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## Genetic variability analysis for various yield attributing traits in rice genotypes

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### Abstract

An experiment was conducted using a randomized complete block design to estimate genetic variability of ten rice genotypes. Analysis of variance for yield and yield contributing traits showed significant ( $p < 0.01$ ) variation among the genotypes. Results of genetic analyses showed a higher phenotypic coefficient of variation compared to their corresponding genotypic coefficient of variation for all the traits measured, which indicates that the traits were influenced by environment. The magnitude of difference between phenotypic coefficient of variance (PCV) and genotypic coefficient of variance (GCV) was less for the traits indicating little influence of environment. The higher estimates of PCV and GCV were observed for number of filled grains panicle<sup>-1</sup> (27.53; 26.84), number of unfilled grains panicle<sup>-1</sup> (26.76; 25.28) and plant height (23.14; 23.00) indicates possibility of genetic improvement through direct selection for these traits, while days to 50% flowering, days to maturity, panicle length, number of effective tillers plant<sup>-1</sup>, fertility (%), 1000 Seed weight and yield panicle<sup>-1</sup> showed low PCV and GCV values indicating the need for creation of variability by hybridization or mutation followed by selection. High heritability values (>60%) along with high genetic advance and genetic advance as percentage of mean were found for all the traits indicating prevalence of additive gene action, which provides good scope for further improvement by selection.

**Keywords:** Genetic variability, Heritability, Genetic advance, Rice genotypes

### Introduction

Rice (*Oryza sativa* L.) is one of the most important food crops in the world. It is a staple food crop for more than half of the world's human population. Bangladesh stands fourth with 52.2 million tons as China occupies the first place with 206.5 million tons in the world's production table of 479.3 million tons (FAOSTAT, 2014). Yield and yield contributing parameters are the most widely targeted traits for rice improvement programmes worldwide. The improvement of a crop is largely dependent on the nature and magnitude of available genetic variability, heritability and the transfer of desired characters into new varieties. The success of breeding programmes can be enhanced when variability within the existing germplasm is high, which allows the plant breeder to more rapidly produce new varieties or improve existing ones (Meena and Bahadur, 2013, 2014; Ranganatha *et al.*, 2013; Yared and Misteru 2016). Hence, knowledge of key genetic parameters is crucial for any crop improvement program, providing precise information for selection. Genetic parameters like the genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability and genetic advance (GA) are useful biometric tools for measuring genetic variability (Aditya *et al.*, 2011). Hence, characterising the genetic background of rice and determining breeding values should be done before carrying out any improvement programme (Agong *et al.*, 2001). Yield is a complex polygenic character, resulting from multiple interactions between many yield contributing traits.

Considering the above facts, the present research study was undertaken to estimate genetic variability, heritability and genetic advances among yield and yield contributing traits for rice genotypes. This investigation provides information that could lead to the development of desirable rice genotypes for salt tolerant in future breeding programmes.

## Materials and Methods

The present experiment was carried out in the Net House of the Plant Breeding Division at Bangladesh Institute of Nuclear Agriculture (BINA), Mymensingh during the period from June to December 2015. Ten rice genotypes including seven landraces and three released varieties viz., Hogla, Dakh Shail, Kute Patnai, Ghunshi, Mondeshor, Tal Mugur, Nona Bokhra, Binadhan-8, Binadhan-10 and BRRI dhan47 were used as plant material. The experiment was carried out in a Randomized Complete Block Design with five replications. Management practices such as irrigation and fertilization were performed by following the standard procedures (IRRI 2002). Other intercultural operations were done whenever necessary.

Morphological data were collected at appropriate growth stage of rice plant following the standard evaluation system indicated by IRRI (IRRI 2002). The characters that were evaluated included days to 50% flowering, days to maturity, plant height (cm), panicle length (cm), number of effective tillers plant<sup>-1</sup>, number of filled grains panicle<sup>-1</sup>, number of unfilled grains panicle<sup>-1</sup>, fertility (%), 1000 Seed weight (g) and yield panicle<sup>-1</sup>(g).

The recorded data for different parameters were assembled and organized properly for statistical analysis using MSTAT-C. Genotypic and phenotypic variances were estimated according to the formula given by (Johnson *et al.*, 1955). Heritability was estimated according to the formula suggested by (Johnson *et al.*, 1955 and Hanson 1961). Genotypic and phenotypic coefficient of variance was estimated according to (Burton, 1952 and Singh *et al.*, 1997). Estimation of GA was done following formula given by (Johnson *et al.*, 1955 and Allard, 1975) and GA% was calculated by the formula suggested by (Comstock *et al.*, 1952).

## Results and Discussion

### Analysis of variance

The analysis of variance showed (Table 1) that the difference among genotypes for all the traits under study were highly significant for genotypes, treatment and genotypes-treatment interaction. This indicated that the genotypes were possessing inherent genetic variances among themselves with respect to the characters studied. Similar results were reported by (Bekele *et al.*, 2013).

**Table 1. Analysis of variance for different morphological plant characters of ten rice genotypes**

Characters	df	Days to 50% flowering	Days to maturity	Plant height (cm)	Panicle length (cm)	No of effective tillers plant <sup>-1</sup>	No of filled grains panicle <sup>-1</sup>	No of unfilled grains panicle <sup>-1</sup>	Fertility (%)	1000 seed weight (g)	Yield panicle <sup>-1</sup> (g)
Replication	4	28.93	15.72	60.18	0.27	0.338	26.60	2.134	18.28	4.07	0.032
Genotypes (A)	9	2070.09**	2896.07**	15050.54**	96.72**	7.789**	11531.17**	1261.581**	1435.60**	251.71**	3.334**
Treatment (B)	3	105.17**	734.05**	3139.77**	250.04**	90.413**	30740.87**	7858.686**	14941.98**	725.27**	42.503**
Ax B	27	28.27*	53.58**	220.75**	85.23**	2.202**	703.28**	599.999**	750.24**	84.79**	0.706**
Error	156	16.55	23.07	25.97	2.28	0.435	11.28	0.924	5.26	5.59	0.015

\*\* Indicates significant at 0.01 probability level and \* indicates significant at 0.05 probability level

### Estimate of genetic parameters

Estimates of phenotypic ( $\delta^2_p$ ) and genotypic variances ( $\delta^2_g$ ), phenotypic coefficient (PCV) and genotypic coefficient of variance (GCV), heritability (%), genetic advance (GA) and genetic advance as percent of mean (GA%) are shown in Table 2. High phenotypic and genotypic variances were recorded with plant height 750.58 and 741.49, respectively. High phenotypic and genotypic variances were equally observed for number of filled grains panicle<sup>-1</sup> (569.64 and 541.39), days to maturity (144.50 and 142.12) and days to 50% flowering (103.39 and 102.09), respectively. The low values of phenotypic and genotypic variances were observed with the characters yield panicle<sup>-1</sup> (0.16 and 0.13), number of effective tillers plant<sup>-1</sup> (0.372 and 0.279) and panicle length (0.620 and 0.575), respectively. In general, the phenotypic variances were higher than genotypic variances for all the characters.

**Table 2. Phenotypic ( $\delta^2p$ ) and genotypic variance ( $\delta^2g$ ), phenotypic coefficient (PCV) and genotypic coefficient of variance (GCV), heritability (%), genetic advance (GA) and genetic advance as percent of mean (GAM) for all the traits**

Characters	Phenotypic variance ( $\delta^2p$ )	Genotypic variance ( $\delta^2g$ )	PCV (%)	GCV (%)	Heritability (%)	GA	GAM
Days to 50% flowering	103.39	102.09	9.63	9.57	98.75	20.68	19.59
Days to maturity	144.50	142.12	8.74	8.67	98.36	24.36	17.71
Plant height (cm)	750.58	741.49	23.14	23.00	98.79	55.75	47.09
Panicle length (cm)	0.620	0.575	3.44	3.32	92.73	1.50	6.58
No of effective tillers plant <sup>-1</sup>	0.372	0.279	11.73	10.16	75.14	0.94	18.15
No of filled grains panicle <sup>-1</sup>	569.64	541.39	27.53	26.84	95.04	46.73	53.90
No of unfilled grains panicle <sup>-1</sup>	37.08	33.08	26.76	25.28	89.21	11.19	49.18
Fertility (%)	36.33	34.27	7.93	7.70	94.32	11.71	15.41
1000 Seed weight (g)	9.79	8.35	14.77	13.64	85.25	5.49	25.94
Yield panicle <sup>-1</sup> (g)	0.16	0.13	20.44	18.54	82.23	0.68	34.63

The phenotypic coefficients of variance (PCV) were ranged from 3.44% for panicle length to 27.53% for number of filled grains panicle<sup>-1</sup>, whereas genotypic coefficients of variance (GCV) were ranged from 3.32% for panicle length to 26.84% for number of filled grains panicle<sup>-1</sup>. According to Siva Subramanian and Menon (1973) PCV and GCV values more than 20% are regarded as high, whereas values less than 10% are considered to be low and values between 10 and 20% to be moderate. Based on this delineation, PCV and GCV values were high for plant height, number of filled grains panicle<sup>-1</sup> and number of unfilled grains panicle<sup>-1</sup>; low for days to 50% flowering, days to maturity, panicle length and fertility percent; medium for number of effective tillers plant<sup>-1</sup> and 1000 seed weight. The yield panicle<sup>-1</sup> was recorded with high PCV and moderate GCV.

The current study suggests that phenotypic variance ( $\delta^2p$ ) and phenotypic coefficient variance (PCV) were higher than their corresponding genotypic variance ( $\delta^2g$ ) and genotypic coefficient of variance (GCV) respectively for all the characters studies, indicating that the expression of these characters was influenced by environment. Similar results were reported by (Dutta *et al.*, 2013; Singh *et al.*, 2014; Tuhina-Khatun *et al.*, 2015) in rice. The trait like yield panicle<sup>-1</sup> which show higher difference between PCV and GCV indicated that environmental effect on the expression of those traits is higher.

Heritability analysis estimates the relative contributions of differences in genetic and non-genetic factors to the total phenotypic variance in a population. It is an important concept in quantitative genetics, particularly in selective breeding. The heritability estimation varied from 75.14% to 98.79%, respectively for number of effective tillers plant<sup>-1</sup> and plant height. All the characters studies had high heritability (>60%). This result indicates that these characters could be easily improved by selection. The most important function of the heritability in the genetic study of quantitative characters is its predictive role to indicate the reliability of the phenotypic value as a guide to breeding value (Falconer and Mackay 1996 and Al-Tabbal *et al.*, 2012). High heritability estimates for those traits indicated a high response to selection in these traits. Similar results were also reported by (Al-Tabbal *et al.*, 2012; Dutta *et al.*, 2013; Raffi *et al.*, 2014), which support the present findings.

Genetic advance (GA) under selection refers to the improvement of characters in genotypic value for the new population compared with the base population under one cycle of selection at a given selection intensity (Wolie *et al.*, 2013). The high value of GA was recorded with plant height (55.75) and the low (0.68) with yield panicle<sup>-1</sup>. Estimates of GA for yield panicle<sup>-1</sup> was (0.68 g) indicating that whenever we select the best, 1% high yielding genotypes as parents, average grains yield panicle<sup>-1</sup> of progenies could be improved by 0.68 g panicle<sup>-1</sup>. Genetic advance as percent mean expected (GAM) had a general range between 6.58% for panicle length and 53.90% for number of filled grains panicle<sup>-1</sup>. Among the characters high values of GAM (>20%) were recorded for plant height, number of filled grains panicle<sup>-1</sup>, number of unfilled grains panicle<sup>-1</sup>, 1000 seed weight and yield panicle<sup>-1</sup>. It was moderate (10 to 20%) for days to 50% flowering, days to maturity and fertility percent; low (<10%) for only panicle length.

Heritability and the genetic advance are also important selection parameters. It is more useful as a selection tool when considered jointly with heritability. The estimates of genetic advance can help to understand the type of gene action of various polygenic characters. (Johnson *et al.*, 1955) suggested that high heritability estimates along with the high genetic advance is more helpful in predicting gain under selection than heritability estimates alone. Thus, the heritability estimates will be reliable if accompanied by high genetic advance. (Patel *et al.*, 2012) also observed highest heritability for days to 50% flowering, plant height, total tillers, panicle length, number of filled grain panicle<sup>-1</sup>, number of unfilled grain panicle<sup>-1</sup> and grains yield m<sup>-2</sup>.

The present study revealed high heritability accompanied with high genetic advance as percent of the mean for plant height, number of filled grains panicle<sup>-1</sup>, number of unfilled grains panicle<sup>-1</sup>, 1000 seed weight and yield panicle<sup>-1</sup>; high heritability and moderate genetic advance as percent of the mean for days to 50% flowering, days to maturity and fertility percent; These results could be explained by additive gene action and their selection may be done in early generations. Similar findings have been reported by (Wolie *et al.*, 2013 and Ogunbayo *et al.*, 2014) on rice and (Reza *et al.*, 2015) on wheat. Panicle length, days to 50% flowering, days to maturity and fertility percent had low to moderate genetic advance as percent of the mean indicates non-additive gene effects; suggesting that these characters could be improved by developing varieties through recurrent selection method (Ogunbayo *et al.*, 2014).

The results of the present study on variability, heritability and genetic advance indicated scope for improvement of rice grain yield through selection, using parameters like the genetic coefficient of variation, heritability and GA and are of great importance when developing an efficient breeding program for rice, because when there is sufficient genetic variation, breeders can exploit additive gene effects, transgressive segregation, and heterosis to improve yield.

## Acknowledgements

The authors are thankful to the Plant Breeding Division, Bangladesh Institute of Nuclear Agriculture (BINA), Mymensingh. Financial support from Ministry of Science and Technology, Bangladesh is also acknowledged.

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