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Genetic Variability and Inter-relationship between Yield and Yield Components in Jhum Rice (*Oryza sativa* L.) Genotypes of Khagrachhari District in Bangladesh

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Abstract

The present investigation consists of 47 rice genotypes and the experiment was conducted during Aus season, 2016 in Randomized Block Design with three replications. The data were recorded for 13 quantitative characters to study genetic variability, heritability, genetic advance, correlation coefficient analysis and path analysis. Analysis of variance among 47 genotypes showed a significant difference for all characters studied. The highest genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were observed for grain yield followed by the number of effective tillers, the number of filled grains per panicle and 1000 grain weight indicating that these characters could be used in selection for the crop improvement program. High estimates of heritability was observed for grain yield, grain length, plant height, number of filled grain per panicle, 1000 grain weight and days to 50% flowering. High genetic advance was observed for the number of filled grains per panicle and plant height, indicating predominance of additive gene effects and possibilities of effective selection for the improvement of these traits. Grain yield showed positive association with number of effective tiller and number of filled grain per panicle at genotypic in conjunction with phenotypic level. Days to maturity possessed the highest positive direct effect and significant indirect correlation with yield.

Keywords: Genetic variability, heritability, path co-efficient and rice (*Oryza sativa* L.)

1. Introduction

Rice is a major food source for more than half of the world's population. Rice is also the major crop of Bangladesh. This crop plays an important role in feeding the huge population of the small country. Rice yield improvement is a priority to meet its rising demand owing to a constant increase in population. Considering this context, assessment of variability in rice crop for grain yield and yield attributes is essential for successful exploitation and improvement of yield through effective breeding.

Jhum rice is a unique kind of plant genetic resource which is cultivated through hilly areas of Bangladesh. The local farmers usually grow low yielding local landraces. More than 300 local jhum rice landraces have been collected from various hilly districts of Bangladesh and conserved in Bangladesh Rice Research Institute (BRRI) genebank (Islam *et al.*, 2017). Further, grain yield depends on various component characters and knowledge of correlations among yield component traits and yield is of great importance in the selection of elite genotypes for breeding program. Path analysis also helps in determining the direct and indirect causes of association and formulation of effective breeding strategies for the development of better genotypes (Sameera *et al.*, 2016).

The existence of variability in germplasm provides the basis for selection of elite germplasm that may be used either as an end product in form of improved variety or can be used as starting material in several breeding program intended to accomplish diverse objectives (Singh *et al.*, 2017). Genetic parameters such as GCV and PCV are the extent of genetic variation present in germplasm and the extent to which genotype is influenced by the environment. Heritability along with genetic advance reflects the reliability of the transmission of trait variation to the next generation. Genotypic correlation among grain quality trait is an indicator of stable association between traits and helps in indirect selection.

2. Materials and Methods

2.1 Plant materials, experimental site and experimental design

Forty seven jhum rice genotypes were collected from Khagrachhari district of Bangladesh were grown under during Aus seaon 2016. The experiment was conducted following a Randomized Complete Block design with three replicates for each treatment at the experimental field of BRRI, Gazipur. Geographically, the place is located at about 23° 59′ 35.8″ N latitude and E 90.24′ 27″ E longitude with an elevation of 15 meters from the sea level and is characterized by subtropical climate. The soil of the experimental site was clay loam in texture.

2.2 Transplantation and management practices

Twenty days-old seedlings from each entry were transplanted using single seedling per hill in 2.4 m^2 plot with 25cm and 20cm space between rows and plants, respectively. Fertilizers were applied @ 80:60:40:12 kg N: P: K: S h^{-1}. However, except N, the other fertilizers were applied at final land preparation. Nitrogen was applied in three equal splits, at 15 days after transplanting (DAT), at 35 DAT, and just before flowering. Intercultural operations and pest control measures were performed as and when necessary.

2.3 Data collection

Five plants were randomly selected and were evaluated for yield and its component traits. The traits studied were: Flag leaf length (cm), flag leaf width (cm), culm diameter (mm), panicle length (cm), plant height (cm), days to flowering, days to maturity, effective tiller number (ET), panicle length (cm), 1000 grain weight (g), number of filled grains per panicle, grain length (mm), grain breadth (mm), and yield per hill (g) for 47 samples collected from different areas of Khagrachari (Table 1).

2.4 Statistical analysis

Genotypic and phenotypic co-efficient of variation were calculated following the methodology delineated by Burton (1952), while the estimates of heritability and genetic advance were computed as per the procedures elaborated by Burton and Devane (1953) and Johnson *et al.* (1955), respectively. Normal Pearson's correlation and path coefficient analysis was undertaken using R software (version 3.2.1). Furthermore, genotypic and phenotypic correlation co-efficients were calculated with Multi Environment Trait Analysis with R (META-R) software.

3. Results and Discussion

Information on mean, range, PCV, GCV, heritability, genetic advance and genetic, advance in percent of mean for yield and yield component traits are presented in Table 2. The relative values of genotypic and phenotypic coefficient of variation provide important information on the magnitude of variation. Higher phenotypic co-efficient of variation compared to genotypic co-efficient of variation was recorded for all the traits studied in the present investigation, indicating the influence of the environment. Similar findings were reported earlier by Islam *et al.* (2016) and Aker *et al.* (2018a).

A wide range of phenotypic coefficient of variation (5.74% - 32.77%) and genotypic coefficient of variation (5.68% - 30.76%) was observed for the traits studied. Besides, highest (32.77%) phenotypic co-efficient of variation for grain yield in the present investigation was noticed to be closely and essentially associated with high genotypic co-efficient of variation for the trait, demonstrating the little influence of environment and presence of high genetic variability for the trait in the experimental material. Hence, selection on the basis of phenotype in these genotypes can also be effective for the improvement of grain yield. Similar results were reported earlier by Mishra and Verma (2002).However, moderate (16-30%) genotypic and phenotypic coefficients of variation were recorded in the present study for 1000 grain weight, number of filled grains per panicle and number of effective tiller. These results are in partial conformity with the findings of Bornare *et al*. (2014) for no. of effective tiller and 1000 grain weight. In contrast, low (<10%) estimates of genotypic and phenotypic coefficients of variation were observed in the present study for plant height, panicle length, days to 50% flowering and days to maturity indicating low variability for these characters in the present experimental material and therefore little scope for improvement of these traits.

Table 1. Information on local name and place of collection of 47 Jhum rice genotypes

Sl. No.	Genotypes	District	Sl. No.	Genotypes	District
1	Kamarang (gol)	Khagrachhari	25	Maloty	Khagrachhari
2	Binnidhan	Khagrachhari	26	Binni Dhan	Khagrachhari
3	Asasuri	Khagrachhari	27	Kotoktara	Khagrachhari
4	Banor binni	Khagrachhari	28	Cholokka binni	Khagrachhari
5	Company (boro)	Khagrachhari	29	Kuttosa binni	Khagrachhari
6	Choroi (sada)	Khagrachhari	30	Galon (sada)	Khagrachhari
7	Suri dhan	Khagrachhari	31	Ameo	Khagrachhari
8	Company (gol)	Khagrachhari	32	Chamaful	Khagrachhari
9	Bodakusum	Khagrachhari	33	Churi dhan (sada)	Khagrachhari
10	Jakton binni	Khagrachhari	34	Binni dhan	Khagrachhari
11	Kainchole	Khagrachhari	35	Galon (Red)	Khagrachhari
12	Binnidhan(lal)	Khagrachhari	36	Wasa	Khagrachhari
13	Longapura binni	Khagrachhari	37	Galon (Red)	Khagrachhari
14	Mala Dhan	Khagrachhari	38	Full badam	Khagrachhari
15	Choroi (lal)	Khagrachhari	39	Mashusai mokom	Khagrachhari
16	Pidi	Khagrachhari	40	Solai	Khagrachhari
17	Galon (lal)	Khagrachhari	41	Nola binni	Khagrachhari
18	Binni (sada)	Khagrachhari	42	Ameosori	Khagrachhari
19	Kamarang	Khagrachhari	43	Badia	Khagrachhari
20	Galon (gol)	Khagrachhari	44	Shailangma	Khagrachhari
21	Modhu maloty	Khagrachhari	45	Kamarang	Khagrachhari
22	Koborok	Khagrachhari	46	Mongshe	Khagrachhari
23	Hori binni	Khagrachhari	47	Ameo dhan	Khagrachhari
24	Company	Khagrachhari			

Similar findings were reported earlier by Akter *et al.* (2018b) for panicle length, days to 50% flowering and days to maturity. High (>90%) estimates of heritability were recorded for all the traits studied excluding flag leaf length, culm diameter, panicle length and number of effective tiller in the present investigation (Table 2). Similar findings were reported earlier by Islam *et al.* (2018) and Islam *et al*. (2019).

These results are in conformity with the reports of Idris *et al*. (2013) for 1000-seed weight and plant height; Bisne *et al*. (2009) for ear bearing tillers per hill; Dhanwani *et al*. (2013) for days to 50 per cent flowering; Chakrabarty *et al*. (2019) for filled grains per panicle and Kundu *et al.* (2008) for grain yield per plant. A perusal of the results on genetic advance revealed the highest value (40.13%) on number of filled grain per panicle, moderate value (>10%) for plant height. The estimation of genetic advance in per cent of mean was also high (>20%) for number of effective tiller, number of filled grains per panicle, 1000 grain weight, grain length and grain yield. These results are in conformity with the findings of Babu *et al.* (2012) for the number of filled grains per panicle; and Dhanwani *et al.* (2013) for 1000 grain weight and grain yield per plant. Further, low (<5%) estimates of genetic advance were recorded in the present investigation for flag leaf width, culm diameter, panicle length, number of effective tiller, grain length, grain breadth and yield.

Table 2. Estimation of genetic parameters of different quantitative characters in 47 Jhum rice landraces

Character	Mean	Range	V_p	V_g	PCV	GCV	h^2_b	GA (5%)	GAPM
FLL	41.88	27.00-58.00	26.76	22.51	12.35	11.33	84.10	6.87	16.41
FLW	1.80	1.20-2.40	0.07	0.05	13.25	12.65	90.23	1.34	19.10
CD	4.91	3.38-6.10	0.49	0.37	13.23	12.47	88.85	0.91	18.58
PL	28.79	23.20-35.60	5.75	4.06	7.57	7.00	85.43	2.94	10.22
PH	121.44	94.00-147.00	95.91	94.26	9.02	7.99	91.31	15.29	12.59
DF	92.22	75.00-116.00	45.62	44.84	7.32	7.26	93.30	9.49	11.38
DM	118.52	103.00-145.00	46.35	45.36	5.74	5.68	91.86	8.53	8.88
ET	6.45	2.00-14.00	5.05	4.83	28.14	27.44	86.35	1.74	48.06
TGW	22.30	12.85-31.60	18.78	18.39	17.40	17.21	90.30	7.41	33.23
FG	117.83	47.60-189.00	1119.48	1103.88	28.40	26.20	94.61	40.13	37.24
GL	8.79	6.45-11.68	1.46	1.35	14.74	13.70	95.45	1.90	21.59
GB	3.04	2.32-3.84	0.15	0.12	11.54	11.16	93.50	0.52	17.05
Y	5.90	2.19-12.30	6.36	6.23	32.77	30.76	91.97	3.98	47.55

V_p= Phenotypic variance, V_g =Genotypic variance, PCV = Phenotypic coefficient of variation, GCV = Genotypic coefficient of variation, h^2_b = Heritability (Broad sense), GA = Genetic advance, GAPM = Genetic advance in per cent of mean

(FLL= Flag leaf length, FLW= Flag leaf width, CD= Culm diameter, PL= Panicle length, PH=Plant height, DF= Days to 50% flowering, DM=Days to maturity, ET= Number of effective tiller, TGW=Thousand grain weight, FG= Number of filled grains per panicle, GL= Grain length, GB=Grain breadth, Y=Yield per hill)

Low (<15%) estimates of genetic advance in per cent of mean were also noticed for panicle length, plant height, days to 50% flowering and days to maturity in the present investigation. These results are in conformity with the findings of Seyoum *et al.* (2012). High heritability coupled with high genetic advance in per cent of mean was recorded for grain yield, number of filled grain per panicle, number of effective tiller and 1000 grain weight indicating that the high heritability observed due to additive gene effects and selection may be effective for these characters. Similar observations were reported by Adilakshmi and Girijarani (2012) for 1000-seed weight and Madhavilatha *et al.* (2005) for grain yield per plant.

Further, information on genetic variation along with heritability and genetic advance estimates has been reported to give a better idea about the efficiency of selection (Burton, 1952). In the present study, high GCV and PCV coupled with high heritability and high genetic advance in per cent of mean were observed for grain yield indicating the pre-ponderance of additive gene action and therefore scope for improvement of the trait through selection. Similar results were reported earlier by Mohana Krishna *et al.* (2009).

The genotypic and phenotypic correlations for yield and yield components are showed in Table 3. Flag leaf width possessed positive association with culm diameter. Panicle length showed a highly significant and positive correlation with plant height (Rangare *et al*., 2012) both at genotypic and phenotypic levels. Moreover, days to 50% flowering had a highly significant positive correlation with culm diameter. Days to maturity also showed a significant positive correlation with culm diameter and days to 50% flowering. Furthermore, the number of effective tiller showed a negative association with flag leaf width, culm diameter, days to 50% flowering and days to maturity at genotypic as well as phenotypic level but showed positive association with plant height at the genotypic and phenotypic level. Grain breadth has a negative but significant association with both days to 50% flowering and days to maturity; however, it showed a positive significant association with 1000 grain weight. In connection to that, 1000 grain weight possessed a negative correlation with the number of filled grains per panicle but had a positive significant association with grain length and grain breadth. The number of effective tiller and number of filled grain per panicle showed significant positive correlation with yield, but negatively significant association with grain length at genotypic along with phenotypic level. Hence, the number of effective tiller and filled grain per panicle should be given prior attention in rice improvement program because of their major influence on yield. This finding was in accordance with Hasan *et al.* (2010), Manikyaminnie *et al.* (2013), Sudharani *et al.* (2013), Idris *et al.* (2013) and Adilakshmi and Girijarani (2012).

Path coefficient analysis was done to partition the direct and indirect effects of different yield contributing traits on the yield of rice. Path coefficient analysis (Table 4) revealed that days to maturity possessed the highest positive direct effect on the yield that also made the indirect effect positive and significant. Grain length had a higher negative direct effect on yield, which also had negative indirect effect on total correlation. Moreover, the negative direct effect was observed for flag leaf width, days to flowering, effective tiller and plant height. On the other hand, the number of filled grains per panicle, 1000 grain weight and panicle length exhibited positive direct effect along with a positive correlation with yield.

The residual effect of the present study was 0.560 which indicated that 56% of the variability was accounted for 13 yield contributing traits included in the present investigation. The rest amount of variability might be controlled by other yield contributing traits that were not considered in the present study.

Table 3. Genotypic (rg) and phenotypic (rp) correlations among yield and yield contributing characters in Jhum rice genotypes

Traits		FLL	FLW	CD	PL	PH	DF	DM	ET	TGW	FG	GL	GB
FLW	rg	0.167											
	rp	0.137											
CD	rg	0.247	0.284*										
	rp	0.244	0.301*										
PL	rg	0.037	0.007	-0.165									
	rp	0.060	0.062	-0.185									
PH	rg	-0.098	-0.051	-0.143	0.632**								
	rp	-0.085	-0.032	-0.147	0.618**								
DF	rg	0.159	0.022	0.372**	0.019	0.052							
	rp	0.152	0.014	0.366**	0.027	0.055							
DM	rg	0.163	-0.021	0.319*	-0.018	0.009	0.980**						
	rp	0.156	-0.033	0.317*	-0.006	0.013	0.977**						
ET	rg	-0.153	-0.434**	-0.376**	0.147	0.340**	-0.340**	-0.350**					
	rp	-0.139	-0.424**	-0.365**	0.128	0.335**	-0.337**	-0.345**					
TGW	rg	-0.155	0.221	-0.178	-0.030	-0.307*	-0.271	-0.275	-0.221				
	rp	-0.155	0.211	-0.172	-0.015	-0.303*	-0.273	-0.278*	-0.216				
FG	rg	-0.013	-0.192	0.199	0.253	0.265	0.270	0.228	0.068	-0.377**			
	rp	-0.004	-0.176	0.187	0.232	0.259	0.273	0.232	0.062	-0.373**			
GL	rg	0.133	0.148	0.078	-0.161	-0.277*	0.046	0.055	-0.234	0.532**	-0.467**		
	rp	0.114	0.116	0.088	-0.123	-0.267	0.041	0.047	-0.227	0.529**	-0.459**		
GB	rg	-0.130	0.336*	-0.081	0.104	-0.108	-0.544**	-0.554**	-0.022	0.596**	-0.214	0.079	
	rp	-0.119	0.321*	-0.067	0.111	-0.104	-0.547**	-0.547**	-0.021	0.586**	-0.210	0.074	
Y	rg	-0.031	-0.274	-0.092	0.220	0.110	0.051	0.075	0.640**	-0.165	0.439**	-0.523**	0.012
	rp	-0.007	-0.235	-0.108	0.168	0.094	0.087	0.087	0.530**	-0.156	0.432**	-0.507**	0.019

*, **Significant at 5% and 1% levels, respectively

(FLL= Flag leaf length, FLW= Flag leaf width, CD= Culm diameter, PL= Panicle length, PH=Plant height, DF= Days to 50% flowering, DM=Days to maturity, ET= Number of effective tiller, TGW=Thousand grain weight, FG= Number of filled grains per panicle, GL= Grain length, GB=Grain breadth, Y= Yield per hill)

Table 4. Partitioning of genotypic correlation into direct (bold phase) and indirect components of 47 genotypes of jhum rice

	FLL	FLW	CD	PL	PH	DF	DM	ET	TGW	FG	GL	GB	Y
FLL	**0.074**	-0.030	-0.008	0.002	0.006	-0.067	0.088	0.009	-0.027	-0.003	-0.063	-0.009	-0.029
FLW	0.010	**-0.226**	-0.010	0.002	0.003	-0.009	-0.013	0.025	0.043	-0.044	-0.072	0.030	-0.260
CD	0.017	-0.062	**-0.035**	-0.018	0.009	-0.155	0.170	0.020	-0.034	0.043	-0.038	-0.005	-0.087
PL	0.001	-0.004	0.005	**0.127**	-0.040	-0.007	-0.009	-0.010	-0.004	0.056	0.078	0.009	0.200
PH	-0.006	0.009	0.004	0.075	**-0.068**	-0.023	0.005	-0.023	-0.060	0.064	0.143	-0.011	0.109
DF	0.011	-0.004	-0.012	0.002	-0.004	**-0.451**	0.552	0.022	-0.053	0.065	-0.023	-0.054	0.050
DM	0.011	0.005	-0.010	-0.002	-0.001	-0.438	**0.568**	0.022	-0.055	0.055	-0.027	-0.054	0.740**
ET	-0.010	0.085	0.010	0.019	-0.023	0.145	-0.187	**-0.068**	-0.040	0.015	0.116	-0.003	0.060
TGW	-0.010	-0.048	0.006	-0.003	0.021	0.121	-0.155	0.014	**0.200**	-0.091	-0.275	0.059	-0.163
FG	-0.001	0.041	-0.006	0.029	-0.018	-0.120	0.128	-0.004	-0.075	**0.243**	0.242	-0.022	0.436*
GL	0.009	-0.031	-0.002	-0.019	0.019	-0.020	0.030	0.015	0.105	-0.112	**-0.522**	0.008	-0.522**
GB	-0.006	-0.066	0.002	0.011	0.007	0.234	-0.298	0.002	0.113	-0.051	-0.041	**0.103**	0.010

Residual Effect = 0.560

*, **Significant at 5% and 1% levels, respectively

(FLL= Flag leaf length, FLW= Flag leaf width, CD= Culm diameter, PL= Panicle length, PH=Plant height, DF= Days to 50% flowering, DM=Days to maturity, ET= Number of effective tiller, TGW=Thousand grain weight, FG= Number of filled grains per panicle, GL= Grain length, GB=Grain breadth, Y= Yield per hill)

4. Conclusions

The presence of genetic variability in a crop is an utmost prerequisite for the improvement of economically important traits like yield in rice. From this study, we conclude that the jhum rice possessed sufficient amounts of variability for yield and its associated traits. The traits number of filled grains per panicle, 1000 grain weight and panicle length had a positive correlation with grain yield (GYD) and hence can be used as selection indices for improving grain yield in rice. Moreover, the presence of high heritability and significant positive correlation between yield and its component traits in Jhum rice genotypes, confirm its suitability for pre-breeding materials.

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