Published with Open Access at Journal BiNET
Vol. 30, Issue 02: 2559-2569
Journal of Bioscience and Agriculture Research
Journal Home: www.journalbinet.com/jbar-journal.html

Genetic analyses of advanced breeding lines of rice (*Oryza sativa* L.) based on morphological traits

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Article received: 15.05.2023; Revised: 01.08.2023; First published online: 30 August, 2023

ABSTRACT

Breeders rely on the genetic variability among advanced breeding lines derived from diverse parents to select the most suitable genotypes or traits for a hybridization program. This study examined forty rice genotypes, evaluating their genetic variability, heritability, clustering patterns, trait associations, principal component analysis and path analysis for yield-contributing characteristics. The experiment followed a randomized complete block design (RCBD) with three replications. The results showed that the genotypes exhibited a broad spectrum of genetic variability for all traits examined. The phenotypic coefficient of variation (PCV) slightly exceeded the genotypic coefficient of variation (GCV) for all traits, implying that environmental factors had negligible influence on trait expression. The GCV ranged from 2.67% for days to 80% maturity to 8.29% for grain yield. High heritability (>60%) and moderate genetic advance as a percentage of the mean (>10%) were observed for plant height (14.55%), yield (14.75%), and panicle length (10.13%), while low genetic advance as a percentage of mean was observed for the number of panicles per hill (6.48), days to 50% flowering (5.96), and days to 80% maturity (5.1). Grain yield exhibited significant positive correlations with the number of panicles per hill ($r = 0.33$, $P<0.001$), panicle length ($r = 0.24$, $P<0.01$), days to 50% flowering and days to 80% maturity ($r = 0.18$, $P<0.05$) at the phenotypic level. The genotypes were grouped into four distinct clusters, each exhibiting unique combinations of trait values. Notably, Cluster 2 displayed high mean values for plant height (101.0 cm), the number of panicles per hill (10.9), panicle length (24.3 cm), days to 50% flowering (130.0 days), days to 80% maturity (154.0 days), and yield (6.43 t/ha), Cluster 4 exhibited a noteworthy number of panicles/hill (11.3). The first three principal components reported approximately 82% of the total variation. Path analysis revealed that the number of panicles per hill had the highest positive direct effect on grain yield at the levels of genotypic (0.30) and phenotypic (0.28). Considering these six yield-contributing traits, it is recommended to crossbreed genotypes from cluster 2 with those from cluster 4 to develop high-yielding rice breeding lines.

***Key Words**: Rice grain yield, Genetic variability, Heritability, Genetic advance, Clustering, Correlation analysis and Path analysis.*

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Cite Article: Rahman, M. A., Islam, M. R., Islam, A. K. M. S., Munna, N. A., Razu, M. A. U. and Rana, M. M. (2023). Genetic analyses of advanced breeding lines of rice (*Oryza sativa* L.) based on morphological traits. Journal of Bioscience and Agriculture Research, 30(02), 2559-2569.
Crossref: https://doi.org/10.18801/jbar.300223.309

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I. Introduction

Rice, a staple food in Asia and Africa, is a popular cereal grain that serves as a primary dietary component for over half the global population (Liu et al., 2014). Rice is low in fiber and fat but rich in calories and nutrients like magnesium, phosphorus, manganese, selenium, iron, folic acid, thiamine, and niacin (Fukagawa et al., 2019). In Bangladesh, rice is vital as the primary food source for more than 169 million individuals. It plays a significant role in the country's rural economy, generating nearly 48% of employment opportunities in rural areas (Hassan, 2021). Bangladesh has secured third place worldwide in rice production for four years, with an estimated production output of 38.4 million tonnes (FAO, 2022). In Bangladesh, the rice sector significantly contributes, accounting for half of the agricultural GDP and one-sixth of the national income (Sayeed et al., 2018). Rice is vital for this country's survival, and sustainable rice production is crucial for food security. Breaking the rice yield plateau is crucial to meeting the demands of the growing population.

Heritability is crucial in determining a trait's response to selection and predicting the transmission of desirable characteristics from parents to offspring during breeding (Acquaah et al., 2009). In the case of high-yielding rice breeding, it's essential to comprehend the nature and extent of genetic variation, the relationship between yield and other agronomic traits, and the impact of environmental factors on the expression of traits. Indirect selection for yield is feasible if the component traits are strongly heritable and positively associated with yield (Roy and Shil, 2020). To breed high-yielding rice, it's crucial to understand the variance and relationships between genotypes and the impact of the environment on traits. If component traits are heritable and linked to yield, indirect selection for yield is possible (Guo, 2021). High heritability and genetic advancement are closely linked, enabling breeders to quickly identify and enhance desirable traits. Breeding success greatly relies on population variations. Rice plants exhibit significant morphological variation, including plant height, tiller count, flowering days, yield, and related components. Analysing genetic variability, heritability, and relationships among these yield-related traits helps assess genetic resources and guides the selection of successful breeding approaches (Larik et al., 2000).

Principal component analysis (PCA) simplifies complex datasets by extracting critical information to reduce dimensionality while preserving important features (Ringnér et al., 2008). Correlation analysis can be a useful tool for understanding the relationships between different traits in rice and identifying genotypes with desirable traits (Ndour et al., 2016). Identifying genetic relationships and divergence in genetic resources helps select suitable breeding parents. This minimizes the use of closely related parents, preventing genetic depression and preserving genetic variation (Suvi et al., 2020). Genetically distant parents can achieve higher heterosis upon crossing (Chakravarthi and Naravaneni, 2006). Path analysis in rice cultivation examines correlations and the direct/indirect influence of variables on growth and yield (Vida et al., 2006). This method helps distinguish which traits have a direct impact on yield and which traits have an indirect influence on yield. By utilizing this approach, it is possible to determine which traits should be prioritized for selection in breeding programs to enhance yield (Chandra et al. 2007). The study involved the assessment of 40 rice genotypes to analyze genetic variability, heritability, clustering, trait association, principal component analysis (PCA), and path analysis for six key yield contributing traits, providing valuable insights for rice breeding and improvement.

II. Materials and Methods

Thirty-one advanced breeding lines and nine released varieties of BRRI tested in the regional yield trial under a favourable rice breeding program were employed in this investigation (Table 01). The experiment was carried out from December 2019 to April 2020 in the BRRI Regional Station Satkhira,

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geographically located at 22°45'11.7"N latitude and 89°06'29.4"E longitude. The field experiment followed a randomized complete block design (RCBD) with three replications. Each plot measured 11.6 sq. m, measuring 5.8 meters in length and 2 meters in breadth. Seedlings of each genotype, aged 35 days, were transplanted at 20 cm × 20 cm spacing. Fertilizer application included 260 kg urea, 100 kg TSP, 120 kg MOP, 110 kg gypsum, and 10 kg ZnSO4 per hectare. All fertilizers except urea were applied at final land preparation. Urea application and crop management practices were done according to Biswas et al. (2016).

Table 01. List of 40 rice genotypes evaluated for six characters at BRRI Regional Station, Satkhira, during Boro 2019-20

SL	Designation	SL	Designation
G1	IR100740-89-B-2	G21	BRC302-18-1-2-1
G2	BR8899-17-1-1-1-1-1	G22	BR9667-54-2-2-97
G3	TP30433	G23	BR9669-21-2-1-19
G4	IR100004-19-B-1	G24	BR9669-23-3-2-23
G5	IR100722-B-B-B-B-16	G25	BR9669-15-3-2-31
G6	BR8905-17-2-3-3-1-1	G26	BR9880-27-4-1-18
G7	TP26717	G27	BR9891-19-2-2-8
G8	BR8905-17-2-3-3-1-4	G28	BR9891-11-2-2-20
G9	BR8902-38-7-1-1-1-1	G29	BR9891-17-2-2-23
G10	TP29654	G30	BR9891-8-2-1-41
G11	BRH11-9-11-4-5B-HR3	G31	BR9891-18-1-2-7
G12	BRH11-2-1-3-8B	G32	BRRI dhan28 (CK)
G13	BRH11-2-4-9B	G33	BRRI dhan29 (CK)
G14	BRH9-7-4-1B	G34	BRRI dhan50 (CK)
G15	BRH13-2-4-6-4B	G35	BRRI dhan58 (CK)
G16	IR 12A 177	G36	BRRI dhan63 (CK)
G17	BRC297-15-1-1-1	G37	BRRI dhan74 (CK)
G18	BRC302-2-1-2-1	G38	BRRI dhan81 (CK)
G19	BRC269-15-1-1-3	G39	BRRI dhan84 (CK)
G20	BRC298-18-2-3	G40	BRRI dhan89 (CK)

Data collection

Ten plants were utilised from each replication to measure plant height (cm), number of panicles per hill, and panicle length (cm). Days to flowering were recorded when 50% of the plants were headed, and growth duration was measured when 80% of the grains in the panicles were matured. Grain yield (t/ha) was calculated using the grain weight of whole plots adjusted to 14% moisture.

Statistical analysis

The R Statistical Software version 4.1.2 was used to perform analyses (https://www.R-project.org/). The R package (https://cran.r-project.org/package=doebioresearch) was utilized to carry out ANOVA and mean comparisons test, LSD for morphological data. Phenotypic and genotypic variance and GCV and PCV were measured according to Singh & Chaudhary (1985). The broad-sense heritability (h^2b) of all characters was determined using the equation given by Falconer (1983). The R package "variability" (https://cran.r-project.org/package=variability) was used to estimate genetic parameters in this study. Genetic Advance (GA) was calculated as per the equation by Allard (1960). Principal component analysis (PCA) was done using STAR v.2.0.1. Correlation analysis was done by Statistix 10 (Statistix, 2013).

III. Results

Analysis of Variance (ANOVA)

The analysis of variance showed significant ($p \leq 0.01$) variations among the different rice genotypes for all the evaluated traits (Table 02). The genotypes BR9669-23-3-2-23 had the highest plant height (111.3±2.5 cm) followed by BR9667-54-2-2-97 (110.9±3.1 cm) and the lowest plant height found in TP29654 (76.4±1.5 cm). The maximum plant height was found in BRRI dhan89 (105.7±2 cm) and the lowest in BRRI dhan63 (82.2±1.8 cm) among the checks in Table 02.

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Table 02. Yield and agronomic performance of forty rice genotypes in Satkhira during Boro 2019-20

SL	Designation	PH	NP/H	PL	DF	DM	Y (t/ha)
G1	IR100740-89-B-2	88.3±1.7	12.6±0.7	22.1±0.6	128±0.9	154±0.9	5.5±0.2
G2	BR8899-17-1-1-1-1-1	99.3±1.9	11.5±0.7	24±0.2	125±0.9	149±0.9	6.82±0.3
G3	TP30433	92±1.7	10.4±0.6	23.4±0.7	129±1.5	152±1.8	6.26±0.2
G4	IR100004-19-B-1	101.4±2.4	10.8±0.4	23.5±0.7	125±0.9	149±0.6	6.91±0.3
G5	IR100722-B-B-B-B-16	96±1.3	11.5±0.8	25.1±0.3	128±1.2	152±1.5	6.35±0.2
G6	BR8905-17-2-3-3-1-1	89.9±2.6	8.6±0.6	22.6±0.6	128±1.8	151±2.1	4.71±0.2
G7	TP26717	96.1±2.2	10.7±0.4	24.6±0.3	126±0.7	151±0.7	6.49±0.2
G8	BR8905-17-2-3-3-1-4	93.3±2.2	11.2±0.8	23.7±0.3	132±0.7	156±0.7	6.14±0.3
G9	BR8902-38-7-1-1-1-1	100.8±1.6	10.4±0.7	24.2±0.4	128±0.9	151±1.2	6.87±0.3
G10	TP29654	76.4±1.5	10.7±0.7	20±0.2	127±0.6	151±0.3	6±0.3
G11	BRH11-9-11-4-5B-HR3	89.9±1.7	10.8±0.3	22.4±0.2	124±0.9	150±0.9	5.91±0.3
G12	BRH11-2-1-3-8B	105.2±2.4	9.7±0.6	22.4±0.3	132±0.9	158±0.9	6.72±0.2
G13	BRH11-2-4-9B	101.6±2	10.8±0.8	23.4±0.2	131±0.9	157±1.3	7.12±0.3
G14	BRH9-7-4-1B	108±1.5	9.4±0.2	25.4±0.8	135±0.9	159±0.9	6.61±0.2
G15	BRH13-2-4-6-4B	91.3±2.4	10.4±0.5	23.1±0.3	125±1.2	149±1.2	5.94±0.3
G16	IR 12A 177	94.4±1.3	11±0.3	25.4±0.2	130±1.5	153±1.5	6.22±0.3
G17	BRC297-15-1-1-1	101.3±3.4	13±0.7	24.4±0.2	125±0.7	151±0.7	6.18±0.2
G18	BRC302-2-1-2-1	106.4±3.6	10.1±0.5	23.1±0.6	122±0.9	148±0.9	5.89±0.3
G19	BRC269-15-1-1-3	89.8±1.5	10.1±0.5	23.7±0.4	125±0.6	151±0.6	5.35±0.2
G20	BRC298-18-2-3	99.7±2.3	11.2±0.4	24.1±0.4	126±0.7	150±0.6	5.38±0.2
G21	BRC302-18-1-2-1	96.8±1.6	10.1±0.3	24.6±0.5	125±0.6	149±0.7	5.78±0.3
G22	BR9667-54-2-2-97	110.9±3.1	12.4±0.7	25.7±0.2	130±1.5	154±1.5	6.05±0.3
G23	BR9669-21-2-1-19	101.4±2.1	11±0.5	25±0.5	129±0.9	153±0.6	6.31±0.2
G24	BR9669-23-3-2-23	111.3±2.5	11.5±0.8	25.3±0.3	131±1.2	156±1	5.54±0.2
G25	BR9669-15-3-2-31	99.6±2	9.4±1	22.3±0.4	127±0.9	153±0.3	5.11±0.2
G26	BR9880-27-4-1-18	106.6±2.3	11.4±0.6	24.3±0.7	136±0.7	160±0.7	5.6±0.2
G27	BR9891-19-2-2-8	99.9±2.5	10.5±1.4	24.2±0.4	131±1.2	154±0.9	6.06±0.3
G28	BR9891-11-2-2-20	107.8±1.8	8.9±0.5	24±0.3	126±0.9	149±0.9	4.93±0.2
G29	BR9891-17-2-2-23	91.6±2	10.2±0.4	21.3±0.7	130±0.9	153±0.9	6.1±0.2
G30	BR9891-8-2-1-41	110.1±2.6	9.9±0.9	23±0.5	131±0.9	155±0.9	5.24±0.3
G31	BR9891-18-1-2-7	95±3.1	11.3±0.2	22.2±0.2	130±0.7	154±0.6	5.56±0.2
G32	BRRI dhan28 (CK)	92.6±2.4	10.7±0.3	23.2±0.4	119±1.2	141±1	5.96±0.2
G33	BRRI dhan29 (CK)	98±1.9	11.1±1	25.8±0.3	133±0.7	157±0.9	6.6±0.3
G34	BRRI dhan50 (CK)	83.7±2	9.6±0.3	21.6±0.2	128±0.6	152±0.9	5.72±0.3
G35	BRRI dhan58 (CK)	96.8±2.2	11.2±0.8	21.4±0.4	131±0.6	155±0.6	6.58±0.2
G36	BRRI dhan63 (CK)	82.2±1.8	10.5±0.6	23.4±0.2	126±0.3	149±0.3	6.04±0.3
G37	BRRI dhan74 (CK)	90.7±2.7	10.9±0.5	22.4±0.2	123±0.7	146±0.3	6.03±0.3
G38	BRRI dhan81 (CK)	93.6±2	10.4±0.5	21.7±0.6	117±0.7	143±0.6	5.92±0.2
G39	BRRI dhan84 (CK)	97.6±2.1	11.2±0.7	25.9±0.7	121±0.9	143±0.7	6.04±0.3
G40	BRRI dhan89 (CK)	105.7±2	11.4±0.6	24.5±0.5	134±1.2	156±0.6	6.85±0.3
$LSD_{(0.05)}$		3.09	0.9	0.6	1.33	1.33	0.37
CV(%)		3.9	10.33	3.16	1.28	1.08	7.41
Significant		***	***	***	***	***	***

PH–Plant height (cm), NP/H–Number of panicles per hill, PL–Panicle length (cm), DF–Days to 50% flowering, DM– days to 80% maturity, and Y– Yield (t/ha)

The genotypes BRC297-15-1-1-1 had the highest number of panicles (13±0.7) followed by IR100740-89-B-2 (12.6±0.7) and the lowest number of panicles found in BR8905-17-2-3-3-1-1 (8.6±0.6). Among the checks, the highest number of panicles was found in BRRI dhan89 (11.4±0.6) and lowest number of panicles was found in BRRI dhan50 (9.6±0.3).

The genotypes BRRI dhan84 had the highest panicle length (25.9±0.7cm) followed by BRRI dhan29 (25.8±0.3 cm). Among the advanced breeding lines, the highest panicle length was noted in BR9667-54-2-2-97 (25.7±0.2cm), followed by IR 12A 177 (25.4±0.2 cm).

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The genotypes BR9880-27-4-1-18 showed the highest days to 50% flowering (136±0.7 days) accompanied by BRH9-7-4-1B (135±0.9 days) and the lowest days to 50% flowering documented in BRC302-2-1-2-1 (122±0.9 days) among the advanced breeding lines. Among the checks, the highest days to 50% flowering were displayed in BRRI dhan89 (105.7±2 cm) and lowest days to 50% flowering were found in BRRI dhan63 (82.2±1.8 cm).

The genotypes BR9880-27-4-1-18 had the highest days to 80% maturity (160±0.7 days) followed by BRH9-7-4-1B (159±0.9 days) and the lowest days to 80% maturity found in BRC302-2-1-2-1 (148±0.9 days) among the advanced breeding lines. BRRI dhan29 took the longest duration to reach 80% maturity (157±0.9 days), followed closely by BRRI dhan89 (156±0.6 days), while BRRI dhan28 had the shortest duration (141±1 days).

The genotypes BRH11-2-4-9B had the highest yield (7.12±0.3 t/ha) accompanied by IR100004-19-B-1 (6.91±0.3 t/ha) and the lowest yield found in BR8905-17-2-3-3-1-1 (4.71±0.2 t/ha) among the advanced breeding lines. Among the checks, the highest yield was found in BRRI dhan89 (6.85±0.3 t/ha), followed by BRRI dhan29 (6.6±0.3 t/ha) and the lowest yield was found in BRRI dhan50 (5.72±0.3 t/ha).

Table 03. Estimation of genetic parameters for morphological characters of forty rice genotypes

Trait	Mean ± SEM	σ^2p	σ^2g	σ^2e	PCV (%)	GCV (%)	ECV (%)	H^2 (%)	GA	GAM
PH	97.32±2.19	73.23	58.85	14.38	8.79	7.88	3.89	80	14.16	14.55
NP/H	10.72±0.64	1.66	0.43	1.22	12.02	6.15	10.33	26.18	0.7	6.48
PL	23.55±0.43	2.32	1.76	0.55	6.47	5.64	3.16	76.06	2.39	10.13
DF	127.72±0.94	18.66	15.97	2.67	3.39	3.13	1.28	85.67	7.62	5.96
DM	151.83±0.94	19.11	16.44	2.67	2.87	2.67	1.08	86.04	7.74	5.1
Y	6.03±0.26	0.45	0.29	0.2	11.12	8.29	7.41	65.61	0.89	14.75

PH–Plant height (cm), NP/H–Number of panicles per hill, PL–Panicle length (cm), DF–Days to 50% flowering, DM– days to 80% maturity, and Y– Yield (t/ha), σ^2g- genotypic variance, σ^2p- phenotypic variance, σ^2e- error variance, GCV, PCV, ECV- genotypic, phenotypic and environmental coefficient variation, H^2- heritability, GA- Genetic Advance and GAM- Genetic Advance as a Percentage of Mean.

Genetic factors were evaluated to determine the genetic variability for specific traits existing among the genotypes (Table 03). The phenotypic variance was partitioned into genotypic, phenotypic and error variance to assess the heritable component of overall variability. The results indicated that the variability among genotypes was mainly due to genotypic variance, with low values for error variance, except for the number of panicles/hills. The PCV values for all traits were higher than their corresponding GCV values. Y (8.29%) and PH (7.88%) recorded high values of GCV followed by NP/H (6.15%), PL (5.64%), DF (3.13%) and DM (2.67%). The highest value of ECV was observed in NP/H (10.33%) followed by Y (7.41%) (Table 03). Broad-sense heritability was high for the days to maturity (86.04%), very closely with DF (85.67%), followed by PH (80.0%), PL (76.06%), Y (65.61%), and NP/H (26.18%). The genetic advance was found to be highest for PH (14.16%), DM (7.74%) and DF (7.62%). The genetic advance as a percentage of mean of PH (14.55) was the highest followed by Y (14.75) and PL (10.13).

Principal component analysis of traits

The principal component analysis (PCA) results showed that the first four principal components (PC1 to PC4) explain almost 93% of the variance in the data (Table 04). PC1 demonstrated the highest level of variance (42%) out of all the PCs, while PC2 showed a lesser amount of 22% variance. The remaining PCs from PC3 to PC4 showed 18% and 11% of the total variance, respectively. Four PCs can be used to show the quantity and contribution of top-performing genotypes and variables to total variability.

Correlation analysis of the Characteristics

A Pearson's correlation coefficient matrix was shown in Figure 01 to highlight the significance of the variables under examination in rice breeding programmes and to understand the strength and nature of the relationship. The study revealed a noteworthy and favorable correlation between yields and

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various characteristics, such as the number of panicles per hill (r = 0.33, P<0.001), panicle length (r = 0.24, P<0.01), as well as the days to 50% flowering and 80% maturity (r = 0.18, P<0.05). It was also found that there was a weak, non-significant positive correlation between plant height and yield. Additionally, positive cross-associations were observed between plant height and traits viz. panicle length, days to 50% flowering, and days to 80% maturity (*r* = 0.46, 0.29 and 0.33, respectively).

Table 04. Variables contribution to overall variability (PC1–PC4) of rice genotypes

Variables	PC1	PC2	PC3	PC4
PH	0.43	-0.13	-0.55	0.11
NP/H	0.19	-0.56	0.40	-0.67
PL	0.37	-0.45	-0.46	0.00
DF	0.54	0.39	0.18	-0.08
DM	0.54	0.40	0.19	-0.11
Y	0.25	-0.40	0.51	0.72
Eigen Values	2.51	1.34	1.06	0.68
Variance (%)	0.42	0.22	0.18	0.11
Cumulative	0.42	0.64	0.82	0.93

PH–Plant height (cm), NP/H–Number of panicles per hill, PL–Panicle length (cm), DF–Days to 50% flowering, DM– days to 80% maturity, and Y– Yield (t/ha)

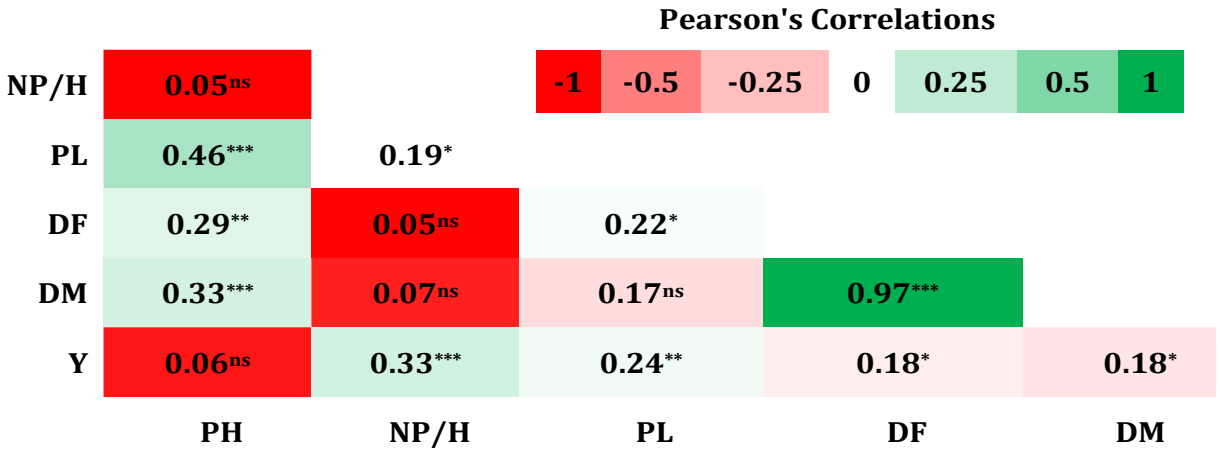

Figure 01. Correlation among different morphological traits.

PH–Plant height (cm), NP/H–Number of panicles per hill, PL–Panicle length (cm), DF–Days to 50% flowering, DM– days to 80% maturity, and Y– Yield (t/ha), ns-non significant (p>=0.05), *p<0.05, **p<0.01, ***p<0.001

Cluster analysis

The utilization of cluster analysis facilitated the exploration of similarities and evaluated the potential for hybridization among different rice accessions. Cluster analysis was done with relative mean values for each trait. Cluster 1 and Cluster 4 were characterized by fifteen and twelve genotypes, respectively. Clusters 2 and 3 had four and nine genotypes, respectively. From the cluster mean, we observed that Cluster 2 is characterized by a high mean value for plant height and panicle length, days to 50% flowering, and days to 80% maturity and yield, whereas Cluster 3 is characterized by a high mean value of the number of panicles per hill (Table 05).

Table 05. Cluster means for different traits among 40 rice genotypes

Variables	Cluster 1	Cluster 2	Cluster 3	Cluster 4
PH	87.7	101	100	96.3
NP/H	10.8	10.9	9.8	11.3
PL	22.1	24.3	23.4	23.8
DF	127	130	126	120
DM	151	154	151	145
Y	5.87	6.43	5.3	6.03

PH–Plant height (cm), NP/H–Number of panicles per hill, PL–Panicle length (cm), DF–Days to 50% flowering, DM– Days to 80% maturity, and Y– Yield (t/ha)

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Euclidian distance coefficients were measured for all rice genotypes based on all traits investigated. The UPGMA dendrogram grouped 40 rice genotypes into four clusters (Figure 02).

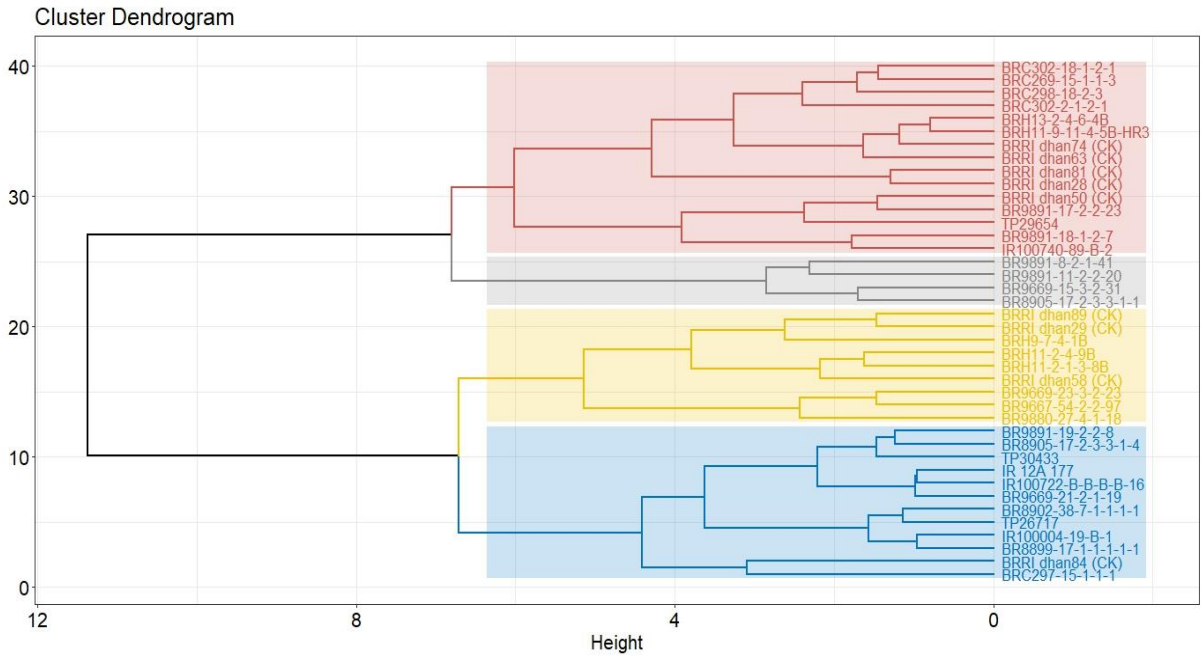

Figure 02. Dendrogram (Complete linkage and Euclidean Distance) showing clusters of forty rice genotypes

Path analysis of the traits

Simple correlation estimates alone cannot accurately determine the individual contributions of traits to yield. Path coefficient analysis can partition the correlations into direct and indirect effects to better understand the cause-and-effect relationship. This analysis allows for a more accurate interpretation of the impact of each trait on yield by considering their direct and indirect effects through other attributes. The path coefficient analysis showed that plant height (0.12), number of panicles per hill (0.30) and days to 50% flowering (0.46) had a direct positive effect at the genotypic level, while panicle length (-0.04) and days to 80% maturity (-0.35) had a direct negative impact at the genotypic level (Table 06).

Table 06. Genotypic path coefficient analysis of forty rice genotypes

Variables	PH	NP/H	PL	DF	DM
PH	**0.12**	0.03	-0.02	0.18	-0.15
NP/H	0.01	**0.30**	-0.01	0.04	-0.04
PL	0.07	0.10	**-0.04**	0.10	-0.06
DF	0.05	0.02	-0.01	**0.46**	-0.34
DM	0.05	0.03	-0.01	0.45	**-0.35**

Residual effect (genotypic) = 0.88

PH–Plant height (cm), NP/H–Number of panicles per hill, PL–Panicle length (cm), DF–Days to 50% flowering, DM– days to 80% maturity, and Y– Yield (t/ha)

The path coefficient analysis showed that the number of panicles/H (0.28), panicle length (0.21), days to 50% flowering (0.01) and days to 80% maturity (0.15) had a direct positive effect at the phenotypic level (Table 07) where plant height (-0.10) had a direct negative effect at the phenotypic level. The residual effect at the genotypic level was 0.88 and phenotypic level was 0.84.

Table 07. Phenotypic path coefficient analysis of forty rice genotypes

Variables	PH	NP/H	PL	DF	DM
PH	**-0.10**	0.01	0.10	0.00	0.05
NP/H	-0.01	**0.28**	0.04	0.00	0.01
PL	-0.05	0.06	**0.21**	0.00	0.03
DF	-0.03	0.01	0.05	**0.01**	0.15
DM	-0.03	0.02	0.04	0.01	**0.15**

Residual effect (genotypic) = 0.84

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IV. Discussion

Genetic variability is essential in crop improvement programs for selecting superior genotypes. Therefore, assessing the extent of genetic variation is crucial to determining the potential advancements in breeding material for various traits. In this study, the analysis of variance (ANOVA) revealed significant ($p \leq 0.01$) differences among the genotypes of forty genotypes for all measured morphological traits (Table 02). These findings indicate the presence of ample genetic variations among the genotypes, offering an opportunity to select better parents for the crossing program to maximize yield. Moreover, it allows rice breeders to develop desired traits through selection and hybridization, optimizing the breeding process. In two separate studies, Abarshahr et al. (2011)and Chandra et al. (2007) reported significant variations among 30 and 57 rice genotypes, respectively, with varying quantitative characters. Shahriar et al. (2014) also found similar results for all tested traits in 34 rice genotypes.

Assessment of genetic parameters

Our results showed close GCV and PCV, suggesting the negligible environmental influence on trait expression. At the same time, higher differences between PCV and GCV indicate a greater contribution of environmental factors to the phenotypic coefficient of variation (Singh & Choudhary, 1996).

For most of the traits studied, the estimates of the coefficient of variation, including GCV and PCV, were similar, representing minimal environmental influence on their expression. However, the number of panicles/hill and yield showed a significant difference between GCV and PCV, suggesting that the environment plays a crucial role in their expression. Higher differences between PCV and GCV indicate a greater contribution of environmental factors to the phenotypic coefficient of variation (Singh and Choudhary, 1996). Therefore, selection based solely on phenotype might not be effective for these traits. Our experiment found that the observed traits showed high significance in ANOVA, but the GCV values were relatively low (<10%), ranging from 2.67% to 8.29% (Table 03). This indicates less genetic variation for a particular trait within a population. Prasad et al. (2017) reported similar trends with close estimates of GCV and PCV, with slightly higher values for PCV. However, the coefficient of variation alone cannot accurately estimate the potential improvement in quantitative traits, as stated by Falconer (1983). Burton and Devane (1953) proposed combining GCV estimates with heritability for a more comprehensive assessment. This approach considers genetic and environmental factors, enhancing understanding of genetic improvement achievable through phenotypic selection (Allard, 1960). In the current investigation, nearly all traits except the number of panicles/hill (26.18%) and yield (65.61%) displayed high estimates of broad-sense heritability (>60%). Behera et al. (2018) discovered low heritability for effective tillers but high grain yield. Johnson et al. (1955) emphasized the significance of estimating heritability and genetic advance for phenotype-based selection. Traits with high heritability and genetic advance are the primary targets for selection based on morphology. In our study, plant height and panicle length had high heritability and moderate genetic advance (Chakraborty and Hazarika, 1994), indicating that these traits are suitable for selection based on morphology. Plant height was highly heritable with a moderate genetic advance by Kumar (1994)and Maurya et al. (1986). The traits of 50% flowering and 80% maturity, measured in days, exhibited higher heritability but low genetic advance as a percentage of the mean, suggesting that the potential improvement in these traits through selective breeding is limited. However, selecting the trait will not result in significant improvement. Similar findings were reported by Gupta et al. (1999). In our study, yield demonstrated high heritability and moderate genetic advance, indicating that the trait is influenced mainly by genetic factors, and that there is potential for improvement through selective breeding. Conversely, Li et al. (1991) found moderate heritability and the maximum genetic advance for yield per plant.

Principal component analysis (PCA)

PCA estimates the eigenvalues and contributions of six variables of forty rice genotypes (Table 04). Eigenvalues were utilized to measure the impact of each variable on total variations (Nuruzzaman et al., 2019). PC1 revealed that genotypes differed significantly in days to 50% flowering, days to 80% maturity, plant height, panicle length, yield, and the number of panicles/hill, explaining 42% of the total variance. The first three principal components accounted for over 80% of the variance. Similarly, Islam et al. (2020) found that the first four components explained more than 80% of the variation, with PC1 contributing 42% overall. Anyaoha et al. (2018) reported that flowering days and grain yield played prominent roles among seventy-seven Nigerian rice genotypes.

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Assessment of correlation coefficients

The yield had a moderately positive relationship with the number of panicles per hill and a weakly positive relationship with the number of days to 50% flowering, the number of days to 80% maturity, and the panicle length. Adhikari et al. (2018)made similar observations, and Gyawali et al. (2018) also found a positive correlation between panicle length and grain yield.

Cluster analysis

Oyekunle et al. (2015) demonstrated that cluster analysis effectively distinguishes homogeneous variables with varying degrees of similarity through dendrograms. The hierarchical cluster analysis of the yield-related traits resulted in grouping the 40 rice genotypes into four main clusters, as shown in Figure 02. Cluster 1 contained the highest number of genotypes (15), while cluster 2 had the lowest number of genotypes (4). Ahmadikhah et al. (2008) classified 58 rice varieties into four groups based on 18 morphological traits, while Veasey et al. (2008) categorized 23 rice populations into 10 distinct groups using 20 morphological characteristics.

Estimation of path coefficient

Dewey and Lu (1959) utilized path coefficient analysis, which breaks down correlation coefficients into direct and indirect effects, to aid plant selection. According to Grafius (1959), the yield may not be determined by a single gene but rather by the multiplicative interaction of multiple genes that control different components. Days to 50% flowering and the number of panicles per hill directly impacted yield (Table 06 and Table 07). Hossain et al. (2018) also observed similar findings, with the number of grains per panicle having the most significant effect on grain yield, followed by the number of panicles per hill. Days to 80% maturity and panicle length had positive and negative impacts on yield, contrary to the findings of Hossain et al. (2018).

V. Conclusion

The findings of this study highlight the presence of significant genetic variation among the genotypes for the traits examined. The slightly higher PCV compared to GCV implies that the expression of these traits is marginally affected by environmental factors. The substantial range of GCV values across traits indicates differences in the genetic composition of the genotypes. The traits with high heritability and moderate genetic advancement, such as plant height, yield, and panicle length, can be selectively improved through breeding programs. On the other hand, traits like the number of panicles per hill, panicle length, days to 50% flowering, days to 80% maturity, and yield have a limited response to genetic factors, suggesting that other non-genetic factors play a more significant role in their expression. These findings contribute to our understanding of the genetic and environmental factors influencing trait variability and can aid in developing strategies for rice improvement and agricultural productivity. The positive correlation between grain yield and the number of panicles per hill, panicle length, days to 50% flowering, and days to 80% maturity at the phenotypic level suggests that these traits could be used as selection criteria to improve grain yield. The path analysis revealed that the number of panicles per hill had the maximum positive direct effect on grain yield at both genotypic and phenotypic levels. These findings can aid in developing strategies for improving rice yield. Future studies should use multilocation trials and molecular marker studies to better understand the interaction between genes and the environment in explaining variability in rice traits and their expression.

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