

# Assessment of Genetic Variability and Correlation of Yield Components of Elite Rice Genotypes (*Oryza sativa* L.)

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## ABSTRACT

The study was conducted to evaluate the extent of variability among the elite rice (*Oryza sativa* L.) genotypes for yield and yield components. Sixteen elite rice genotypes were evaluated for yield and yield contributing characters in Bangladesh Rice Research Institute, Regional Station, Satkhira. Highest grain yield ( $t\ ha^{-1}$ ) was observed in BR(Bio)8333-BC5-2-16, which was followed by BR16, BRRI dhan28, BRRI dhan58 and BRRI dhan29. BR7671-37-2-2-37-3-P3 had the highest number of grains per panicle with minimum thousand grain weight. Correlation analysis revealed that the number of panicles per plant (0.301), days to 50% flowering (0.606) and grain yield per plant (0.393) had the significantly positive contribution to grain yield. After evaluation of yield components, four genotypes namely BR(Bio)8333-BC5-1-20, BR(Bio)8333-BC5-2-16, BR(Bio)8333-BC5-2-22 and BR(Bio)8333-BC5-3-10 were selected as outstanding genotypes, which can be used as potential breeding materials for variety development or in the crossing program to enrich the rice gene pool in Bangladesh.

**Key words:** Variability, correlation, yield components, elite rice genotypes.

## INTRODUCTION

Rice (*Oryza sativa* L.) is one of the pivotal staple cereal crops feeding more than half of the world population. In view of the growing population, the basic objective of the plant breeders would always be towards yield improvement of staple food crops. Sufficient rice production is the key to ensure food security in Bangladesh. In fact, 'Rice security' is synonymous to 'Food security' in Bangladesh as in many other rice growing countries (Brolley, 2015). Rice security is not just an economic issue but also an important parameter for determining social and political stability (Nath, 2015). More food will be required in future because of increasing population. Population of Bangladesh will reach 215.4 million in 2050, when 44.6 MT of clean rice will be needed (Kabir *et al.*, 2015). Theoretically, rice still has great yield potential to be tapped and there are many ways to raise rice yield, such as building of irrigation works, improvement of soil conditions, agronomic

management techniques and breeding of high yielding varieties. The knowledge on the nature and magnitude of genetic variation in respect of quantitative characters like yield and its components is essential for effective crop improvement. Selection of high yielding varieties based only on grain yield will not be much effective unless adequate information on genetic parameters and association between them are available to formulate hybridization and selection program for further improvement, because the estimate of the mean serves as a basis for eliminating the undesirable genotypes.

Information on correlations of characters, direct and indirect effects contributed by each character towards yield will be an added advantage in aiding the selection process. Correlation establishes the extent of association between yield and its components and also brings out relative importance of their effects, thus giving an obvious understanding of their association with grain yield.

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Ultimately, this kind of analysis could help the breeder to design his selection strategies to improve grain yield. Therefore, the present investigation is carried out with the objective of studying the analysis and character associations in rice genotypes for yield improvement.

## MATERIALS AND METHODS

Sixteen elite rice genotypes including five standard check varieties namely, BR16, BRRI dhan28, BRRI dhan58 and BRRI dhan29 were grown at Bangladesh Rice Research Institute, Regional Station, Satkhira, Bangladesh during Boro season 2016-17. The experiment was laid out in a Randomized Complete

Block Design with three replications. Seeding was done on 09 December 2016 and 35 days old seedlings were transplanted. Twenty cm distance was maintained between the rows and 15 cm between the plants. Single seedling was used for transplanting and unit plot size was 10.2 m<sup>2</sup>. TSP and MOP were applied at the rate of 100 kg/ha and 120 kg/ha, respectively during final land preparation. Urea was applied at the rate of 260 kg/ha in three splits at 10 and 30 days after transplanting and 5 days before panicle initiation. A hand weeding was done at 25 days after transplanting. Others intercultural operations and pest control measures were done as and when necessary.

**Table 1. Genotypes with passport data are used for this study.**

Code	Genotype	Parentage	Source
GEN1	BR(Bio)8333-BC5-1-1	BRRI dhan29/IRBB60	BRRI
GEN2	BR(Bio)8333-BC5-1-20	BRRI dhan29/IRBB60	BRRI
GEN3	BR(Bio)8333-BC5-2-16	BRRI dhan29/IRBB60	BRRI
GEN4	BR(Bio)8333-BC5-2-22	BRRI dhan29/IRBB60	BRRI
GEN5	BR(Bio)8333-BC5-3-10	BRRI dhan29/IRBB60	BRRI
GEN6	BRC266-5-1-1-1	BR16/90060-TR1252-8-2-1	BRRI
GEN7	BRC266-5-1-2-1	BR16/90060-TR1252-8-2-1	BRRI
GEN8	BR8523-36-2-2-6	IR 77512-128-2-1-2 / BR 6817-25-2-2	BRRI
GEN9	BR16 (Ck.)	IR1416-131-5/IR1364-37-3-1//IR1544A-E666	BRRI
GEN10	BR7671-37-2-2-37-3-P3	BRRI dhan29/ IR68144	BRRI
GEN11	BR8626-19-5-1-2	BR7166-5B-6/ SHEW WAR TUN// BRRI dhan47	BRRI
GEN12	BR8626-10-5-1	BR7166-5B-6/ SHEW WAR TUN// BRRI dhan47	BRRI
GEN13	BR8109-29-2-2-3	BM9821/Parija	BRRI
GEN14	BRRI dhan28 (Ck.)	BR6 (IR28)/Purbachi	BRRI
GEN15	BRRI dhan58 (Ck.)	Somaclonal line of BRRI dhan29	BRRI
GEN16	BRRI dhan29 (Ck.)	BG90-2/BR51-46-5	BRRI

Source: BRRI (2013) and BRRI (2019).

## Data collection of agronomic traits

Data were collected at days to 50% flowering, plant height (cm), number of tillers per plant, number of panicles per plant, grains per panicle, grain yield per plant, panicle length (cm), thousand-grain weight (g), fertility (%) and yield (t ha<sup>-1</sup>). Days to flowering has been recorded as soon as 50% of the panicles appeared. Five plants were randomly selected excluding the border rows and avoiding the missing hills around for recording data on

plant height in centimeter. Numbers of tillers were recorded in maximum tillering stage. The plant height was measured from ground level to tip of the tallest panicle excluding awns. Panicles were harvested from each individual plant at maturity, properly labelled and placed in net bags separately and air-dried at room temperature for one week. Percentages of spikelet fertility, thousand grain-weight and grain yield per plot were estimated by given formula:

$$\text{Spikelet fertility (\%)} = \frac{\text{Number of filled grains}}{\text{Number of filled grains} + \text{number of unfilled grains}} \times 100$$

$$\text{Yield (t/ha)} = \frac{100 - \text{Grains moisture content (\%)}}{100 - 14} \times \text{Plot yield}$$

## Statistical Analysis

Genotypic variance, mean comparisons of different traits, coefficient of variation (CV) was measured by STAR software (version 2.0.1) and PB Tools software (version 1.3). Analysis of variance was used to test the significance of variance sources, while Tukey's Honest Significant Difference (HSD) test (p = 0.05) was employed to compare the differences among treatment means. The correlation coefficient analysis was conducted to find the relationship of different traits.

## RESULTS

### Genetic variability

The analysis of variance shows highly significant genetic variations ( $P \leq 0.01$ ) among the genotypes for days to 50 % flowering, plant height, number of tillers per plant, number of panicles per plant, number of grains per panicle, grain yield per plant, panicle length, thousand-grain weight, grain fertility and grain yield (Table 2). Coefficient of variation (CV) for days to 50 % flowering, plant height, number of tillers per plant, number of panicles

per plant, number of grains per panicle, grain yield per plant, panicle length, thousand-grain weight, grain fertility and grain yield were 0.92, 2.42, 7.11, 14.07, 12.93, 5.33, 4.40, 12.92, 6.75 and 4.35% respectively (Table 2).

It was observed that mean values for the studied traits ranged from 105 to 120 days for days to 50 % flowering, 88.6 to 116.3 cm for plant height, 8 to 14.3 for number of tillers per plant, 8.4 to 15.4 for number of panicles per plant, 158.6 to 299 for number of grains per panicle, 19.7 to 27.7 g for grain yield per plant, 21.3 to 25.6 cm for panicle length, 16.1 g to 24.7 g for thousand grain weight, 69.4 to 85.7 for grain fertility and 5.18 to 7.58 t ha<sup>-1</sup> for grain yield (Table 3). The highest and the lowest yield was observed in GEN1 (BR (Bio) 8333-BC5-1-1) and GEN8 (BR8523-36-2-2-6), respectively. On the other hand, the longest days to 50% flowering was found in GEN1 (BR(Bio)8333-BC5-1-1) (120 days) and the earlier days to 50% flowering was found in GEN8 (BR8523-36-2-2-6) that was 105 days. Figure 1 shows comparison between days to 50% flowering

and yield (t ha<sup>-1</sup>) of four selected outstanding genotypes along with the check varieties. Among the genotypes, GEN2 (BR(Bio)8333-BC5-1-20), GEN3 (BR(Bio)8333-BC5-2-16), GEN4 (BR(Bio)8333-BC5-2-22) and GEN5 (BR(Bio)8333-BC5-3-10) produced 0.84 to

1.67 t ha<sup>-1</sup>, 0.92 to 1.75 t ha<sup>-1</sup>, 0.82 to 1.65 t ha<sup>-1</sup> and 0.79 to 1.62 t ha<sup>-1</sup> higher compared to the check varieties BR16 (6.56 t ha<sup>-1</sup>), BRRI dhan28 (5.83 t ha<sup>-1</sup>), BBRI dhan58 (6.66 t ha<sup>-1</sup>) and BRRI dhan29 (6.21 t ha<sup>-1</sup>), respectively (Fig. 1).

**Table 2. Genotypic variations of the yield contributing traits in 16 rice genotypes.**

Source of variation	DF	50F	PH	TILL	PP	GP	GYP	PL	TGW	F (%)	Yd
Genotype	15	60.2**	129.6**	12.1**	12.7**	6596.6**	19.2**	4.4**	13.9**	87.7**	1.67**
Rep	2	0.3 <sup>NS</sup>	16.6 <sup>NS</sup>	2.1 <sup>NS</sup>	1.5 <sup>NS</sup>	1234.8 <sup>NS</sup>	0.5 <sup>NS</sup>	1.8 <sup>NS</sup>	25.5 <sup>NS</sup>	18.6 <sup>NS</sup>	0.1 <sup>NS</sup>
Error	30	1.1	6.1	0.6	2.8	908.2	1.6	1.1	6.7	28.5	0.1
Mean		114.0	102.3	11.0	11.8	233.2	23.4	23.6	20.1	79.2	6.7
CV%		0.92	2.42	7.11	14.07	12.93	5.33	4.40	12.92	6.75	4.35

\*\* indicate significantly different at 1%, NS= Non significance. CV denote co-efficient of variation. Indicators: 50F= days to 50% flowering, PH= plant height (cm), TILL= number of tillers per plant, PP= number of panicles per plant, GP= grains per panicle, GYP= grain yield per plant (g), PL= panicle length (cm), TGW= thousand grain weight (g), F (%) = fertility (%) and Yd= yield (t ha<sup>-1</sup>).

**Table 3. Mean comparison of different traits of the genotypes through Tukey's Honest Significant Difference (HSD).**

Code	50F	PH	TILL	PP	GP	GYP	PL	TGW	F (%)	Yd
GEN1	120a	102.3ce	9.6gh	11.8a-d	225.6a-f	20.8ef	22.9a-d	18.7ab	83.0ab	7.10a-c
GEN2	117ab	104.3b-d	9.3g-i	11.1a-d	215.0b-f	21.8d-f	23.3a-d	20.1ab	83.5ab	7.50ab
GEN3	116bc	102.0c-e	9.3g-i	11.8a-d	204.3c-f	22.0d-f	23.0a-d	20.5ab	83.1ab	7.58a
GEN4	118ab	106.3bc	8.0i	13.2a-d	227.0a-f	22.1d-f	23.6a-d	21.2ab	81.9ab	7.48ab
GEN5	117ab	111.0ab	9.3g-i	15.1ab	271.0a-e	21.9d-f	23.7a-d	18.8ab	81.6ab	7.45ab
GEN6	110de	104.6bd	12.6b-d	8.4d	158.6f	25.2a-d	25.6a	21.5ab	70.2ab	6.51c-e
GEN7	112d	95.6e-g	14.0ab	10.2b-d	186.6e-f	23.8b-e	24.6a-c	18.1ab	76.3ab	6.40c-e
GEN8	105g	116.3a	8.6hi	10.2b-d	195.6d-f	19.7f	24.6a-c	19.9ab	74.7ab	5.18g
GEN9	118ab	92.3fg	14.3a	8.9cd	171.3f	24.7a-d	23.5a-d	24.7a	78.2ab	6.58ce
GEN10	113cd	102.6c-e	12.0c-e	13.1a-d	299.0ab	20.5ef	23.5a-d	16.1b	77.3a-d	5.40fg
GEN11	112de	98.6d-f	11.3d-f	13.8a-c	287.0a-d	27.2ab	23.9a-d	20.5ab	85.5a	7.10a-c
GEN12	116bc	88.6g	10.6e-g	10.6a-d	219.3b-f	26.8a-c	21.3d	23.0ab	77.6a-d	7.06a-d
GEN13	113cd	104.6b-d	13.3a-c	15.4a	288.0a-c	27.7a	24.1a-d	16.9ab	72.5cd	7.19a-c
GEN14	106fg	102.3c-e	10.3fg	10.2b-d	225.3a-f	21.5d-f	21.6cd	20.8ab	85.7a	5.83e-g
GEN15	109ef	102.0c-e	10.3fg	13.3a-d	315.6a	26.0a-c	22.4b-d	20.0ab	85.3a	6.66b-e
GEN16	118ab	103.3cd	13.3a-c	11.4a-d	240.6a-f	23.3c-f	25.4ab	20.0ab	69.4d	6.21d-f
Maxi.	120	116.3	14.3	15.4	299.0	27.7	25.6	24.7	85.7	7.58
Mini.	105	88.6	8.0	8.4	158.6	19.7	21.3	16.1	69.4	5.18
LSD <sub>0.05</sub>	1.64	3.96	1.25	2.63	48.76	1.96	1.66	4.15	8.45	0.46

Mean with the same letter in a column are not significantly different each other at 0.05 % probability level. GEN=Genotypes, Maxi.=Maximum, Mini.=Minimum and LSD=Least Significant Difference . Indicators: 50F= days to 50% flowering, PH= plant height (cm), TILL= number of tillers per plant, PP= number of panicles per plant, GP= grains per panicle, GYP= grain yield per plant (g), PL= panicle length (cm), TGW= thousand grain weight (g), F (%) = fertility (%), and Yd= yield (t ha<sup>-1</sup>).

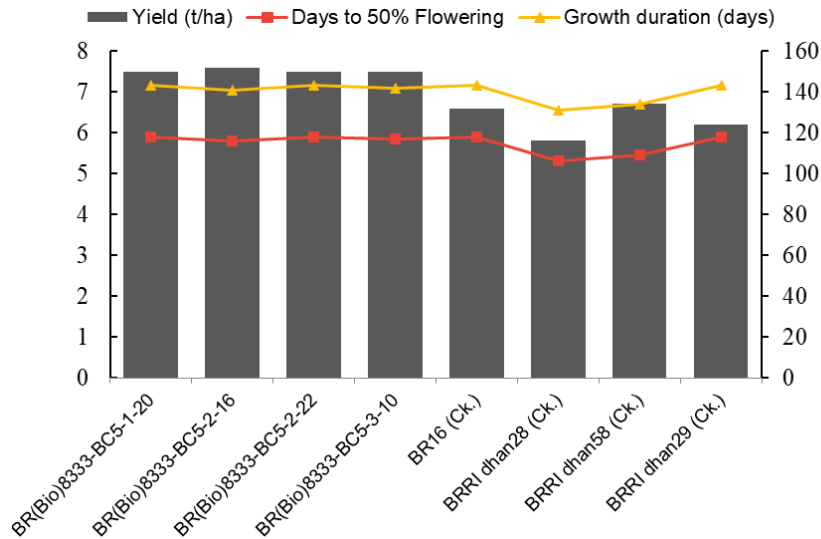


Fig. 1. Comparison between days to 50% flowering and yield ( $t\ ha^{-1}$ ) of four selected outstanding genotypes along with four checks.

### Correlation analysis

Out of ten characters, only three viz. days to 50% flowering, number of panicles per plant

and grain yield per plant showed significantly positive correlations with the grain yield (Table 4).

Table 4. Pearson correlation coefficients among the yield contributing traits using genotypes means

Particulars	50F	PH	GYP	TILL	PP	GP	PL	TGW	F (%)
PH	-0.283	1							
GYP	-0.005	-0.431**	1						
TILL	0.011	-0.437**	0.438**	1					
PP	0.124	0.191	0.098	-0.217	1				
GP	-0.037	0.118	0.138	-0.115	0.692**	1			
PL	-0.013	0.262	-0.093	0.317*	-0.065	-0.165	1		
TGW	0.075	-0.227	0.129	0.061	-0.582**	-0.371**	-0.026	1	
F (%)	0.012	-0.058	-0.125	-0.425**	0.301*	0.202	-0.444**	0.008	1
Yd	0.606**	-0.124	0.393**	-0.242	0.301*	0.041	-0.212	0.071	0.232

\*\* and \* indicate significantly different at 1% and 5% respectively, NS: Non-significance Indicators: 50F= days to 50% flowering, PH= plant height (cm), TILL= number of tillers per plant, PP= number of panicles per plant, GP= grains per panicle, GYP= grain yield per plant (g), PL= panicle length (cm), TGW= thousand grain weight (g), F (%) = fertility (%) and Yd= yield ( $t\ ha^{-1}$ ).

Correlation coefficients between different agronomic traits and grain yield have shown explicitly in Fig 2. Plant height and panicle length had shown negative and non-significant correlation with grain yield. However, grains per panicle, thousand-grain weight and spikelet fertility percentages showed non-significant but positive correlation with grain yield. Days to 50 % flowering exhibited negative and non-significant correlations with plant height. Number of tillers per plant showed positive and significant correlation with grain yield per plant and panicle length. Number of panicles per plant exhibited positive and significant correlation with grains per panicle and percent spikelet fertility. Significantly positive correlation was observed between number of panicles per plant and percent spikelet grain fertility.

## DISCUSSION

### Genetic variability

Highly significant genetic variations ( $P \leq 0.01$ ) suggested that the studied genotypes had considerable variability for effective selection. The minimum days to 50 % flowering was (105 days) observed in GEN8 (BR8523-36-2-2-6), while the maximum value (120 days) was recorded in GEN1 (BR(Bio)8333-BC5-1-1). Among the tested entries, GEN1 (BR(Bio)8333-

BC5-1-1) showed significant difference from the checks BRR1 dhan28 and BRR1 dhan58. Weiya *et al.*, (2008) also observed variations in heading days among several genotypes and they identified a regulatory gene responsible for this variation. Therefore, it is suggested that these lines should be further studied to confirm their consistent performance. The minimum plant height (88.6 cm) was recorded in GEN12 (BR8626-10-5-1), while maximum plant height (116.3 cm) was observed in GEN8 (BR8523-36-2-2-6). Hussain *et al.*, (2005) reported that transplantation time, water and soil condition, planting and sowing method affect plant height in rice. In case of delayed planting in photosensitive rice, plant height is also influenced by different sets of planting time (Biswas *et al.*, 2019).

The minimum tillers per plant (8.0) were produced by rice genotype GEN4 (BR (Bio)8333-BC5-2-22). The GEN9 (Check BR16) produced maximum (14.3) number of tillers per plant. This observation was supported by Zahid *et al.*, (2005), who studied twelve genotypes of coarse rice to check their yield performance and reported highly significant variation for different traits including the number of productive tillers per plant, which is an important yield component in rice.

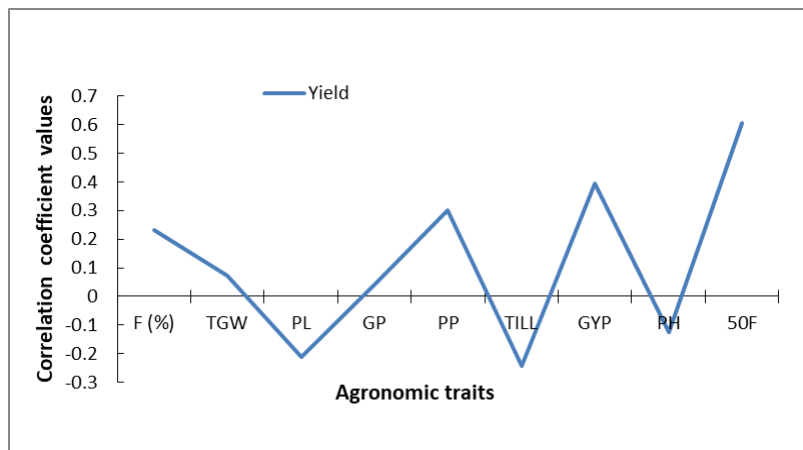


Fig. 2. Correlation coefficients between different agronomic traits and grain yield.

Minimum number of panicles was found in GEN13 (BR8109-29-2-2-3) and maximum in GEN6 (BRC266-5-1-1-1). The least number of filled grains per panicle was observed in the genotype GEN6 (BRC266-5-1-1-1), while the maximum was in GEN10 (BR7671-37-2-2-37-3-P3). Tahir *et al.*, (2002) reported highly significant variation for the grains per panicle for different genotypes.

Minimum grain yield per plant (19.7 g) was recorded in GEN8 (BR8523-36-2-2-6) and maximum (27.7 g) was recorded in GEN13 (BR8109-29-2-2-3). The shortest panicle length (21.3 cm) was recorded in GEN12 (BR8626-10-5-1) while the longest panicle length (25.6 cm) in GEN6 (BRC266-5-1-1-1). Ifftikhar *et al.*, (2009) studied genetic variability for various traits and found that this trait is under the genetic control and could be used in the selection process of some desirable traits.

Minimum thousand grain weight (16.1 g) was recorded by GEN10 (BR7671-37-2-2-37-3-P3), while maximum (24.7 g) were recorded by GEN9 (check BR16). The findings are in with Tahir *et al.*, (2002), who reported highly significant variation among different traits and observed that these traits are under the control of genotypic difference among the genotypes.

Minimum (69.4) and maximum (85.7) grain fertility percentage were recorded in GEN16 (BRR1 dhan29) and in GEN14 (BRR1 dhan28), respectively. The highest grain yield (7.58 t ha<sup>-1</sup>) was recorded by GEN3 (BR(Bio)8333-BC5-2-16), while the lowest (5.18 t ha<sup>-1</sup>) was recorded by GEN8 (BR8523-36-2-2-6). The same variability was reported by Zahid *et al.*, (2005), who studied twelve genotypes of coarse rice to check their yield performance and reported highly significant variation for different traits. This variation in the grain yield might be due to the environment (Mahapatra, 1993) or the correlation of grain yield per plant with various yield contributing characteristics like; fertility of soil, flag leaf area, number of grains per panicle and grain weight.

Days to 50% flowering of selected four genotypes were 10-12 and 7-9 days longer than the check varieties BRR1 dhan28 and BRR1 dhan58, respectively, but similar in days to 50% flowering with the check varieties BR16 and BRR1 dhan29 (Fig 1).

### Correlation analysis

The association between days to 50% flowering and yield was significant and positive, which means that the late maturing variety produced higher yield. Positive relation of grain yield with panicles per plant was reported by Zahid *et al.*, (2005) and Golam *et al.*, (2011). Zahid *et al.*, (2005) studied 14 genotypes of basmati rice and reported that plant height has negative correlation with yield. Golam *et al.*, (2011) and Kim *et al.*, (1999) reported positive contribution of grains per panicle towards grain yield, which is agreement with the present findings. Eidikohnaki *et al.*, (2013), Haider *et al.*, (2012), Kiani and Nematzadeh (2012), Seyoum *et al.*, (2012), Akinwale *et al.*, (2011) reported the positive association of grain yield with filled grains per panicle. Prasad *et al.*, (2001) observed that a day to 50 % flowering was negatively correlated with plant height, which supported the present study. It was observed that plant height showed significantly negative correlation with grain yield per plant and productive tillers per plant which was supported by Prasad *et al.*, (2001). Rasheed *et al.*, (2002) reported a positive association between fertility percentage and grain yield per plant.

### CONCLUSION

In this study, sixteen Boro rice genotypes showed extensive variability for yield and yield related traits. Correlation analysis revealed that three agronomic traits such as number of panicles per plant (0.301), 50% flowering (0.606) and grain yield per plant (0.393) had the significantly positive contribution to grain yield. The number of

panicles per plant showed significantly positive correlation with grains per panicle and spikelet fertility percentages. Though the growth duration of GEN2 (BR(Bio)8333-BC5-1-20), GEN3 (BR(Bio)8333-BC5-2-16), GEN4 (BR(Bio)8333-BC5-2-22) and GEN5 (BR(Bio)8333-BC5-3-10) genotypes were longer but possessed 0.79 to 1.75 t ha<sup>-1</sup> higher grain yield than the check varieties (BR16, BRRI dhan28, BRRI dhan29 and BRRI dhan58). Therefore, these genotypes were identified as high yielders among all genotypes. The gathered information can be useful for rice research and the selected rice genotypes can be used as potential breeding materials for variety development or use in the breeding program as parents after further evaluations in multi-locations in Bangladesh.

#### AUTHORS' CONTRIBUTION

SKD and RFD generated idea; SKD, MI and RFD coordinated the experiment/research/project; SKD, MI, and RFD developed methodology; SKD, MK and MMEA provided scientific insights; SKD and RFD gathered data; SKD and MMEA carried out analysis and synthesis; SKD, MK, and MMEA did the writings all versions of the manuscript; SKD, MK, MMEA and TLA performed critical review and editing; All authors read and approved the final manuscript

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#### DECLARATION OF INTERESTS

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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