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Multivariate Analysis of Growth and Yield Traits of Aman Rice Genotypes in Barishal Region of Bangladesh

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ABSTRACT

Rice (*Oryza sativa* L.) is the most important staple crop worldwide in terms of production and cultivation area. In rice breeding efforts, the degree of genetic diversity is a significant factor in selecting appropriate genotypes. This study was carried out to determine genetic diversity among fifteen rice genotypes by assessing different morphological yield traits using multivariate analysis. Our results record significant variation with considerable values for certain specific traits for certain genotypes indicating genetic diversity among the genotypes. Cluster analysis categorized genotypes into four clusters based on growth and yield characteristics. Significant variations were observed in plant height, panicle length, number of effective tillers per plant, and grain yield. The highest yielding rice genotype was IR18A1075 (6.35 t/ha), followed by IR17A1633 (6.31 t/ha). The maximum distance (43.74) was identified between cluster centroids in cluster III and cluster IV, showing genetic dissimilarity among genotypes that can be used in hybrid breeding program. Cluster II genotypes exhibited the maximum grain yield potential (5.52 t/ha) indicating the possible usefulness of these genotypes for rice improvement purposes and can be cultivated for increased grain yield.

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Introduction

Rice (*Oryza sativa* L.) is one of the most important staple food crops, maintaining the diets of more than half of the world's population (Lakshmi, 2022). The primary food crop in Bangladesh is rice, which provides a considerable portion of people's livelihoods and greatly affects the economy (Rahman, 2022). Around 158.9 million individuals in Bangladesh consume rice as the key food source (BBS, 2017). Most of the farmers prefer rice as major crop instead of other crops due to its wide adaptability in various ecosystems and less cultivation risk. Ninety percent of the world's supply of rice is grown in Asia (Niaz, 2022). Broad distribution of rice across continents and sub-continents is an evidence of its diverse genetic makeup (Naaz, 2022). Rice production in Bangladesh has gained notable progress over the last few decades and which has continued in recent years. However, genetic diversity and different environmental and human induced factors inhibits overall production of rice. Therefore, development of climate-smart varieties with improved yield should be the main focus of plant breeder for sustaining Bangladeshi rice production and future food security. Genetic diversity play important role for choosing efficient breeding strategies and creates an option for the breeder to select desirable traits and use them in making new combinations (Garris *et al*. 2005). In Bangladesh rice breeding program mainly focus on yield enhancement with effective genetic improvement of rice to cope with the growing demand associated with adaptability in different environments. Bangladesh has developed a large number of rice varieties adapted in the different agro-ecosystems of the country (Al Mamun *et al*. 2021). Breeders practice different techniques for the selection and identification of improved rice varieties. Multivariate analysis is the most commonly used popular genetic variability evaluation tool utilized by rice breeders for assessing genetic variability. Researchers have been able to classify and estimate the diversity of a variety of rice by using agro-morphological characters and multivariate analyses (Varthini, 2017). Therefore, the objective of the study was to determine the degree of diversity to identify suitable genotypes for rice hybridization based on morphological traits.

Materials and Methods

Experimental site, layout and plant material

The experimental work was carried out at the research field of the Bangladesh Institute of Nuclear Agriculture (BINA) substation in Barishal of Banglaesh. It is located at 22◦53′ N latitude and 90◦34′ E longitude and 11.2 m above the sea level. The soil of the research field was silty clay. The climate of the experimental field was a hot humid tropic under the rain forest with temperature ranging from 22 °C to 25 °C. The experiment was conducted in a Randomized Complete Block Design (RCBD) with three replications. The seeds of fifteen genotypes were stored at 480 degrees Celsius for 72 hours, soaked for a day, and then treated with Bavistin for 5 minutes before sowing. Seeds were directly sowed on the wet field. The fertilizers N:P:K:S:Zn/ha were supplied at 60:20:40:100:10 kg/ha, respectively. Nitrogen was applied in stages at 15, 30, and 50 days after sowing (DAS). Standard cultural management was performed and plant protection measures were taken following the suggestion of BRRI. Weed control was performed with the application of herbicide. Hand weeding was done in time.

Data Collection of observed morphological traits

The data for all traits were recorded from five plants in each input for each replication and data on yield was collected from each plot. Morphological data that were collected included: days to maturity (DM), plant height (cm) (PH), effective tiller (ET), panicle length (PL), filled grains per panicle (FG), and thousand seed weight (1000 seed wt.).

Multivariate Analysis

Univariate analysis of the individual character was performed using mean values for all characters and computed using the microsoft excel computer tool. The collected data were subjected to multivariable analysis was calculated using the statistical software packages of Minitab ver.14. Duncan's Multiple Range Examine (DMRT) was used to test the differences between genotype means for all the characteristics. MSTAT-C was used to calculate the mean, range, and CV%. Rstudio-4.1 was used to compute the genotypic and phenotypic co-efficient of variation, Broad sense heritability, and expected genetic advance for several traits under selection. Minitab software was used to calculate cluster analysis and distance between clusters.

Result and Discussion

All the fifteen rice genotypes exhibited significant ($p \le 0.01$) variation for all the traits evaluated (Table 1). Days to 50 percent flowering could be used as good indicator for better improvement of grain yield of rice. Significant variation was observed among the genotypes regarding the days to 50% flowering (Table 1). Maximum days to 50% flowering (142 days) were recorded in genotype BRRIdhan-76, followed by BRRI dhan-77 (139 days) respectively, while the minimum days to 50% flowering was recorded in IR17A3163, IR18A1910, IR17A3163 (116 days) followed by IR17A1633, IR17A2210, IR18A1800, (117days) and IR17A3089, IR18A1075, Binadhan-23 (118 days), respectively (Table 1). Ali *et al.* 2014 have also reported variations in days to 50% flowering in different rice genotypes. The variation of flowering time may be due to the genetic structure of the different genotypes under specific environmental conditions. Crop maturity is related to the optimal harvesting time, grain yield and post-harvest quality of rice (wang, 2021). Significant differences on days to maturity were recorded among different genotypes (Table 1). The maturity period ranged from 116 to 142 days (Table 1). Maximum maturity days (142 days) were recorded in genotypes BRRIdhan-76 followed by BRRI dhan-77 (139 days) while minimum maturity days (116 days) were recorded in IR17A3163, IR17A3163, IR18A1910, IR17A3163 followed by (117 days) IR17A1633, IR17A2210 and IR18A1800 (Table 1). Variation in days to maturity in different rice genotypes also reported by Sabouri *et al*. (2008). The genotypes that took maximum days for maturity may be due to having grain sterility or fail to mature due to environmental barriers. Plant height is an important growth factor that is closely related to rice yield and quality (Reddy and Redd, 1997). It is a complicated trait controlled by a number of genes and various environmental factors (Rahman *et al*. 2018). Significant variation was observed in plant height and the range of plant height varied from 93.67 to 136.33 in Binadhan-17 and IR18A1029, respectively (Table 1). Variation in plant height of various rice genotypes was also observed by Rasheed *et al*. (2002). All the fifteen genotypes produced effective tillers at a range between 10.66 and 15.11 in IR17A2210 and BRRI dhan-77, respectively (Table 1) may showed relatively stable condition of this character in varying environmental conditions (Tahir *et al*. 2004). The panicle length was found to be variable between 21.67 and 29.47 in IR17A3006 and IR17A3163, respectively while filled grain ranged from 53.67 to 102.20 gm in IR17A3163 and IR18A1800, respectively (Table 1). Significant differences were observed on the yield (tons per hectare) of rice genotypes (Table 1). Maximum yield (6.35 t/ha) was recorded in IR18A1075, followed by 6.31 t/ha in IR17A1633 respectively (Table 1). The minimum paddy yield **(**3.86 t/ha**)** was recorded in IR17A2210 rice genotypes. Number of grains/panicle and the panicle length are not closely related with yield as some genotypes have longer panicles but a smaller number of grains/panicles. Our results are contradictory to Biswass *et al*. (1998) where they observed higher number of effective tillers per hill and higher number of grains per panicle showed higher yield in rice. The observed results of phenotypic traits indicating the existence of substantial variability among the genotypes taken for the study. Significant variation among different rice genotypes were earlier reported by Singh *et al*. (2020), Kumari *et al*. (2019) and Ranjith *et al*. (2018).

Table 1. Mean values of various growth and yield traits of fifteen rice genotypes

Genotype	Days to Maturity (DM)	Plant Height (cm) (PH)	Effective tiller (ET)	Panicle length (cm) (PL)	Filled grain (FG)	1000 seed wt.	Yield (t/ha)
IR17A1633	117±1.16^{fgh}	105.67±1.53^{h}	13.33±0.58^{abc}	26.57±0.51^{def}	73.47±1.50^{g}	23.90±1.23^{cd}	6.31±0.43^{a}
IR17A3056	120±1.00^{cd}	124.33±2.08^{e}	10.89±1.02^{d}	24.43±0.51^{hi}	77.80±2.31^{f}	27.87±0.67^{abc}	4.86±1.09^{abc}
IR18A1029	120±0.58^{cde}	136.33±2.08^{ab}	13.67±0.58^{ab}	25.33±0.58^{gh}	82.00±3.61^{def}	25.67±2.89^{abcd}	5.86±1.10^{ab}
IR17A2210	117±0.58^{fgh}	131.00±1.00^{cd}	10.66±1.76^{d}	24.53±0.42^{hi}	85.33±2.52^{bcd}	24.93±1.93^{bcd}	3.86±1.15^{c}
IR17A3089	118±0.58^{def}	130.33±1.53^{cd}	13.00±1.00^{bc}	26.93±0.06^{cde}	86.73±2.05^{bc}	22.30±2.39^{d}	5.62±1.31^{ab}
IR18A1075	118±1.73^{defg}	129.67±2.08^{cd}	14.00±1.00^{ab}	25.87±0.06^{fg}	85.67±3.06^{bcd}	25.10±1.82^{abcd}	6.35±0.58^{a}
Binadhan-17	116±0.58^{fgh}	93.67±1.53^{i}	13.55±1.07^{abc}	27.17±0.76^{cde}	81.00±1.00^{def}	22.47±1.04^{d}	6.30±0.27^{a}
IR18A1910	116±0.58^{h}	132.67±2.52^{bc}	12.44±0.70^{bcd}	25.27±0.68^{gh}	81.33±2.31^{def}	25.50±4.00^{abcd}	5.78±1.28^{ab}
BRRI dhan-76	142±3.00^{a}	137.67±2.52^{a}	12.99±1.68^{bc}	26.20±0.53^{efg}	89.33±2.52^{b}	28.37±0.06^{ab}	5.84±1.40^{ab}
IR17A3006	118±0.58^{efgh}	113.33±3.51^{fg}	12.11±0.39^{bcd}	21.67±0.42^{j}	66.00±1.91^{h}	27.13±2.50^{abc}	5.81±0.35^{ab}
IR18A1762	121±0.58^{c}	127.67±2.08^{de}	13.33±1.00^{abc}	24.13±0.70^{i}	78.60±0.72^{ef}	29.23±0.99^{a}	5.51±0.73^{abc}
BRRI dhan-77	139±1.00^{b}	133.00±3.00^{bc}	15.11±0.96^{a}	27.77±0.59^{bc}	62.67±3.79^{h}	25.70±3.32^{abcd}	5.35±0.96^{abc}
IR17A3163	116±1.00^{gh}	112.33±2.52^{g}	13.44±1.07^{abc}	29.47±0.61^{a}	53.67±3.21^{i}	25.03±2.06^{abcd}	4.15±0.84^{bc}
Binadhan-23	118±1.53^{def}	116.67±1.53^{f}	13.33±1.16^{abc}	28.73±1.11^{ab}	83.20±3.30^{cde}	25.77±1.70^{abcd}	5.21±0.30^{abc}
IR18A1800	117±0.58^{fgh}	114.67±0.58^{fg}	11.55±0.51^{cd}	27.50±0.50^{cd}	102.20±2.11^{a}	26.03±2.27^{abcd}	5.11±0.45^{a}

Genetic diversity assessment is crucial for any crop improvement program (Mehmood *et al*. 2021). Multivariate analysis is a useful tool for assessing and measuring the genetic divergence among the given genotypes with respect to characters that were considered together (Khadakabhavi *et al*. 2014, Mounika and Lal, 2018). Mean sum of square, genotypic variances ($σ^2$g), phenotypic variances ($σ^2$P), heritability, genotypic co-efficient of variation (GCV), phenotypic co-efficient of variation (PCV), genetic advance and genetic advance as percent of mean, GA (%) for all the yield contributing traits are presented in Table 2. The phenotypic variance was higher than the genotypic variance for all the traits. The filled grain per panicle showed the highest range of phenotypic and genotypic variations among the traits followed by the plant height, panicle length, 1000 seed weight, while yield displayed the least variation. A similar finding was reported by Khan *et al*. 2023 for filled grain per panicle and single plant yield. Wide and narrow difference between PCV and GCV for the characters implies their susceptibility and resistance to environmental fluctuation respectively. Divergence among the genotypes related to the variation present in particular trait. The difference between genotypic and phenotypic coefficient of variation (GCV and PCV) indicates the extent of environmental effect on a specific trait (Asante *et al*. 2019). Kumar, 2019 classified the magnitude of GCV and PCV values as low (< 10%), moderate (10-20%) and high (> 20%) scale (Kumar, 2019). In the current study, PCV was larger in magnitude compare to the corresponding GCV for all the studied traits (Table 2), indicate significant influence of environment on the expression of these traits. Considerable environmental influence on rice traits was also observed by many others researchers. Similar results are delineated by Rashid *et al*. 2017; and Gyawali *et al*. 2018; Lalitha *et al*. 2019. PCV ranges from 1.49 to 16.15 and GCV ranges from 1.37 to 15.32 per cent among the seven quality attributing parameters (Table 2). High magnitude of GCV and PCV was obtained only for yield and filled grain respectively, and the rest of the characters had shown moderate to low GCV and PCV values (Table 2). Very minimal differences between GCV and PCV values were noted for dry matter and 100 seed weight indicated least influenced of environment on those traits.

Table 2. Estimation of genetic parameters of fifteen rice genotypes based on yield contributing traits

Traits	Min	Max	Mean	σ^2g	σ^2e	σ^2P	GCV	ECV	PCV	h^2b (%)	GA	GA (% mean)
DM	114	121	117.46	2.59	0.50	3.09	1.37	0.60	1.49	83	3.03	2.58
PH	104	139	126.11	94.53	4.95	99.48	7.70	1.76	7.90	95	19.52	15.48
ET	9.33	15.66	12.89	1.03	1.11	2.14	7.89	8.17	11.36	48	1.45	11.29
PL	21.2	30.0	26.11	3.80	0.35	4.15	7.46	2.26	7.80	91	3.84	14.71
FG	50.0	104.2	79.2	136.26	5.65	141.92	14.72	3.00	15.02	96	23.56	29.72
HSW	19.8	29.9	25.57	3.14	3.82	6.96	6.93	7.64	10.31	45	2.45	9.59
Y	4.45	8.10	6.68	1.04	0.11	1.16	15.32	5.11	16.15	89	2.00	29.95

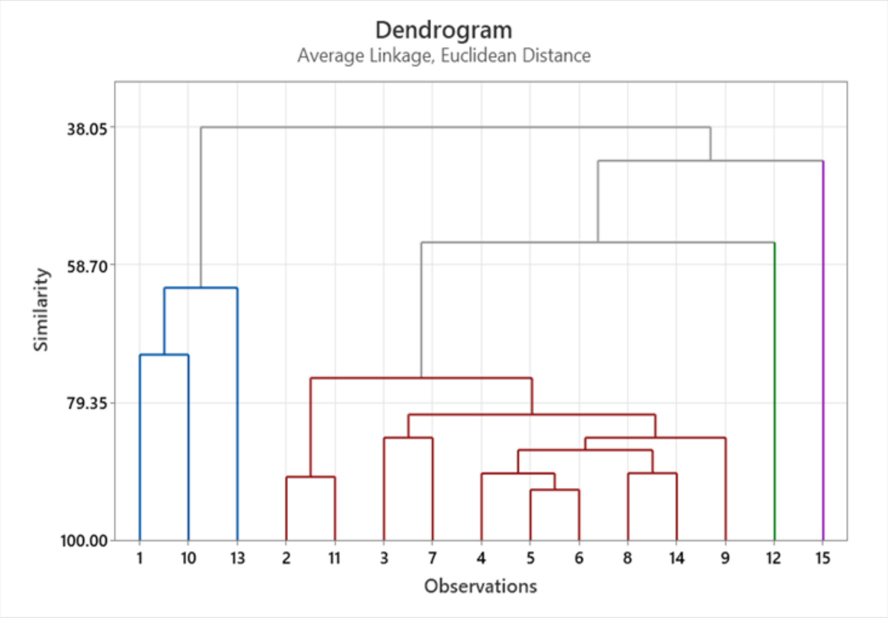
DM-Days to Maturity, PH-Plant Height, ET-Effective tiller, PL-Panicle length, FG-Filled grain per panicle, 1000 seed wt., Yield

Table 3. Grouping of 15 rice genotypes by Euclidean Method

Cluster	Number of genotypes	Name of genotypes
Cluster 1	3	IR17A1633, IR17A3006, IR17A3163
Cluster 2	10	IR17A3056, IR18A1029, IR17A2210, IR17A3089, IR18A1762, Binadhan-17, IR18A1910, BRRI dhan-76, IR17A3006 and Binadhan-23
Cluster 3	1	BRRI dhan-77
Cluster 4	1	IR18A1800

Heritability acts as predictive instrument for the selection of a particular trait. Higher heritability as well as high genetic advance are considered ideal indicators for selection and breeding purposes (Ogunbayo *et al*. 2014). Heritability value was classified by Johnson *et al*. as low (< 30%), moderate (30-60%) and high (> 60%) (Johnson *et al*. 1995). Moderate to high heritability (45-96%) percentage was observed among the different traits studied in the study (Table 2). Among the traits, high heritability was observed for filled grain per panicle (96%), plant height (95%), and Panicle length (91%) respectively, indicate the predominance of the genetic factor and less influenced by environment in their expression. Therefore, the selection would be effective for these traits. Results of the present study closely agree with the earlier reports of Pandey *et al*. (2009) who observed significant variations among 40 rice accessions for 12 quantitative traits. High heritability coupled with high genetic advance as percent of mean was recorded for filled grain per panicle and plant height and yield indicating predominance of additive gene effects for controlling the respective traits (Table 2). These findings were corroborated by Singh *et al*. (2005) for plant height; Sanker *et al*. (2006) for plant height, panicle length, grain per panicle, Kishore *et al*. (2008) for plant height, 50 per cent flowering (Singh *et al*. 2005; Sanker et al. 2006; Kishore et al. 2008). However, days to maturity and panicle length had recorded a high heritability coupled with low genetic advance as per cent of mean indicating the role of non- additive gene effects for the characters. The 15 rice genotypes were grouped in 4 clusters based on growth and yield traits

(Table 3, Figure 1). Among the 4 clusters, cluster II was the largest and displayed the highest overall genetic similarity followed by clusters I (3). Clusters III and IV were the smallest, each containing only one genotype (Table 3, Figure 1). Similar results were also reported in soybean by khan *et al*. (2022), in wheat by Al-Ashkar *et al*. (2020), in maize by Bista *et al*. (2022) and in chillis by Ahmad *et al*. (2022).



Here,
1= IR17A1633, 2= IR17A3056, 3= IR18A1029, 4= IR17A2210, 5= IR17A3089, 6= IR18A1075, 7= Binadhan-17, 8= IR18A1910, 9= BRRI dhan-76, 10= IR17A3006, 11= IR18A1762, 12= BRRI dhan-77, 13= IR17A3163, 14= Binadhan-23 and 15= IR18A1800

Figure 1. Dendogram of 15 rice genotypes using Euclidean method

Table 4. Cluster mean for yield and yield related characters in rice genotypes

Variable	Cluster I	Cluster II	Cluster III	Cluster IV	Grand centroid
Days to Maturity	116.780	117.900**	116.00*	116.67	117.467
Plant Height (cm)	110.443*	131.267	133.00**	114.67	126.111
Effective tiller	12.960	12.786	15.11**	11.55*	12.893
Panicle length (cm)	25.900	25.879*	27.77**	27.50	26.117
Filled grain	64.377	83.099	62.67*	102.20**	79.266
1000 seed wt.	25.353*	25.587	25.70	26.03**	25.577
Yield (t/ha)	5.42	5.52**	5.35	5.11*	6.683

*Minimum value **Maximum value

The mean values for plant height (cm), effective tiller number and panicle length were all highest in cluster III, out of the four possible cluster (Table 4). For the trait yield cluster II had the highest value. Cluster III also had the lowest average mean of days to maturity and the filled grains. The grouping pattern showed that there was no link between genetic divergence and geographic diversity, which has been a source of debate for a long time. There have also been similar observations (Chandramohan, 2016; Ranjith, 2018).

The lowest distance between cluster centroids was found between cluster III and cluster II (20.99), which shows that the genotypes are similar (Table 5). The highest distance was found between cluster III and cluster IV (43.74), which shows that the genotypes are different. Srinivas *et al*. (2018) and Tripathi *et al*. (2018) both came up with the same results when they looked at rice. Kumar *et al*. 2019 stated that distance clusters of genotypes can be used in hybridization programme to get a wide range of differences between genotypes.

CONCLUSION

Multivariate analysis-based grouping would potentially be applied in selection of diverse parents which can be used for future breeding programs. Based on these analyses, the cluster analysis revealed the presence of genetic variation in the genotypes studied. Cluster III and IV had the greatest distance between cluster centroids, showing genetic dissimilarity. Crosses between parents from the most diverse clusters are likely to have the most heterosis. The highest yielding rice genotype was found in IR18A1075, followed by IR17A1633 and Binadhan-17. These genotypes might be the promising rice genotypes and cultivating those can increase grain production.

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