Acta Scientifica Malaysia (ASM)

DOI: http://doi.org/10.26480/asm.02.2023.50.59

ISSN: 2521-5051 (Print)
ISSN: 2521-506X (Online)
CODEN: ASMCCQ

RESEARCH ARTICLE

GENETIC ANALYSIS OF LOCAL AMAN RICE (*ORYZA SATIVA* L.) GENOTYPES BASED ON MORPHOLOGICAL TRAITS

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ARTICLE DETAILS

Article History:

Received 20 August 2023
Revised 23 September 2023
Accepted 28 October 2023
Published 04 November 2023

ABSTRACT

Rice is the staple food for the majority of the global populations and the nutritional traits improvement is the prime priority for rice breeding. The study was carried out with 30 local rice varieties including two checks during the aman season of 2021 at BIRTAN, Noakhali, Bangladesh. Significant differences were found among the cultivars for the studied parameters. The lowest days to maturity were observed in both RS 40 and RS 56. The highest grain yield per plant was observed in RS 31, followed by RS 17 and RS 22 as compared with check. The number of panicles and filled grains per panicle were the most contributing variables. Genetic distances of genotypes ranged from 0.086 to 4.262. Considering the overall diversity pattern, grain yield, and other agronomic traits, RS17, RS22, RS29, RS31, and RS42 have been selected as promising genotypes for further yield and nutritional traits improvement through hybridization.

KEYWORDS

Genetic Divergence, Correlation, Regression, Principal Component Analysis, plant characters.

1. INTRODUCTION

Rice (*Oryza sativa* L.) is one of the major cereal crops with the particular preference of global importance for more than half of the world's population (Sahu et al., 2017). Rice landraces take a crucial part in food and nutrition security in addition to disease and pest resistance and resilience to climate change, which is essential for human survival in the face of undesired climate change on Earth. An estimated 90% of the world's rice is produced and consumed in Asia, where rice is the staple food for 50% of the population (Bhattacharjee et al., 2002; Islam et al., 2018; Tenorio et al., 2013). Rice has been harvested, consumed, and cultivated by more people worldwide for over 10,000 years than any other crop (Onyango, 2014). In developing countries, people eat white rice, although many rice varieties with black, red, and purple kernels are cultivated (Ahmad et al., 2015; Patel et al., 2014). Pigmented rice possesses a high levels of phenolic and anthocyanin content in the pericarp with a red to dark purple color (Ichikawa et al., 2001; Rathna Priya et al., 2019). Anthocyanin is well known as a healthy functional food ingredient because of its antioxidant activity, anti-inflammatory, and anticancer effects as well as lowering cholesterol levels (Kaur et al., 2017; Nam et al., 2006; Rathna et al., 2019).

A breeding program could be successful depending on the amount of genetic variability and the extent of heritability of the desired traits (Arunachalam, 1981; Ragvendra et al., 2011). The main breeding goal of rice breeding programs is to break the yield ceiling by utilization of genetic resources with desirable genes with the noble intention of feeding the ever-increasing humankind. Rice improvement considering yield as well as abiotic and biotic stresses with the exploitation of local rice genetic resources is a major goals for the rice breeders (Al-Amin et al., 2013; Alam et al., 2012; Moniruzzaman et al., 2013). Grain yield is a complex trait that depends on several yield-related characters besides showing poor response to direct selection. Therefore, understanding the nature and extent of genetic variation that leads to the heritability of quantitative traits such as yield and yield-related components is the key to efficient genetic improvement (Islam et al., 2018; Rashid et al.,2012;Salim et al., 2013; Sarif et al., 2020). The genetic diversity study is the prerequisite for crop improvement. Knowledge of genotype diversity and genetic distance also assist to identify parental lines for hybridization programs (Alam et al., 2016, 2020; Haque et al., 2022; Mia et al., 2022).

Principal component analysis (PCA) is an important tool for diversity analysis that helps to identify plant characters that classify distinctness among potential genotypes and traits of interest. It is a powerful tool for the characterization and identification of desired traits and genotypes for purposeful breeding (Alam et al., 2021; Chakravorty et al., 2013). Local aman rice germplasm could be a great source for rice improvement for abiotic and biotic stresses due to changing climate (Emi et al., 2021). Although there are different local rice cultivars cultivated in the coastal region of Bangladesh, their diversity has not been well studied. Therefore, this study was conducted to estimate the genetic diversity of 30 brown, black, and red rice genotypes on the basis of yield and yield-related traits.

2. MATERIALS AND METHODS

2.1 Study area and the design of the Experiment

The study was carried out at the research field of BIRTAN, Noakhali, Bangladesh, during the Aman season of 2021. A total of 30 Aman rice genotypes were collected from different locations in Bangladesh. The study was organized in a randomized complete block design (RCBD) with three times of each treatment. Each plot was 5 m long and 1.2 m wide, whereas row-to-to-row distance was maintained at 0.2 m and plant-to-to-plant distance 0.15 m. Twenty-five days old seedlings were transplanted to the main field. All necessary intercurtural operations and plant protection measures were done during the crop growing period. Data was collected on yield and yield related important agronomic characters from selected individual plants from each plot.

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DOI:
10.26480/asm.02.2023.50.59

Cite The Article: Mohammad Zahir Ullah, Md. Sarowar Alam, Md. Samsuzzaman, Md Nurul Huda (2023). Genetic Analysis of Local Aman Rice (*Oryza Sativa* L.) Genotypes Based on Morphological Traits. *Acta Scientifica Malaysia, 7(2): 50-59.*

2.2 Data Analysis

Principal component analysis (PCA) was performed to compute the traits, which estimated more of the total variation. The collected data was standardized to mean zero and variance of one before computing principal component analysis. The principal component-based correlation matrix was analyzed by OPSTAT software (Sheoran et al., 1998). The 10 highest and 10 lowest genetic distances of rice genotypes was estimated using Euclidean distance (ED) calculated from quantitative traits after standardization (Sneath and Sokal, 1973). The genotypes were grouped into various clusters, whereas intra and inter-cluster distances and mean performance for the characters were analyzed.

3. RESULTS AND DISCUSSION

3.1 Plant Traits Mean Performance

The analysis of variance revealed that the genotypes showed highly significant differences ($p<0.01$) among the studied characters (Table 1). It is indicated that the existence of adequate variation among the genotypes for yield and yield contributing characters and consequently, there is a possibility for efficient selection. Days to first flowering (84) and fifty percent flowering (92) were lower in Shaita but higher in RS24 which were 130 days and 139 days, respectively. Days to maturity was the highest (168) for RS32 and the lowest (135) for RS30. Highest plant height (188.67 cm) was observed in RS40 but the lowest values were found for RS50 and RS51, respectively. The highest number of effective tillers per plant was found in RS 31 (34.33) and it was statically similar to RS 22 (33.00). The highest and lowest filled grains per panicle were observed in RS 56 (325.33) and RS 50 (79.33), respectively. The maximum grain yield per plant was noted in RS 31 (60 g). The minimum grain yield was noted in RS 50 (6.33 g) due to its lowest filled grains per panicle.

DFF: days to first flowering, D50F: days to 50% flowering, DM: days to maturity, PH: plant height (cm), TTP: Tillers per plant, ETP: effective tillers per plant, PL: panicle length (cm), GPP: grains per panicle, FGP: filled grains per panicle, UGPP: unfilled Grains per panicle and GYP: grain yield per plant (g).

Effective tillers per plant are the most essential component of yield. Satapathy *et al.*, observed that the number of effective tillers per plant leads to higher yield (Satapathy et al., 2015). The highest number of effective tillers per plant was found in RS 31 and RS 22. The number of filled grains per panicle is affected by the grain set amount that was reported by Tsuneo Kato (Kato, 2010). I our present study, the highest and lowest filled grains per panicle were observed in RS 56 and RS 50, respectively. The poor grain filling in rice is the consequence of low translocation and segmentation of assimilates into grains (sink) compared to inadequate biomass production (source) (Puteh et al., 2014). Grain yield is a major trait which determines the genetic ability of a variety. The maximum grain yield per plant was noted in RS 31 (60 g). Comparable finding was demonstrated by Subramani *et al.* (Subramani et al., 2014). The minimum grain yield was noted in RS 50 (6.33 g) due to its lowest filled grains per panicle. These findings were in agreement with other studies with rice (Sary et al., 2022; Tyeb et al., 2013).

Table 1: Mean Performance of 30 Aman Rice Cultivars Based on 11 Morphological Traits

	DFF	**D50F**	**DM**	**PH**	**TTP**	**ETP**	**PL**	**GPP**	**FGP**	**UGPP**	**GYP**
RS17	115^{l}	120^{h}	160^{d}	179^{ab}	19^{bcd}	19^{b-e}	25^{e-k}	244.33^{d-h}	243.33^{de}	1^{g}	49^{b}
RS22	112^{m}	120^{h}	149^{g}	118.67^{hi}	33.33^{a}	33^{a}	27.33^{b-g}	266.67^{b-f}	260^{bcd}	6.67^{efg}	48^{b}
RS24	130^{a}	139^{a}	158^{e}	167.67^{bcd}	19.67^{bcd}	19.67^{b-e}	25.33^{d-k}	106^{opq}	80^{k}	26^{b}	16^{kl}
RS19	107^{n}	115^{i}	149^{g}	121^{hi}	24.33^{bc}	24.33^{bc}	28.67^{a-e}	297.33^{bc}	291^{abc}	5.67^{efg}	28^{fg}
RS25	124^{ef}	130^{cde}	164^{c}	172.67^{abc}	24.67^{bc}	24.67^{bc}	27.33^{b-g}	176^{jklm}	164.33^{ghi}	11.67^{c-g}	12^{m}
RS23	117^{jk}	126^{efg}	164^{c}	167.67^{bcd}	17.67^{cd}	17.67^{c-f}	29^{a-d}	130.33^{nop}	105^{jk}	25.33^{bc}	18.27^{k}
Shaita	84^{r}	92^{l}	132^{m}	141.67^{fg}	19^{bcd}	19^{b-e}	20.67^{l}	98.33^{pq}	91^{k}	7.33^{efg}	31.67^{e}
BRRI dhan80	102^{o}	110^{j}	148^{h}	142.33^{fg}	27.67^{ab}	27.67^{ab}	26.55^{c-i}	215.33^{h-k}	198^{fg}	17.33^{b-e}	38^{d}
RS28	96^{q}	106^{k}	144^{j}	143.67^{fg}	15^{d}	14.67^{def}	27^{b-h}	245.33^{d-h}	228.33^{def}	17^{b-f}	41^{c}
RS29	123^{fg}	132^{cd}	167^{b}	148.67^{efg}	16.33^{cd}	16.33^{c-f}	27.67^{b-f}	275.33^{bcd}	267.67^{bcd}	7.67^{efg}	46^{b}
RS30	96^{q}	106^{k}	135^{l}	155.67^{c-f}	13^{d}	9^{f}	27.33^{b-g}	207.33^{h-k}	189.67^{fgh}	17.67^{b-e}	8.33^{n}
RS31	116^{kl}	119.33^{h}	146^{i}	154.33^{def}	34.33^{a}	34.33^{a}	28.67^{a-e}	302^{bc}	288.33^{abc}	13.67^{b-g}	60^{a}
RS32	125de	128.67^{defg}	168^{a}	165.33^{b-e}	13^{d}	13^{def}	26.33^{c-i}	143^{mno}	139.33^{ij}	3.67^{efg}	17^{kl}
RS33	128^{b}	137^{a}	167^{b}	170^{bcd}	13.33^{d}	13.33^{def}	24.67^{f-l}	156^{lmn}	150.33^{hi}	5.67^{efg}	22$^{h j}$
RS34	106^{n}	114.67^{i}	146^{i}	157^{cdef}	14.67^{d}	13.67^{def}	24.33^{f-l}	174^{klm}	166.33^{ghi}	7.67^{efg}	17^{kl}
RS35	112^{m}	121^{h}	146^{i}	142.67^{fg}	20^{bcd}	20^{bcde}	23.33^{h-l}	194.33^{i-l}	189.67^{fgh}	4.67^{efg}	30^{ef}
RS36	116^{kl}	124.67^{g}	135^{l}	157.67^{c-f}	24.67^{bc}	24.33^{bc}	30.67^{ab}	308.33^{b}	296.67^{ab}	11.67^{c-g}	30^{ef}
RS37	126^{cd}	133.33^{bc}	146^{i}	169^{bcd}	18.33^{cd}	18.33^{cde}	26^{c-j}	176.67^{j-m}	171.33^{ghi}	5.33^{efg}	25^{gh}
RS38	127^{bc}	136^{ab}	154^{f}	155.33^{c-f}	13^{d}	13^{def}	23.67^{g-l}	103.67^{opq}	101.67^{jk}	2^{g}	12^{m}
RS39	121^{hi}	127.33^{efg}	146^{i}	170.67^{bcd}	11.33^{d}	11^{ef}	28.67^{a-e}	198.67^{i-l}	195^{fg}	3.67^{efg}	25^{ghi}
RS40	100^{p}	107.33^{jk}	127^{n}	188.67^{a}	12.33^{d}	12.33^{def}	32.33^{a}	224$^{e ghi}$	161.33^{ghi}	62.67^{a}	12^{m}
RS56	112^{m}	118^{hi}	127^{n}	133^{gh}	16.33^{cd}	15^{def}	29.67^{abc}	347.67^{a}	325.33^{a}	22.33^{bcd}	32^{e}
RS50	117^{jk}	125^{fg}	149^{g}	87.67^{k}	12.33^{d}	11^{ef}	21^{l}	81.67^{q}	79.33^{k}	2.33^{fg}	6.33^{n}
RS51	118^{j}	126^{efg}	149^{g}	79.67^{k}	13^{d}	12^{def}	21.67^{kl}	85.33^{q}	83.67^{k}	1.67^{g}	6.45^{n}
RS48	120^{i}	129^{def}	146^{i}	92.67^{jk}	13^{d}	13^{def}	23^{ijkl}	175.67^{j-m}	168.33^{ghi}	7.33^{efg}	8^{n}
RS52	122^{gh}	130^{cde}	146^{i}	108.67^{ij}	12^{d}	12^{def}	27.67^{b-f}	264^{c-g}	248.67^{cde}	15.33^{b-g}	14^{lm}
RS45	120^{i}	129.33^{de}	143^{k}	113.33^{i}	17^{cd}	16.67^{c-f}	25^{e-k}	272^{bcd}	270^{bcd}	6.67^{efg}	28^{fg}
RS41	116^{kl}	126^{efg}	135^{l}	106^{ij}	11.33^{d}	11.33^{def}	22.33^{jkl}	104^{opq}	93.67^{k}	10.33^{d-g}	12^{m}
RS42	121^{hi}	129^{def}	143^{k}	120^{hi}	20.33^{bcd}	20.33^{bcd}	24.67^{f-l}	267^{b-e}	264^{bcd}	3.33^{efg}	36^{d}
RS47	120^{i}	128^{defg}	143^{k}	93.67^{jk}	20.33^{bcd}	20^{b-e}	24^{f-l}	219.33^{hij}	214^{ef}	5.33^{efg}	47^{b}
Min	**84.00**	**92.00**	**127.00**	**79.67**	**11.33**	**9.00**	**20.67**	**81.67**	**79.33**	**1.00**	**6.33**
Max	130.00	139.00	168.00	188.67	34.33	34.33	32.33	347.67	325.33	62.67	60.00
F test	**	**	**	**	**	**	**	**	**	**	**
CV (%)	0.67	1.72	1.23	6.63	21.07	26.13	7.70	11.57	12.05	65.10	6.77

Same letter(s) in a column did not differ significantly at $p \leq 0.05$ by DMRT; * and ** = Significant at 5 and 1% level of probability, respectively; NS = Not significant, CV (%) = coefficient of variation.

DFF: days to first flowering, D50F: days to 50% flowering, DM: days to maturity, PH: plant height (cm), TTP: Tillers per plant, ETP: effective tillers per plant, PL: panicle length (cm), GPP: grains per panicle, FGP: filled grains per panicle, UGPP: unfilled Grains per panicle and GYP: grain yield per plant (g).

3.2 Correlation and Regression

Days to first flowering showed a highly significant and positive correlation with days to fifty percent flowering (0.974**), days to maturity (0.577**) but a negative relationship with unfilled grains per panicle (-0.280**). Days to fifty percent flowering had a very strong positive association with days to maturity (0.549**) but a negative relation with unfilled grains per panicle (-0.293**) Days to maturity had a significant positive relationship with plant height (0.242*) but a negative relationship with grains per plant. Plant height showed a highly significant positive correlation with panicle length (0.461**) but a negative relationship with tiller per plant. Total tillers per plant showed a highly significant positive correlation with effective tillers per plant (0.986**) and significant relation with filled grains per panicle. Panicle length had a strong positive correlation with grains per plant (0.583**), filled (0.494**), and unfilled grains per plant (0.517**). Again, grains per plant showed a highly significant relationship with filled grains per panicle (0.984**). A highly significant and positive correlation was observed of grain yield per plant with total tillers per plant (0.458**), effective tillers per plant (0.573**), grains per panicle (0.607**), and filled grains per panicle (0.637**) (Table 2). It showed the significance of these characters for the increase of rice yield in the T. Aman season. These findings are in line with the results of other previous studies (Babu et al., 2012; Bagheri et al., 2011). Similar trends of results were also observed in other previous studies with rice, peanut, and hyacinth bean (Rashid et al.,2012, Samsuzzaman et al., 2023).

Grain yield per plant had a negative relationship with unfilled grains per panicle, which indicated that grain yield per plant reduces with the increase of unfilled grains per panicle. Plant height showed positively significant association with panicle length that was similar to other findings (Babu et al., 2012; Konate et al., 2016; Sadeghi, 2011). Positive and significant correlations were recorded for the number of effective tillers per plant with panicle length, the number of grains per panicle, and filled grains per panicle. Deepa Shankar *et al.* also observed similar results in another study (Sankar et al., 2006). Linear regression analysis of grain yield per plant based on all yield-related components is shown in Table 3. Grain yield exhibited a significant linear regression coefficient with days to maturity (0.249*), plant height (0.110**), tillers per plant (0.242**), and effective tillers per plant (0.384**). Linear regression analysis showed that the selection of the best regression equation done by a backward elimination technique exhibiting that days to maturity, plant height, tillers per plant, and effective tiller per plant were the highly efficient yield contributing variables.

Table 2: Pearson Correlation Matrix of 11 Morphological Attributes on Yield of Rice Genotypes

	D50F	DM	PH	TTPP	ETPH	PL	GPP	FGP	UFGP	GYPP
DFF	0.974**	0.577**	-0.015	0.047	-0.043	-0.039	-0.109	-0.059	-0.280**	-0.134
D50%F		0.549**	-0.060	0.036	-0.080	-0.072	-0.146	-0.093	-0.293**	-0.181
DM			0.242*	-0.064	0.056	-0.088	-0.255*	-0.200	-0.324**	0.018
PH				-0.232*	0.081	0.491**	0.054	-0.007	0.333**	0.095
TTPP					0.986**	-0.013	0.196	0.211*	-0.081	0.458**
ETPP						0.232*	0.398**	0.403**	-0.020	0.573**
PL							0.583**	0.494**	0.517**	0.195
GPP								0.984**	0.137	0.607**
FGPP									-0.040	0.637**
UGPP										-0.140

* and ** = Significant at 5 and 1% level of probability, respectively.

DFF: days to first flowering, D50F: days to 50% flowering, DM: days to maturity, PH: plant height (cm), TTPP: total tillers per plant, ETPP: effective tillers per plant, PL: panicle length (cm), GPP: grains per panicle, FGPP: filled grains per panicle, UGPP: unfilled Grains per panicle and GYPH: grain yield per plant (g).

Table 3: Linear Regression Coefficients of Vegetative and Reproductive Attributes on The Yield of Rice Genotypes

Attributes	Linear Regression Coefficients (b)	t-Value	Significance
Days to first flowering	0.040	0.097	0.922
Days to 50% flowering	-0.367	-0.901	0.365
Days to maturity	0.249	2.090*	0.037
Plant height (cm)	0.110	2.672**	0.008
Total tillers per plant	0.242	4.161**	0.000
Effective tillers per plant	0.384	2.469**	0.014
Panicle length (cm)	-1.111	-2.223*	0.027
Grains per panicle	-0.056	-0.086	0.931
Filled grains per panicle	0.178	0.274	0.782
Unfilled Grains per panicle	0.009	0.014	0.989

*= significant at 5%, **= significant at 1%, ***= significant at 0.1%

3.3 Principal Component Analysis (PCA)

The principal component analysis (PCA) results comprise the factor scores of every single character among the 30 rice genotypes, eigen values, and percentage of total variance accounted for by the four principal components (PCs). The PCA was grouped into four principal components (PC1 to PC4) with eigen values ranging from 1.117 to 3.609. The percentage of four PCs ranged from 10.2 to 32.8% and the value was 83.2% of the total variation (Table 4). The greater eigenvalues were reflected as the greatest representative of system traits in the principal components. The PC1 revealed 32.8% variability among characters, followed by PC2, PC3, and PC4 showing 22.9%, 17.3%, and 10.2% variability, respectively. The PC1 was comparatively to the upper value that contains days to 50% flowering, effective tillers per plant, panicle length, grains per panicle, filled grains per panicle, and grain yield per plant (Table 5). These characters had more involvement in the total diversity and accountable for the distinction of the clusters. Days to first flowering, days to 50% flowering, days to maturity, effective tillers per plant, unfilled grains per panicle, and grain yield per plant had significant roles in the total genetic diversity and genotypes clustering in PC2.

In PC3, plant height and panicle length had comparatively higher influence on the total genetic diversity and genotypes clustering. In PC4, days to 50% flowering, days to maturity, plant height, grains per panicle, and filled grains per panicle had comparatively more involvement in the total variance. Plant height had the highest involvement and other characters viz. days to first flowering, days to 50% flowering; panicle length, grains per panicle, and filled grains per panicle contributed higher to genetic diversity. The highly contributed traits to total genetic divergence are influenced by additive gene action, which may lead to a better opportunity for crop improvement by selective breeding. In different PCs, there are some important characters which are coming together and have the tendency to stay together, which can be considered to utilize those characters for better and rapid improvement of crop yield and yield-related characters in a breeding program. Biswas *et al.* stated the contribution of the first three principal components caused 82.99% variation (Biswash et al., 2016). Moreover, the first four principal components contributed approximately 72.1% and 76.7% variation (Tuhina-Khatun et al., 2015; Sohrabi et al., 2012). Moreover, this finding is confirmed in other studies (Asante et al., 2019; Biswash et al., 2016).

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Table 4: Eigenvalues of the Principal Components of The Correlation Matrix for 30 Rice Genotypes

	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9	PC10	PC11
Eigenvalues	3.609	2.521	1.902	1.117	0.852	0.423	0.290	0.204	0.073	0.009	0.000
Proportion	32.8	22.9	17.3	10.2	7.7	3.8	2.6	1.9	0.7	0.1	0.0
Cumulative Proportion	32.8	55.7	73.0	83.2	90.9	94.8	97.4	99.3	99.9	100.0	100,0

Table 5: Principal Component Values of The First Four Principal Components for 30 Rice Genotypes Evaluated in 2021.

Traits	**PC1**	**PC2**	**PC3**	**PC4**
Days to first flowering	-0.215	**0.492**	0.247	0.229
Days to 50% flowering	**-0.239**	**0.474**	0.230	**0.263**
Days to maturity	-0.200	**0.393**	0.242	**-0.386**
Plant height (cm)	0.097	-0.065	**0.545**	**-0.469**
Tillers per hill	0.165	0.238	**-0.330**	-0.144
Effective tillers per hill	**0.319**	**0.253**	-0.102	**-0.412**
Panicle length (cm)	**0.353**	-0.028	**0.484**	0.125
Grains per panicle	**0.468**	0.137	0.062	**0.329**
Filled grains per panicle	**0.446**	0.197	0.001	**0.330**
Unfilled Grains per panicle	0.159	**-0.359**	**0.375**	0.025
Grain yield per plant (g)	**0.388**	**0.257**	-0.179	**-0.293**

PC1, first principal component; PC2, second principal component; PC3, third principal component and PC4, fourth principal component.

3.4 Clustering of Genotypes

The 30 rice genotypes were grouped into five different clusters according to the mean values of the genotypes for 11 quantitative characters (Table 6). Cluster V was the largest cluster (33.33%) containing 10 genotypes. Cluster III and cluster II consisted of seven (23.33%) and five genotypes. While, cluster IV and cluster I had four genotypes and one genotype, respectively. The findings indicated that the genotypes under the same cluster showed similarities for many characters, while exhibiting dissimilarity to other genotypes in other clusters on one or more characters. Ahmed *et al.* showed seven clusters in 40 Balam rice genotypes for 17 traits (Ahmed et al., 2015). Similarly, Sohrabi *et al.* stated six clusters in 50 Malaysian upland rice germplasm for 12 characters (Sohrabi et al., 2012). Again, reported five clusters from 35 Aman rice cultivars for 10 characters during the Kharif season (Roy et al., 2004). A group researchers the genotypes within the clusters showed homogeneity (Hossain et al., 2015; Kulsum et al., 2011).

3.5 Scatter Diagram

On the basis of the principal component scores 1 and 2 found from the principal component analysis, a two-dimensional scatter diagram (Z1-Z2) (Figure 1) utilizing component score 1 as X-axis and component score 2 as Y-axis was created. The position of the genotypes in the scatter diagram was distributed into five groups revealing the presence of significant diversity among the genotypes. The clustering pattern confirmed the results gained by diversity analysis. Similar clustering pattern was also confirmed in other studies (Alam et al., 2016, 2021; Hossain et al., 2015).

Table 6: Distribution of 30 Genotypes in Different Clusters

Cluster	No. of genotypes	Name of genotypes	Varietal Code	Percentage
Cluster I	4	G1, G8, G9, G30	RS 17, RS 92, RS 28, RS 47	13.33
Cluster II	5	G2, G10, G26, G27, G29	RS22, RS 29, RS 52, RS 45, RS 42,	16.68
Cluster III	7	G3, G6, G7, G19, G23, G24, G28	RS24, RS23, G54, RS 38, RS 50, RS 51, RS 41,	23.33
Cluster IV	4	G4, G12, G17, G22	RS19, RS 31, RS 36, RS 56,	13.33
Cluster V	10	G5, G11, G13, G14, G15, G16, G18, G20, G21, G25,	RS25, RS 30, RS 32, RS 33, RS 34, RS 35, RS 37, RS 39, RS 40, RS 48,	33.33
Total	30			100

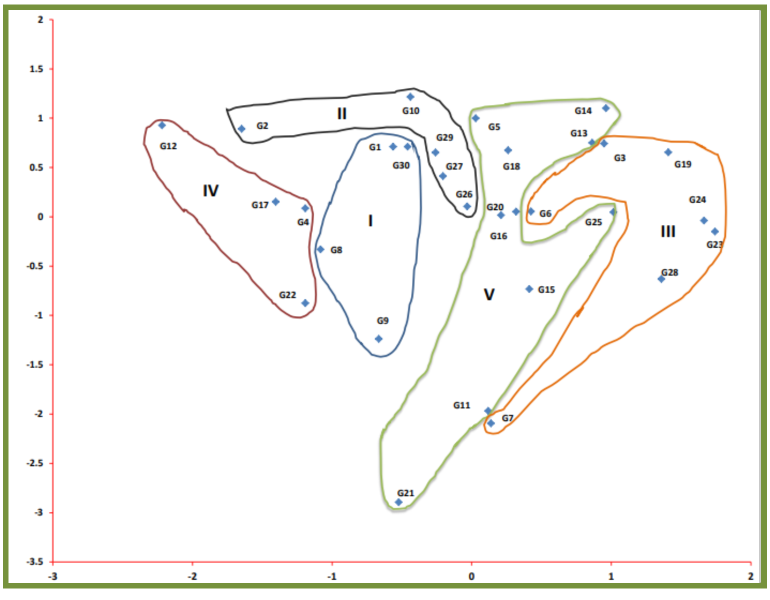

Figure 1: Two-dimensional scatter diagram based on PCA scores for 11 morphological characters of 30 Aman rice genotypes

3.6 Genetic Distances Among Rice Genotypes

The genetic distance for all possible pairs of 30 rice genotypes ranged from 0.086 to 4.262 with the mean (1.78), standard deviation (0.91), and coefficient of variation (50.84%). The maximum genetic distance was observed between G14 and G21 (4.262) whereas the minimum genetic distance was reported between G3 and G13 (0.086) (Table 7). Rice genotypes with greater than average genetic distances can be considered for crossing programs for the combination of their desirable characters. Crossing genotypes with high genetic distance between them has the potential to produce heterotic hybrids. This result is supported by the findings of other studies (Priyanga et al., 2020; Sarif et al., 2020; Sohrabi et al., 2012).

The intra-(bold) and inter-cluster distances (D^2) are presented in Table 8. The highest intra-cluster distance was observed in cluster I (0.509), while the lowest was in cluster V (0.076), which indicates that genotypes within cluster I were the most diverse and genotypes under cluster V were similar or less diverse compared to other clusters' genotypes. On the other hand, in the case of the intercluster distance, the maximum genetic distance was observed between clusters III and IV (300.265), which exhibited a wide range of diversity. Again, the lowest inter-cluster distance was found between clusters I and II (61.786). A group researchers reported that the inter-cluster distance was maximum between clusters II and IV (Biswas et al., 2019). The minimum intercluster distance (61.786) was found between clusters I and II. Mahalingam *et al.* reported that inter-cluster distances ranged from 6.14 to 24.84, greater compared to distances which ranged from 0.0 to 12.11 in Indian and exotic rice (Mahalingam et al., 2012). Hossain *et* noted that intra- and inter-cluster distances ranged from 0.0 to 1.02 and 2.21 to 21.59 in aromatic and fine rice (Hossain and Haque, 2016).

Table 7: Ten Highest and Ten Lowest Inter-Genotypic Distances Among the 30 Rice Genotypes

Highest	Genotypic combination	Distance	Lowest	Genotypic combination	Distance
10 highest inter genotypic distance			10 lowest inter genotypic distance		
1.	G14-G21	4.262	1.	G3-G13	0.086
2.	G12-G21	4.181	2.	G1-G29	0.103
3.	G10-G21	4.111	3.	G6-G20	0.106
4.	G12-G23	4.105	4.	G20-G26	0.115
5.	G19-G21	4.039	5.	G7-G11	0.129
6.	G12-G24	4.001	6.	G23-G24	0.136
7.	G2-G21	3.950	7.	G6-G26	0.218
8.	G5-G21	3.932	8.	G4-G17	0.221
9.	G13-G21	3.923	9.	G27-G30	0.245
10.	G12-G28	3.902	10.	G16-G26	0.257

Table 8: Average Intra-(Bold) and Inter-Cluster Distances (D^2) for 11 Morphological Characters of 30 Aman Rice Germplasm

Cluster No	**1**	**2**	**3**	**4**	**5**
1	**0.509**	61.786	186.947	115.671	78.754
2		**0.237**	240.928	64.717	133.231
3			**0.141**	300.265	117.043
4				**0.450**	187.964
5					**0.076**

Table 9: Cluster Mean Values for 11 Quantitative Traits of 30 Rice Genotypes

Cluster	DFF	D50%F	DM	PH	TTP	ETP	PL	GPP	FGP	UFGP	GYP
Cluster 1	108.25*	116.00*	148.75	139.67	20.50	20.34	25.64	231.08	220.92	10.17	43.75**
Cluster II	119.60**	128.07**	149.60**	121.87*	19.80	19.67	26.47	269.00	262.07	7.93*	34.40
Cluster III	115.57	124.29	148.71	129.38	15.14*	14.81*	23.38*	101.33*	90.62*	10.71	14.67*
Cluster IV	112.75	119.25	139.25*	141.50	24.92**	24.50**	29.42**	313.83**	300.33**	13.34**	37.50
Cluster V	115.80	123.43	149.10	158.44**	15.37	14.83	26.33	182.57	169.57	13.00	17.63

*, ** indicate the lowest and highest mean value of the characters.

DFF: days to first flowering, D50F: days to 50% flowering, DM: days to maturity, PH: plant height (cm), TTP: Tillers per plant, ETP: effective tillers per plant, PL: panicle length (cm), GPP: grains per panicle, FGP: filled grains per panicle, UGPP: unfilled Grains per panicle and GYP: grain yield per plant (g).

3.7 Cluster Mean Analysis

The mean values for all eleven morphological traits are shown in Table 9. The data discovered that diverse clusters displayed the maximum and minimum mean values of specific traits and no one of the clusters exhibited the maximum or lowermost average values of all traits. However, the genotype of cluster IV exhibited the maximum means for total tillers per plant (24.92), effective tillers per plant (24.50), panicle length (29.42 cm), grains per panicle (313.83), and filled grains per panicle (300.33). Similarly, the genotypes of cluster I exhibited the maximum means for grain yield per plant (43.75 g). Whereas the genotypes of cluster V exhibited the maximum mean for plant height (158.44 cm). Therefore, crossing the genotypes of cluster IV with genotypes of cluster I may conceivably achieve the highest mean values for the most studied traits; cluster II and cluster V combine desirable characters in hybrids as well as investigate the genotypes with excellent performance in the next generations. Similar trend was observed in other studies in rice and also recommended to make a cross among rice genotypes grouped into different clusters containing different desirable characters (Hossain and Haque, 2016; Jahan et al., 2020; Mahalingam et al., 2012; Sarif et al., 2020; Sohrabi et al., 2012; Haque et al., 2022; Mia et al., 2022).

4. CONCLUSION

Genetic diversity and morphological characterization are the basic requirements in crop breeding in terms of gene identification, trait and parent selections, etc. In the present study, the highest variability was established in unfilled grain per panicle, effective tillers per plant, and total tiller per plant. Grain yield per plant showed a significant and positive relationship with tiller per plant, effective tillers per plant, grains per panicle, and filled grain per panicle indicating the significance of these characters' selection in a rice breeding program for the improvement of Aman rice grain yield. Linear regression analysis showed that days to maturity, plant height, tillers per plant, and effective tillers per plant were the most potential variables contributing to the yield. The maximum genetic distance was exhibited between genotypes G14 and G21 and the minimum between G3 and G13. Therefore, crossing between genotypes with high genetic distance between genotypes is likely to produce heterotic hybrids. Cluster III and Cluster IV showed the highest inter-cluster genetic distance, indicating that crossing between parents of these two clusters could provide maximum recombination and segregation of progeny. In Conclusion, the rice genotypes viz. RS17, RS22, RS29, RS31, RS42 and RS47 have been noted as promising genotypes according to grain yield and pericarp color for nutritional analysis. Further multilocation trials as well as genetic studies should be done for more precise results and future research needs.

ACKNOWLEDGMENT

The authors are highly thankful to the Bangladesh Institute of Research

Cite The Article: Mohammad Zahir Ullah, Md. Sarowar Alam, Md. Samsuzzaman, Md Nurul Huda (2023). Genetic Analysis of Local Aman Rice (*Oryza Sativa* L.) Genotypes Based on Morphological Traits. *Acta Scientifica Malaysia, 7(2): 50-59.*

and Training on Applied Nutrition (BIRTAN), Arayhazar, Narayangonj for providing technical and financial assistance during the research program.

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