

GENETIC DIVERSITY, CHARACTER ASSOCIATION AND PATH
COEFFICIENT ANALYSIS OF EXOTIC RICE GENOTYPES (*Oryza sativa* L.)

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ABSTRACT

Fifty exotic rice genotypes along with two check varieties were studied to measure the variability among the genotypes for yield and yield contributing characters, estimate genetic parameters, association among the characters and their contribution to yield. High genotypic co-efficient of variation (GCV) was observed for days to 50% flowering, days to first flowering and spikelet sterility whereas low genotypic co-efficient of variation (GCV) was observed for grain length and filled grains per panicle. High heritability with high genetic advance in percent of mean was observed for days to 50% flowering and pollen sterility indicated that this trait was under additive gene control and selection for genetic improvement for this trait would be effective. On the other hand, high heritability with low genetic advance in percent of mean was observed in days to harvesting and grain length which indicated that non-additive gene effects were involved for the expression of this character and selection for such trait might not be rewarding. Correlation studies revealed that highest significant positive association of grain yield was with days to first flowering, days to harvesting, filled grains per panicle followed by grain length at genotypic and phenotypic level. Path co-efficient analysis revealed that maximum direct contribution towards grain yield with days to harvesting followed by filled grains per panicle.

Key words: Rice (*Oryza sativa* L.), genetic diversity, character association, path coefficient.

INTRODUCTION

Rice (*Oryza sativa* L.) is the staple food of about 135 million people of Bangladesh. It provides nearly 48% of rural employment, about two-third of total calorie supply and about one-half of the total protein intakes of an average person in the country. Rice sector contributes one-half of the agricultural GDP and one-sixth of the national income in Bangladesh. Over the last thousand years, rice has been the dominant crop in Bangladesh and it currently accounts for 77% of the total cropped area and over 80% of the total irrigated area. The country is also said to have among the highest per capita consumption of rice (about 170 kg annually), and its food security and economy largely depend on good harvests year after year. In Bangladesh, total rice production area is 115.29 lac ha and total production is 335.40 lac metric tons (BBS, 2010-11). The need for expansion of rice cultivation does not only depend on cultural practices and management, but also on the suitability of rice varieties, which must be drawn from

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existing germplasm that has been collected and conserved by genetic resources centers (Ng *et al.*, 1988). In Bangladesh considerable rice genetic diversity existed as one of the center of origin of rice. However, the diversity is narrowing down due to introduction and expansion of modern rice varieties. Evaluation of potential varieties should form an important constituent of these genotypes because of their in-built genetic variability due to several generations of growing and selection by breeders and farmers. However, the utilization of these rice genetic resources has been limited to only adaptable genotypes (Caldo *et al.*, 1996). A successful breeding program will depend on the genetic diversity of a crop for achieving the goals of improving the crop and producing high yielding and better resistant varieties (Padulosi, 1993). Considering the availability of genetic variability, its scope of yield improvement, the present investigation was undertaken to assess the genetic diversity among the genotypes and to search suitable diverse germplasm as suitable donor parents for the utilization in future breeding program.

MATERIALS AND METHODS

Fifty exotic genotypes and two varieties of rice, collected from Department of Genetics and Plant Breeding of Bangabandhu Sheikh Mujibur Rahman Agricultural University, Salna, Gazipur namely: RG-BU-08-051, RG-BU-08-052, RG-BU-08-053, RG-BU-08-054, RG-BU-08-055, RG-BU-08-056, RG-BU-08-057, RG-BU-08-058, RG-BU-08-059, RG-BU-08-060, RG-BU-08-061, RG-BU-08-062, RG-BU-08-063, RG-BU-08-064, RG-BU-08-065, RG-BU-08-066, RG-BU-08-067, RG-BU-08-068, RG-BU-08-069, RG-BU-08-070, RG-BU-08-071, RG-BU-08-072, RG-BU-08-073, RG-BU-08-074, RG-BU-08-075, RG-BU-08-076, RG-BU-08-077, RG-BU-08-078, RG-BU-08-079, RG-BU-08-080, RG-BU-08-081, RG-BU-08-082, RG-BU-08-083, RG-BU-08-084, RG-BU-08-085, RG-BU-08-086, RG-BU-08-087, RG-BU-08-088, RG-BU-08-089, RG-BU-08-090, RG-BU-08-091, RG-BU-08-092, RG-BU-08-093, RG-BU-08-094, RG-BU-08-095, RG-BU-08-096, RG-BU-08-097, RG-BU-08-098, RG-BU-08-099, RG-BU-08-100, BRR1 dhan28 and BRR1 dhan29 were grown at the experimental farm of Bangabandhu Sheikh Mujibur Rahman Agricultural University, Salna, Gazipur following randomized block design with three replications during December 2008 to May 2009.

The field was divided into three blocks, the blocks were subdivided into 52 plots where genotypes were randomly assigned. The unit plot size was 12.5m × 2.5m. Each plot had two lines. Row to row and plant to plant distances were 25cm and 20cm respectively. Data were recorded for days to first flowering (DFF), days to 50% flowering (50% DF), days to harvesting (DH), pollen sterility (PS), spikelet sterility (SS), filled grains per panicle (FGP), unfilled grains per panicle (UGP), grain length (GL), grain breadth (GB) and grain yield per hill (GYH). Genotypic and phenotypic coefficients of variation were computed according to Burton (1952). The broad sense heritability (h^2_b) and genetic advance as percentage of means were calculated as suggested by Johnson *et al.* (1955). Genotypic and phenotypic correlation coefficients were calculated according to Miller *et al.* (1958) and path coefficient analysis was performed according to method suggested by Dewey and Lu (1959).

RESULTS AND DISCUSSION

The estimates of mean, range, genotypic (GCV) and phenotypic coefficients of variation (PCV), heritability (h^2_b) and genetic advance (GA) as percentage of mean for 10 characters are given in Table 1. The range of variation was much pronounced in most of the characters. The lowest and the highest range of variation were observed in GB and FGP, respectively. The narrow difference between PCV and GCV supported the idea that

environmental effect was less on characters under the present study. The highest and lowest GCV were found in 50%DF and GL, respectively. Heritability estimates in broad sense (h^2b) were relatively higher for all most all the characters studied. High heritability estimates have been found to be very effective for superior genotype selection on the basis of phenotypic performance. Kumar *et al.* (2006) reported that traits exhibiting high heritability along with high to moderate genetic advance suggesting that these characters could be of high importance for selecting better genotypes in rice improvement programme. High values of heritability together with high genetic advance (GA) as percentage of mean were obtained for 50%DF and PS suggesting selection for these characters would give better response. Souroush *et al.* (2005) and Dorosti *et al.* (2004) found the similar results in rice. The results also had close agreement with the findings of Hossain and Haque (2003) and Iftekharuddaula *et al.* (2001).

Table 1. Estimation of genetic parameters of yield and yield contributing characters of 50 exotic rice with 2 check varieties (*Oryza sativa* L.)

Parameters	Range	Mean	GCV (%)	PCV (%)	h^2b (%)	GA (%) of mean
DFF	74.00-98.00	81.85	61.29	66.69	65.89	58.97
50% DF	81.00-103.67	91.25	70.55	75.26	68.55	67.01
DH	111.00-124.00	116.78	45.19	46.95	72.28	17.56
PS	0.133-99.87	36.35	45.74	48.44	69.56	56.88
SS	6.55-53.05	27.74	60.22	74.08	51.55	33.68
FGP	29.00-197.93	103.71	26.91	46.82	25.77	06.04
UGP	5.73-102.33	40.75	30.65	33.35	32.95	37.78
GL	6.27-14.05	9.18	18.07	19.74	65.35	03.90
GB	2.02-4.33	2.90	28.06	31.78	60.82	16.85
GYH	7.82-38.91	26.46	29.35	32.56	46.89	29.69

DFF= days to first flowering, 50% DF= days to 50% flowering, DH= days to harvesting, PS= pollen sterility, SS= spikelet sterility, FGP= filled grains per panicle, UGP= unfilled grains per panicle, GL= grain length, GB= grain breadth and GYH= grain yield per hill

Character Association

Character association analysis among the traits under study of rice (Table 2) revealed that the genotypic correlation coefficients in most of the cases were higher than their corresponding phenotypic correlation coefficients indicating the effects of environment suppressed the phenotypic relationship between these characters. Accordingly, Bai *et al.* (1992) reported that the genotypic correlations were greater than the phenotypic values in medium durated rice varieties. Grain yield was found positive and highly significant association with filled grain per panicle and grain length both at genotypic and phenotypic levels. Similar associations in rice were also reported by Manuel and Palanisamy (1989) and Kennedy and Rangasamy (1998).

Unfilled grains per panicle and spikelet sterility (%) had significant and negative association with grain yield per hill at both genotypic and phenotypic level. Also, grain length showed highly significant and negative correlation with filled grains per panicle at both genotypic and phenotypic level. Similar associations in rice were also reported by Ogunbayo *et al.* (2005).

Path Analysis

Partitioning of genotypic correlations of different genotypes of rice are shown in Table 3. DH had maximum positive direct effect on yield followed by FGP. The direct effect revealed that the characters viz., DH and FGP having high positive correlation with GYH, also had direct positive influence with GYH, suggesting thereby, good scope for the improvement of grain yield by selecting plant types bearing higher days to

harvesting in combination with high FGP. The residual effect of the present study was 0.741 indicating 26% of the variability of grain yield per hill was contributed by the ten characters studied in the path analysis. Similar findings (R=0.766) was found by Mojumder (2009).

Table 2. Genotypic and phenotypic correlations among different characters of 50 exotic rice with two check varieties (*Oryza sativa* L.)

Parameters		50% DF	DH	PS	SS	FGP	UGP	GL	GB	GYH
DFF	r _g	0.49*	0.98**	0.88**	0.52*	0.76**	-0.53*	-0.78**	0.45*	0.82**
	r _p	0.42*	0.87**	0.84**	0.45*	0.73**	-0.64**	-0.74**	0.37*	0.76**
50% DF	r _g		0.54*	0.48*	0.28	0.41*	-0.35	-0.42*	0.24	0.60*
	r _p		0.47*	0.46*	0.25	0.40*	-0.29	-0.40*	0.20	0.42**
DH	r _g			0.95**	0.49*	0.83**	-0.70*	-0.85**	0.48*	1.06**
	r _p			0.92**	0.56*	0.79**	-0.58**	-0.80**	0.41*	0.83**
PS	r _g				0.54*	0.80**	-0.56*	-0.78**	0.47*	-0.80**
	r _p				0.48*	0.76**	-0.67**	-0.82**	0.39*	-1.05**
SS	r _g					-0.41*	0.66**	-0.44*	0.25	-0.41*
	r _p					-0.43*	0.60**	-0.42*	0.21	-0.43*
FGP	r _g						-0.58*	-0.71**	0.40	0.69**
	r _p						-0.48*	-0.67**	0.34*	0.67**
UGP	r _g							0.52*	-0.30	-0.75*
	r _p							0.49*	-0.25	-0.51*
GL	r _g								0.41	0.76**
	r _p								0.34*	0.70**
GB	r _g									0.36
	r _p									0.34

DFF= days to first flowering, 50% DF= days to 50% flowering, DH= days to harvesting, PS= pollen sterility, SS= spikelet sterility, FGP= filled grains per panicle, UGP= unfilled grains per panicle, GL= grain length, GB= grain breadth and GYH= grain yield per hill

Table 3. Path Partitioning of genotypic correlation with grain yield into direct (bold) and indirect effect in 50 exotic rice genotypes with two check varieties

	DFF	50% DF	DH	PS (%)	SS (%)	FGP	UGP	GL	GB	r _g with yield
DFF	-0.809	0.440	0.880	0.851	0.457	0.732	-0.537	-0.743	0.377	0.769
50%DF	0.440	0.239	0.478	0.463	0.249	0.398	-0.292	-0.404	0.205	0.418
DH	0.880	0.478	0.956	0.925	0.497	0.796	-0.583	-0.808	0.410	0.836
PS (%)	0.851	0.463	0.925	-0.895	0.481	0.770	-0.564	-0.782	0.396	0.809
SS (%)	0.457	0.249	0.497	0.481	-0.259	0.414	-0.303	-0.420	0.213	0.435
FGP	0.732	0.398	0.796	0.770	0.414	0.662	-0.485	-0.672	0.341	0.696
UGP	-0.537	-0.292	-0.583	-0.564	-0.303	-0.485	0.356	0.493	-0.250	-0.510
GL	-0.743	-0.404	-0.808	-0.782	-0.420	-0.672	0.493	-0.683	-0.346	-0.706
GB	0.377	0.205	0.410	0.396	0.213	0.341	-0.250	-0.346	0.175	0.358

DFF= days to first flowering, 50% DF= days to 50% flowering, DH= days to harvesting, PS= pollen sterility, SS= spikelet sterility, FGP= filled grains per panicle, UGP= unfilled grains per panicle, GL= grain length, GB= grain breadth and GYH= grain yield per hill

High heritability and GA was observed in 50%DF and PS along with moderate heritability with moderate genetic advance in UGP and SS suggested that these characters could be transmitted to the hybrid progeny and phenotypic selection based on these would be effective. Correlation and path coefficient analysis suggested that during selection more emphasis should be given on DH, FGP and UGP since these characters have high positive correlation and high direct effect on grain yield.

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