha^{-1} in south-east Asian country.

In Bangladesh, research and development of hybrid rice technology was initiated in 1993 with the introduction of rice hybrids and parent materials from International Rice Research Institute (IRRI). Peng *et al*. (2003) reported that the average yield of F_1 hybrid rice was 17% higher than that of *indica* inbred in the 1998 wet season. Significant emphasis is being given to comprehensive analysis of genetic diversity in numerous field crops and maximum exploitation of the genetic resources (Belaj *et al*., 2002). Hybrid Rice Research and Development Consortium (HRDC) were inaugurated in 2008 at IRRI to accelerate the adoption of the technology.

Keeping in view the above facts, a number of 43 IRRI developed hybrid rice genotypes were tested in two different agro-ecological zones of Bangladesh to estimate the nature and magnitude of genetic divergence and characters contributing to the genetic divergence of these genotypes during wet season.

2. Materials and Methods

2.1. Experimental Design and Treatments
On farm trials were conducted with 43 F_1 hybrid rice lines from IRRI along with popular BRAC hybrid Aloran, Shakti-2 and BRRI dhan39 (inbred) in two locations-BRAC Agricultural Research and Development Centre (BARDC), Gazipur and Dashuria Seed Farm, Pabna, respectively in a Randomized Complete Block Design (RCBD) with three replications during wet season of 2013. Each plot measures 4.0 meter long and 2.0 meter wide in BARDC and 3.8 meter long and 2.2 meter wide in Dashuria Seed Farm.

2.2. Crop establishment and management
Seedlings for each genotype were separated, labelled and these were bundled in convenient sizes. Seedlings of each genotype were transplanted in each designated plot. 23-26 days old seedlings of the genotypes were transplanted at one seedling per hill as a standard practice on a straight row at spacing of 20 cm x 20 cm. Gap filling was done a week after transplanting. Urea, TSP, MoP, Gypsum and $ZnSO_4$ fertilizer were applied at 180-80-70-60-10 kg ha^{-1}. The whole amount of TSP, Gypsum, two third of MoP and one third of urea were mixed and applied as basal application. $ZnSO_4$ was applied separately to avoid fixation with Phosphorus. The remaining urea was applied in two equal splits at maximum tillering stage and just before panicle initiation stage. The rest amount of MoP was applied before panicle initiation stage. Weeding was done two to three times and insecticides were applied as and when necessary to keep the fields free from insects-pests. All other recommended cultural management practices were followed to ensure good crop stand.

2.3. Measurements of Parameters
Three hills (excluding border hills) from each plot were selected and tagged after transplanting for taking yield and yield components data at harvest. Morphological data were collected for ten quantitative characters at the appropriate growth stage of rice plants following the description for *Oryza sativa* L. (IRRI, 2002). The crop was harvested at maturity; the weight of grains was adjusted to 14% moisture content. Plant height (cm), panicles no. m^{-2}, days to 50% flowering; growth duration (days), panicle length (cm), spikelet panicle^{-1}, panicle weight (g), spikelet fertility (%), 1000 grain weight (g) and grain yield (t ha^{-1}) were measured.

2.4. Data Analysis
The collected data were analyzed statistically following PCA and Mahalanobis (1936) generalized distance (D^2) extended by Euclidean and clustering by Ward's (1963) method. Statistical analysis was carried out using computer software STAR version 2.0.1 (2014).

3. Results and Discussion

The data obtained across locations showed that there are significant differences among HRDC genotypes for all growth parameters, yield and yield components (Table 1). The plant height (PH) ranges between 108 and 143 cm. Among the genotypes, the highest height of 143 cm was recorded in HRDC 1326 while the lowest, 108 cm in HRDC 1349. Shorter plant height is an important character of the hybrid to withstand lodging. The panicle no. m^{-2} (PM^{-2}) was significantly affected by genotypes which varied from 131 for HRDC 1340 to 239 for HRDC 1350. Days to 50% flowering (FD) and crop growth duration (CGD) was shortest in Shakti-2 and Aloran, taking 79 and 113 days, respectively while the longest in HRDC 1319, taking 102 and 128 days, respectively. The longest panicle (30.57 cm) was produced by HRDC 1326 while the shortest (24.5 cm) by HRDC 1313. The heaviest panicle (4.28 g) was produced by HRDC 1341 while the lightest (1.47 g) by HRDC 1349. Spikelet panicle^{-1} (SP^{-1}) is one of the most important yield components and probably this character will be helpful in breaking the yield plateau. Spikelet panicle^{-1} differs significantly among the tested genotypes. The highest Spikelet panicle^{-1} (272) was recorded in HRDC 1311 and the lowest (114) in HRDC 1343 and 1349, respectively. The highest fertility % (82.4) and 1000-grain wt. (28.85 g) was recorded in HRDC 1340 and 1313, respectively and the lowest (49.9% and 12.90 g) in HRDC 1311. Among the genotypes, the grain yield ranges between 2.48 and 5.65 t ha^{-1}. The highest yield was observed in HRDC 1341 because of produced heaviest panicle and the lowest in HRDC 1311 because of obtained lowest fertility (%) and 1000-grain wt., respectively.

On the basis of D^2 values, by the application of non-hierarchical clustering using covariance matrix, the 43 genotypes were grouped into five clusters (Table 2). Among five clusters, cluster III had the maximum genotypes (15) followed by

cluster V (13 genotypes) and the lowest was found from cluster I (1 genotype).

The inter-cluster distances in all the cases were greater than intra-cluster distances suggesting wider diversity among the genotypes of the distant groups (Table 3). Nayak *et al*. (2004) also found similar trends in rice. The intra-cluster degree of diversity was maximum in cluster III (1.73) indicating that the genotypes in cluster I was more heterogeneous and minimum in cluster I (0.00), since it consisted with one genotype. The maximum inter-cluster distances were observed between cluster I and V (11.63) followed by cluster I and III (10.86), cluster I and II (10.36), cluster II and V (8.46), and the minimum between cluster III and IV (2.35).

From Table 4, it is clearly observed that the highest mean values for fertility percentage, panicle weight and 1000 grain wt. but early flowering and short maturing genotypes were grouped into Cluster II followed by Cluster III and IV. Mean performance of different clusters also revealed that for number of plant height, days to 50% flowering, growth duration, panicle length, panicle weight, fertility (%) and 1000-grain wt., cluster I and cluster II were the most diverged genotype groups. Again, cluster II and V were most diverged for panicle no. m^{-2}, cluster III and IV for spikelet panicle^{-1} and cluster I and IV for grain yield.

Vector 1 obtained from PCA express that growth duration, spikelet panicle^{-1}, fertility (%) and 1000-grain wt. contributed to genetic divergence whereas in vector 2, plant height, panicle no. m^{-2}, spikelet panicle^{-1}, fertility (%) and 1000-grain wt. played important role in genetic divergence for having positive values (Table 5). Choudhury *et al*. (1999) also found that plant height contributed the highest for genetic divergence. Both the vectors had positive values for growth duration, spikelet panicle^{-1}, fertility (%) and 1000-grain wt indicating the highest contributions of these traits towards the divergence among F_1 hybrid rice genotypes.

Table 1. Mean performance of growth parameters, yield and yield components of HRDC genotypes during wet season over two locations

Genotypes	YIELD	PH	PM^{-2}	FD	CGD	PL	PW	SP^{-1}	FER%	TGW
HRDC 1301	5.10	134	167	95	125	29.7	2.75	183	67.6	22.78
HRDC 1303	4.11	132	218	94	121	28.4	2.27	184	59.3	20.55
HRDC 1304	4.22	139	174	94	120	30.1	2.53	174	66.5	22.47
HRDC 1305	4.83	131	168	97	126	30.4	2.68	160	69.9	24.40
HRDC 1306	4.67	137	177	92	122	27.2	2.82	168	66.1	25.70
HRDC 1307	4.12	122	152	88	117	27.8	2.23	207	53.7	20.85
HRDC 1308	4.16	132	156	94	122	28.6	2.60	177	65.7	22.32
HRDC 1309	4.61	130	172	91	122	29.1	2.58	206	67.4	19.55
HRDC 1310	5.02	140	179	96	124	28.1	2.47	173	65.3	22.05
HRDC 1311	2.48	138	164	94	121	30.3	1.75	272	49.9	12.90
HRDC 1312	4.79	134	203	96	126	26.2	2.47	171	65.0	21.57
HRDC 1313	4.63	118	164	84	114	24.5	2.98	151	68.0	28.85
HRDC 1314	4.57	142	167	93	119	27.3	2.85	199	71.2	20.23
HRDC 1315	4.22	122	163	92	119	28.4	2.35	166	60.1	24.53
HRDC 1316	4.05	133	156	87	114	27.3	2.65	190	60.3	23.28
HRDC 1317	3.67	125	138	80	113	27.0	2.57	171	65.4	23.25
HRDC 1318	3.88	125	201	100	124	27.1	2.45	193	69.0	18.87
HRDC 1319	4.18	130	199	102	128	24.8	2.18	170	63.8	19.83
HRDC 1324	4.38	140	157	94	122	29.3	2.30	165	61.0	23.10
HRDC 1325	4.64	136	185	88	116	28.5	2.57	158	68.8	24.15
HRDC 1326	4.20	143	198	91	119	30.5	1.95	171	52.1	21.50
HRDC 1327	4.16	125	163	82	119	27.3	2.10	131	62.8	25.27
HRDC 1328	4.55	124	165	91	121	26.5	2.40	154	62.6	25.47
HRDC 1329	4.17	124	168	91	121	25.7	2.75	173	59.7	26.38
HRDC 1330	5.13	130	162	93	120	26.1	2.50	199	61.8	21.17
HRDC 1331	3.78	127	161	91	118	28.9	2.75	208	68.5	20.05
HRDC 1332	4.66	126	170	91	119	30.1	2.30	197	59.8	19.70
HRDC 1333	4.30	136	158	90	118	29.1	2.63	211	57.1	21.95
HRDC 1334	3.91	117	197	88	116	26.0	2.22	162	60.4	23.55
HRDC 1335	5.06	137	194	86	114	27.2	2.20	157	62.5	22.98
HRDC 1336	4.13	127	170	80	116	25.7	2.68	172	66.8	23.07
HRDC 1338	4.97	139	199	91	120	27.6	2.58	177	60.8	24.63
HRDC 1339	4.77	131	211	91	120	29.3	2.22	139	64.5	25.07
HRDC 1340	4.63	116	131	82	115	25.9	3.63	172	82.4	26.80
HRDC 1341	5.65	131	160	87	115	25.8	4.28	208	78.1	26.40
HRDC 1342	3.78	113	214	81	118	27.7	1.95	150	54.9	23.88
HRDC 1343	5.32	124	225	94	124	28.6	2.02	114	72.6	24.43
HRDC 1347	3.26	123	200	89	122	28.3	2.17	154	54.7	24.78
HRDC 1349	2.86	108	161	80	117	25.5	1.47	114	53.4	23.97
HRDC 1350	2.99	124	239	85	119	27.0	1.80	138	53.2	24.73
Aloran	4.44	125	154	84	113	26.2	2.77	144	70.7	27.37

Continued										
BRRI dhan39	4.45	127	157	87	120	27.1	2.57	143	76.9	23.45
Shakti-2	3.99	134	145	79	114	25.0	3.22	196	64.0	25.63
$LSD_{0.05}$	1.38	7	40	10	12	0.45	0.78	33	12.59	0.93
MEAN	4.31	129	176	89	119	27.6	2.49	173	63.8	23.10
Minimum	2.48	108	131	79	113	24.5	1.47	114	49.9	12.90
Maximum	5.65	143	239	102	128	30.5	4.28	272	82.4	28.85

Legend: PH= Plant height, FD= Days to 50% flowering, CGD= Crop growth duration, PL= Panicle length, PW= Panicle weight, SP^{-1}= Spikelet $panicle^{-1}$, FER %= Fertility % and TGW= 1000-grain wt.

Table 2. Distribution of HRDC genotypes to different clusters as determined by multivariate analysis during wet season over two locations

Cluster	Serial No. of the genotypes	No. of genotypes	Name of genotypes
I	G10	1	HRDC 1311
II	G16 and G34	2	HRDC 1317 and HRDC 1340
III	G3, G4, G5, G9, G12, G14, G19, G20, G22, G23, G24, G31. G39, G41 and G42	15	HRDC 1304, HRDC 1305, HRDC 1306, HRDC 1310, HRDC 1313, HRDC 1315, HRDC 1324, HRDC 1325, HRDC 1327, HRDC 1328, HRDC 1329, HRDC 1336, HRDC 1349, Aloran and BRRI dhan39
IV	G1, G6, G7, G8, G13, G15, G25, G26, G27, G28, G35 and G43	12	HRDC 1301, HRDC 1307,HRDC 1308, HRDC 1309, HRDC 1314, HRDC 1316, HRDC 1330, HRDC 1331, HRDC 1332, HRDC 1333, HRDC 1341 and Shakti-2
V	G2, G11, G17, G18, G21, G29, G30, G32, G33, G36, G37, G38 and G40	13	HRDC 1303, HRDC 1312, HRDC 1318, HRDC 1319, HRDC 1326, HRDC 1334, HRDC 1335, HRDC 1338, HRDC 1339, HRDC 1342, HRDC 1343, HRDC 1347 and HRDC 1350

Table 3. Intra (bold) and inter-cluster distance (D^2) of HRDC genotypes during wet season over two locations

Cluster	I	II	III	IV	V
I	**0.00**				
II	10.36	**0.25**			
III	10.86	4.23	**1.73**		
IV	8.64	3.44	2.35	**0.82**	
V	11.63	8.46	4.34	5.50	**1.09**

Table 4. Cluster means for ten characters of HRDC genotypes during wet season over two locations

Traits	Clusters means				
	I	II	III	IV	V
Yield (t ha^{-1})	2.48	4.15	4.36	4.51	4.25
Plant height (cm)	138	120	128	131	129
Panicle no. m^{-2}	164	134	167	160	208
Days to 50% flowering	94	81	89	90	91
Growth duration (days)	121	114	119	119	121
Panicle length (cm)	30.33	26.45	27.41	27.93	27.63
Panicle weight (g)	1.75	3.10	2.50	2.78	2.19
Spikelet panicle^{-1}	198	171	156	272	160
Fertility (%)	49.97	73.98	65.28	64.64	61.02
1000-grain wt. (g)	12.90	25.03	24.68	22.80	21.99

Table 5. Relative contributions of the ten characters to the total divergence in HRDC genotypes during wet season over two locations

Traits	Vector 1	Vector 2
Yield (t ha^{-1})	-0.191	-0.3114
Plant height (cm)	-0.0106	0.0163
Panicle no. m^{-2}	-0.089	0.042
Days to 50% flowering	-0.1271	-0.1121
Growth duration (days)	0.1073	0.104
Panicle length (cm)	0.2524	-0.0843
Panicle weight (g)	-2.9262	-5.9803
Spikelet panicle^{-1}	0.0719	0.1342
Fertility (%)	0.1705	0.2118
1000-grain wt. (g)	0.3458	0.5889

Table 6. Eigen values and yield percent contribution of 10 characters of HRDC genotypes during wet season over two locations

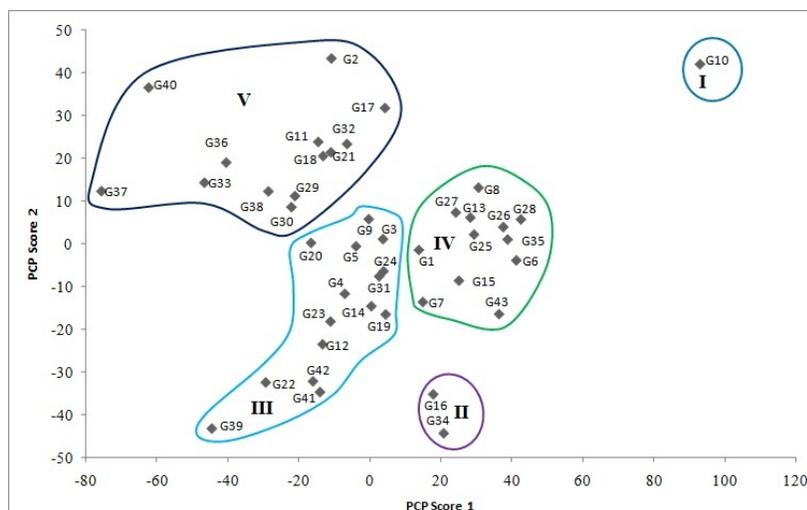| Principle component (PC)	Eigen values	Percent variation	Cumulative % of Percent variation
PC 1	1.7757	35.61	35.61
PC 2	1.6924	33.94	69.55
PC 3	0.7685	15.41	84.96
PC4	0.2751	5.52	90.48
PC 5	0.2202	4.42	94.90
PC 6	0.1056	2.12	97.02
PC 7	0.0765	1.53	98.55
PC 8	0.0614	1.23	99.78
PC 9	0.0082	0.17	99.95
PC 10	0.0025	0.05	100.00

Figure 1. Distribution of 43 genotypes of transplanted Aman rice in a two-dimensional Scatter diagram based on PCA scores superimposed with clusters

The PC 1 and 2 had 35.61% and 33.94% variability among the genotypes for the evaluated traits, respectively. Eigen values associated with each PC, decreased gradually and stopped at 0.0025 (Table 6). On the basis of the principal axes I and II, a two dimension scatter diagram was prepared showing the groups into five clusters of genotypes (Figure 1). The principal component analysis (PCA) showed that the first two components accounted for 69.55% of the total variation and a two dimensional scatter diagram was constructed using component 1 as X-axis and component 2 as Y-axis, reflecting the relative positions of the genotypes. The clustering pattern observed from D^2 analysis was also reflected by this diagram.

4. Conclusions

The overall results showed that Shakti-2 and Aloran was short maturing but the highest grain yield was observed in HRDC 1341 among the tested rice genotypes. Wider genetic diversity among the genotypes of the distant groups was observed. The genotypes under cluster IV gave the highest yield because of produced higher

spikelet panicle^{-1} than other clusters. The highest mean values for fertility percentage, panicle weight and 1000 grain wt. but early flowering and short maturing genotypes were grouped into Cluster II, III and IV. The genotypes under these clusters should therefore be selected, and their seed production feasibility in local condition should be studied before making final selection to submit in SCA trials as wet season hybrid in Bangladesh.

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