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Harnessing Genetic Diversity by Studying Agro-Morphological Traits for Rice Improvement

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ABSTRACT

Studying genetic variability and key agro-morphological traits in rice is crucial for breeding because it identifies superior genotypes and reveals how traits are inherited, enabling breeders to select the best parents for developing new, high-yielding varieties. This process provides the essential data needed to plan effective crosses and make targeted improvements in rice crop. This study investigated the genetic variability and key agro-morphological traits of 33 rice genotypes to identify superior lines for future breeding programs. Understanding the genetic potential of these genotypes is crucial for developing high-yielding, resilient rice varieties. We evaluated ten quantitative traits, including days to 50% flowering, plant height, panicle length, and yield per hill. Data were analyzed using analysis of variance (ANOVA), genetic parameters, correlation coefficients, and multivariate techniques such as principal component analysis (PCA) and cluster analysis to determine genetic relationships and trait associations. Significant genetic variation ($P \leq 0.05$) was observed for all traits. The mean performance analysis identified genotypes with superior traits, such as IR146151-B-B-584-44-3(G-30) for the highest plant height (117.17 cm) and yield hill^{-1} (31.71 gm), and IR146164-B-B-543-165-47(G-24) for the longest flag leaf (42.33 cm). High heritability and genetic advance were recorded for flag leaf length and spikelet fertility, indicating strong additive gene action. Yield hill^{-1} showed a significant positive correlation with the number of effective tillers hill^{-1} (r=0.52), number of grains panicle^{-1} (r=0.72), and spikelet fertility (r=0.69). PCA revealed three principal components that explained 70.54% of the total variance. Cluster analysis grouped the genotypes into four distinct clusters, with the largest inter-cluster distance observed between clusters II and IV (5.45), highlighting their high genetic divergence. The study confirmed substantial genetic variability among the rice genotypes, which can be effectively utilized for crop improvement. The identified high-performing genotypes and traits with high heritability are promising for direct selection. Hybridization between genotypes from divergent clusters, particularly clusters II and IV, is recommended to create new genetic combinations and enhance yield potential in future rice breeding programs.

Keywords: Rice, Yield-traits, Correlation, Principal component analysis, Cluster analysis

INTRODUCTION

Rice is a major food for a large portion of the world's population, particularly in Asia, and its civilization and consumption play a substantial part in comprehensive food security and artistic identity. It's a vital source of energy and, to a lower extent, protein, for billions of people (Asma *et al.*, 2023). Rice provides 21% of global mortal per capita energy and 15% of per capita protein (Samal *et al.*, 2022). Although rice protein ranks grandly in nutritive quality among cereals, protein content is modest. Rice also provides minerals, vitamins, and fiber,

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although all constituents except carbohydrates are condensed by milling. It's the easiest source of food and commodity of significance for the people of Bangladesh (Ahmed *et al.*, 2022). It belongs to the family Gramineae. The quantum of rice grown in Asia is about 90 of the world's rice which alone covers the food demand for about 60 population of the world (Haque *et al.*, 2015). Bangladesh is the third-largest rice producer among the 114 rice growing countries of the world. As rice plays a very important part in traditional diets and in the livelihood of people, it earns a special position in numerous nations. Among all food particulars, the significance of rice is supreme. The global population is adding but rice cultivable land is dwindling. In order to meet up the demand, two ways can be effective expanding the rice growing area and adding productivity or both (Hasan *et al.*, 2015). As there's no possibility of adding cultivated area (Horizontal expansion), development of high yielding kinds is the only option to increase the yield of rice (Vertical expansion).

The future approaches in the advance of rice largely depend on the availability of genetic resources and their effective utilization (Sabar *et al.*, 2024). At present, varietal identification for rice are primarily based on morphological and physiological parameters. During varietal development, plant breeders use several techniques to create genetic variation and select within this diversity, ultimately retaining superior plants after final selection (Joshi *et al.*, 2023). Parental genotypes from arbitrary populations are carefully chosen based on the evidence about genetic diversity. Besides genetic diversity, crop yield not only hang on the different yield contributing characters but also on the factors intricate about environment. In case of rice, yield also depends on the higher number of effective tillers hill^{-1}, number of filled grains panicle^{-1} and 1000-grain weight (Islam *et al.*, 2013). These traits are also associated among themselves. The extent of genetic variability like as, phenotypic and genotypic variances, phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV), broad sense heritability, genetic gain (GA) are highly accountable for the genetic enhancement of any crop based on which the breeding methods are found for its additional improvement. The range of variability is also measured by GCV and PCV. Correlation analysis is used to determine the association among the different traits (Faysal *et al.*, 2022). Principal component analysis (PCA) marks out the plant characters that provide the most in generating variation within a group of entries. The above apparatuses are found to be useful for proper description in further breeding program. Plant characterization has been effectively used in searching out appropriate attributes among individual genotype (Prasanna *et al.*, 2024). Elucidation of morphological and genetic characterization and valuation of diversity is very crucial for future varietal improvement. The objectives of the paper are to assess genetic variability and identify superior genotypes among 33 rice genotypes, and to determine trait correlations and genetic parameters to aid in future breeding programs. The study aims to classify genotypes for strategic parent selection and to identify key traits contributing to variation.

MATERIALS AND METHODS

Plant materials, exploratory site and design

The experiment was set up at the research Farm of Hybrid Rice Division, Bangladesh Rice Research Institute, Bangladesh during Boro 2024-25 following randomized complete block design (RCBD) with three replications. Thirty three rice genotypes were used as plant materials which were collected from different places of Hybrid Rice Development Consortium (HRDC) (Table 1).

Table 1. List of used genotypes.

Genotypes	Code name	Genotypes	Code name
IR146173-B-B-268-22-45	G-1	IR146164-B-B-54-52-41	G-18
IR146173-B-B-268-68-44	G-2	IR146164-B-B-191-15-40	G-19
IR146173-B-B-268-94-4	G-3	IR146164-B-B-191-47-3	G-20
IR146173-B-B-529-134-4	G-4	IR146164-B-B-191-86-4	G-21
IR146173-B-B-529-178-4	G-5	IR146164-B-B-44-122-4	G-22
IR146173-B-B-527-90-44	G-6	IR146164-B-B-543-5-7	G-23
IR146154-B-B-430-188-46	G-7	IR146164-B-B-543-165-47	G-24
IR146154-B-B-430-209-8	G-8	IR146168-B-B-317-122-6	G-25
IR146154-B-B-141-10-1	G-9	IR146168-B-B-15-2-2	G-26
IR146154-B-B-141-174-42	G-10	IR146168-B-B-89-41-4	G-27
IR146154-B-B-547-168-40	G-11	IR146168-B-B-214-81-38	G-28
IR146154-B-B-793-7-30	G-12	IR146151-B-B-439-83-7	G-29
IR146172-B-B-21-86-5	G-13	IR146151-B-B-584-44-3	G-30
IR146172-B-B-136-81-17	G-14	IR146151-B-B-584-82-40	G-31
IR146172-B-B-236-87-40	G-15	IR146151-B-B-1253-16-3	G-32
IR146172-B-B-596-8-10	G-16	IR146151-B-B-1266-13-9	G-33
IR146164-B-B-54-9-54	G-17		

The unit plot size was 75cm × 75cm. Twenty-five days old seedlings were used for transplanting @ one seedling hill^{-1} with the space of row to row is 25cm and plant to plant 15 cm. Recommended doses of fertilizers and manures were applied to the soil. Other intercultural operations were done when needed.

Data Collection

Data on ten quantitative traits such as days to 50% flowering (DFF), days to maturity (DM), plant height (PH), flag leaf length (FLL), number of effective tillers panicle^{-1} (ETH), panicle length (PL), number of grains panicle (NGP), spikelet fertility (SF), thousand grains weight (TGW) and yield hill^{-1} (YH) were recorded from three randomly selected plants of each genotype in each replication. Mean of the three plants for each character were used for statistical analysis.

Statistical Analysis

The collected data were compiled and analyzed using R software (version 3.4.1). The analysis encompassed one-way ANOVA to evaluate variations among genotypes. To differentiate the means, the LSD test was used at a 5% probability level. In order to identify quantitative variation patterns with the eigen vectors and eigen values principal component analysis (PCA) was also carried out.

Estimation of Genetic Parameters

Following the procedures described by Johnson *et al.* (1955) and Allard (1960), genetic parameters such as genetic variance, broad-sense heritability (h^2b), phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), genetic advance (GA), and genetic advance as a percentage of the mean (GA%) were computed. According to the

standards put forth by Deshmukh et al. (1986), the phenotypic coefficient of variation and genotypic coefficient of variation estimates were classified as low (20%). Similarly, Johnson et al. (1955) defined GA% as low (20%), and broad sense heritability (h^2b) as low (0%-30%), medium (31%-60%), and high (>60%).

Estimation of Correlation Co-efficient and Cluster Analysis

The phenotypic and genotypic correlation coefficient was estimated using the formula suggested by Miller *et al.* (1958) and path analysis was performed following formula provided by Dewey and Lu (1959), cluster analysis was performed using Ward's method (Ward, 1963).

RESULTS

Mean Performance Analysis

The analysis of variance (ANOVA) results showed highly significant ($P \leq .05$) variation for all the traits studied (Table 2). The mean performance of ten measurable traits of rice is documented in Table 3. Among the studied genotypes, the minimum number of days to 50% flowering (95 days) was observed in genotype IR146173-B-B-527-90-44(G-6), IR146154-B-B-141-10-1(G-9), IR146154-B-B-141-174-42(G-10), IR146154-B-B-547-168-40(G-11), IR146154-B-B-793-7-30(G-12), IR146172-B-B-21-86-5(G-13), IR146172-B-B-136-81-17(G-14), IR146172-B-B-236-87-40(G-15), IR146168-B-B-317-122-6(G-5), IR146168-B-B-89-41-4(G-27), IR146168-B-B-214-81-38(G-28), in contrast, the maximum number of days to 50% flowering (109 days) was required for the genotype IR146164-B-B-54-9-54(G-1) (Table 3). The minimum number of days to maturity (126 days) was observed in IR146168-B-B-214-81-38(G-28), whereas, the maximum number of days to maturity (143 days) was recorded for the genotype IR146164-B-B-54-9-54 (G-17). The minimum plant height (87.5 cm) was observed in the genotype IR146154-B-B-430-188-46(G-7). One the other hand, maximum plant height (117.17 cm) was recorded in the IR146151-B-B-584-44-3(G-30). The highest flag leaf length (42.33 cm) was found in IR146164-B-B-543-165-47(G-24). In contrast, the lowest flag leaf length (28.5 cm) was observed in the genotype IR146151-B-B-439-83-7(G-29). The highest number of effective tiller hill^{-1} (10) was observed in the genotype IR146154-B-B-793-7-30(G-12) and IR146151-B-B-1266-13-9(G-33). The minimum panicle length (21.17 cm) found in the genotype IR146172-B-B-136-81-17(G-14). The maximum panicle length (30.33 cm) was recorded in IR146164-B-B-44-122-4 (G-22). In addition, the minimum number of grains panicle^{-1} (96.67) was found in IR146164-B-B-44-122-4 (G-22). The maximum (228.67) was observed in the genotype IR146154-B-B-430-188-46 (G-7). The maximum spikelet fertility (87.83%) was recorded in IR146173-B-B-268-22-45 (G-45) and the minimum (53.86%) was found in IR146154-B-B-547-168-40 (G-11). Among the genotypes, the minimum thousand grains weight (19.62 g) was observed in genotypes IR146154-B-B-430-188-46 (G-7) whereas the maximum (26.68 g) weight was found in the genotypes IR146173-B-B-527-90-44 (G-6). The maximum yield hill^{-1} (31.17 g) was recorded in IR146151-B-B-584-44-3 (G-30), followed by IR146154-B-B-430-188-46 (G-7) (28.99 g) and IR146173-B-B-268-94-4 (G-3) (28.01g). The minimum yield hill^{-1} was recorded in IR146154-B-B-547-168-40 (G-11) as 8.47 g.

Genetic Parameters Analysis

The characters which showed very high genotypic variance (σ^2g) and phenotypic variance (σ^2p) were number of grains panicle^{-1} (712.51 and 1249.48, respectively), followed by spikelet fertility (61.99 and 68.75, respectively) and plant height (56.53 and 59.14, respectively) (Table 4). Co-efficient of variation studies showed that the values of phenotypic coefficient of variation were higher in compare to those of the genotypic coefficient of variation for all the individual traits.

Table 2. Analysis of variance (mean square) for ten yield and yield attributing traits.

Source of variance	df	DFF	DM	PH	ETH	FLL	PL	NGP	**SF**	TGW	**YH**
Replication	2	20.525	28.495	0.023	1.7449	2.031	6.3813	53.04	9.02	0.0045	6.102
Genotypes	32	63.99***	77.044***	172.203***	5.2085***	47.79***	14.49***	2674.49***	192.73***4	7.88***	99.58***
Error	64	0.369	0.349	2.609	1.0965	1.934	0.9204	536.97	6.759	0.2464	18.397

*, ** and *** indicate significant at 5%, 1% and 0.1% level of probability, respectively. Here, DFF = Days to 50% flowering, DM = Days to maturity, PH = Plant height (cm), FLL = Flag leaf length (cm), ETH = Number of effective tillers hill^{-1}, PL= Panicle length (cm), NGP= Number of grains panicle^{-1}, SF= Spikelet fertility, TGW= Thousand grains weight (gm) and YH= Yield hill^{-1}

Table 3. Mean performance for ten different morphological traits of rice genotypes grown at BRRI during Boro season of 2024-25.

Genotypes	Code name	DFF	DM	PH	FLL	ETH	PL	NGP	SF	TGW	YH
IR146173-B-B-268-22-45	G-1	95^{n}	127^{j}	89.5^{o}	32^{j-n}	5.18^{k}	25.83^{efg}	222.33^{ab}	87.83^{a}	26.41^{a}	26.67^{a-e}
IR146173-B-B-268-68-44	G-2	99.33^{ij}	132^{h}	102.5^{gh}	30.17^{m-p}	7.17^{c-i}	25^{f-i}	153^{d-k}	79.77^{d-g}	25.27^{b}	22.10^{b-h}
IR146173-B-B-268-94-4	G-3	99^{j}	133^{g}	107.33^{cd}	30.83^{l-o}	8.67^{abc}	26.5^{ef}	158.67^{d-i}	84.98^{abc}	23.98^{cd}	28.01^{abc}
IR146173-B-B-529-134-4	G-4	100.33^{gh}	133^{g}	96.17^{k-n}	33^{i-l}	7^{e-j}	25.5^{e-h}	158^{d-j}	76.87f-k	23.24^{d-g}	19.81^{e-j}
IR146173-B-B-529-178-4	G-5	100^{hi}	134^{ef}	104.33^{e-h}	32.33i-m	6.33^{f-k}	$28.83a^{bc}$	162.67^{c-i}	82.9^{b-e}	22.46^{g-k}	19.13^{f-k}
IR146173-B-B-527-90-44	G-6	95^{n}	128^{i}	93.67^{n}	32.67^{i-l}	7.3^{b-h}	$24h^{i}$	165.5^{c-i}	72.74^{klm}	26.68a	23.59^{b-f}
IR146154-B-B-430-188-46	G-7	100.33^{gh}	133.33^{fg}	87.5^{o}	28.67^{op}	8.67^{abc}	23.83^{j}	228.67^{a}	74.61^{jkl}	19.62^{p}	28.99^{ab}
IR146154-B-B-430-209-8	G-8	96^{m}	133^{g}	97.33^{jkl}	30^{nop}	9^{ab}	23.5^{j}	158.83^{d-i}	75.41^{i-l}	21.93^{klm}	23.61^{b-f}
IR146154-B-B-141-10-1	G-9	95^{n}	127^{j}	95.67^{lmn}	31.33^{k-n}	7.17^{c-i}	25.5^{e-h}	182.33^{c-f}	75.66g-l	21.78^{klm}	21.663^{e-i}
IR146154-B-B-141-174-42	G-10	95^{n}	128^{i}	102.33^{h}	39.33^{cd}	7^{e-j}	28.67^{bc}	187.17^{b-e}	80.97^{c-f}	23.37^{def}	24.6^{b-f}
IR146154-B-B-547-168-40	G-11	95^{n}	128^{i}	95.5^{lmn}	33^{i-l}	6.83^{d-k}	25.67^{efg}	103.5^{lm}	53.86^{q}	22.04^{klm}	8.47^{m}
IR146154-B-B-793-7-30	G-12	95^{n}	127^{j}	96.33^{klm}	32.5^{i-l}	10.17^{a}	25^{f-i}	137.5^{h-l}	68.96^{mn}	21.93^{klm}	21^{d-i}
IR146172-B-B-21-86-5	G-13	95^{n}	132^{h}	97.33^{jkl}	33^{i-l}	8.5^{a-d}	25.67^{efg}	147^{f-k}	73.98^{jkl}	23.19^{d-h}	21.41^{c-i}
IR146172-B-B-136-81-17	G-14	95^{n}	127^{j}	90^{o}	31.67^{j-n}	8^{b-f}	21.17^{j}	147.67^{f-k}	75.71^{g-l}	23.63^{c-f}	21.04^{c-i}
IR146172-B-B-236-87-40	G-15	95^{n}	128^{i}	112.17^{b}	34.5^{f-i}	5.33^{jk}	28.5^{bcd}	197.17^{abc}	63.57^{p}	23.04^{e-i}	15.38^{h-m}
IR146172-B-B-596-8-10	G-16	97^{l}	134^{ef}	96.33^{klm}	32.67^{i-l}	5.17^{k}	27^{de}	120.5^{klm}	72.31^{lm}	23.61^{c-f}	10.92^{lm}
IR146164-B-B-54-9-54	G-17	109^{a}	143^{a}	106^{cdef}	33.33^{h-k}	7.33^{b-h}	25.5^{e-h}	155.83^{d-k}	64.17^{op}	20.39^{op}	15.18^{h-m}
IR146164-B-B-54-52-41	G-18	108^{b}	141^{b}	105^{d-g}	42^{a}	8.17^{b-e}	28.33^{cd}	180.83^{c-f}	78.04^{f-j}	20.78^{no}	24.27^{b-f}
IR146164-B-B-191-15-40	G-19	107^{c}	141^{b}	104^{e-h}	39.67^{bcd}	8.67^{abc}	23.83^{j}	140.5^{g-l}	67.85^{no}	22.11^{j-m}	18.78^{f-k}

Genotypes	Code name	DFF	DM	PH	FLL	ETH	PL	NGP	SF	TGW	YH
IR146164-B-B-191-47-3	G-20	107^{c}	141^{b}	103.67^{fgh}	42.27^{a}	9^{ab}	23.67^{i}	166.67^{c-i}	79.12^{e-i}	21.53^{mn}	24.81^{a-f}
IR146164-B-B-191-86-4	G-21	107^{c}	141^{b}	105^{d-g}	33.67^{g-j}	7.33^{b-h}	23.67^{i}	138.5^{h-l}	66.07^{nop}	22.51^{g-k}	15.23^{h-m}
IR146164-B-B-44-122-4	G-22	99^{j}	134^{ef}	110.67^{b}	35.66667^{efg}	5.5^{ijk}	30.33^{a}	148^{f-k}	73.37^{kl}	21.62^{lm}	12.96^{j-m}
IR146164-B-B-543-5-7	G-23	105^{e}	140^{c}	107.67^{c}	36.33^{ef}	6^{h-k}	26.33^{ef}	177.83^{c-g}	67.75^{nop}	22.89^{f-j}	16.5^{g-l}
IR146164-B-B-543-165-47	G-24	106^{d}	140^{c}	99.67^{ij}	42.33^{a}	6.5^{e-k}	28.167^{cd}	150.33^{e-k}	65.34^{nop}	24.23^{c}	15.043^{i-m}
IR146168-B-B-317-122-6	G-25	95^{n}	128^{i}	97^{kl}	34.5^{f-i}	8.5^{a-d}	24.33^{ghi}	152.83^{d-k}	79.71^{d-h}	22.89^{f-j}	23.83^{b-f}
IR146168-B-B-15-2-2	G-26	102.33^{f}	134.33^{de}	102.17^{hi}	33.17ijk	7.83^{b-g}	24^{hi}	189^{bcd}	83.4^{bcd}	22.15^{j-m}	26.98^{a-d}
IR146168-B-B-89-41-4	G-27	95^{n}	127^{j}	106.33^{cde}	33.67^{g-j}	7.67^{b-h}	26.5^{ef}	162.67^{c-i}	77.67^{f-j}	22.18^{j-m}	22.11^{b-h}
IR146168-B-B-214-81-38	G-28	95^{n}	126^{k}	106.5^{cde}	41.83^{ab}	8.33^{bcd}	24.5^{ghi}	120.83^{j-m}	74.9^{i-l}	25.15^{b}	18.96^{f-k}
IR146151-B-B-439-83-7	G-29	101^{g}	134ef	98.67^{jk}	28.5^{p}	6.17^{g-k}	26.5^{ef}	120.67^{klm}	75.51^{h-l}	22.39^{h-l}	12.67^{klm}
IR146151-B-B-584-44-3	G-30	100^{hi}	134^{ef}	117.17^{a}	37.83^{de}	8.17^{b-e}	29.5^{abc}	188.67^{bcd}	86.54^{ab}	23.74^{cde}	31.71^{a}
IR146151-B-B-584-82-40	G-31	99^{j}	134^{ef}	117^{a0}	40.5^{abc}	6.33^{f-k}	30^{ab}	169.5^{c-h}	83.23^{b-e}	25.88^{ab}	23.18^{b-g}
IR146151-B-B-1253-16-3	G-32	98^{k}	133^{g}	88.67^{o}	36.17^{ef}	7^{e-j}	25.5^{efgh}	96.67^{m}	57.76^{q}	22.29^{i-m}	8.75^{m}
IR146151-B-B-1266-13-9	G-33	101^{g}	135^{d}	93.83^{mn}	35.5^{fgh}	10.17^{a}	28.83^{abc}	129.17^{i-m}	79.87^{d-g}	21.83^{klm}	22.9^{b-g}
Maximum		109	143	117.17	42.33	10.17	30.33	228.67	87.83	26.68	31.71
Minimum		95	126	87.5	28.5	5.17	21.17	96.67	53.86	19.62	8.47
SD		0.45	0.43	1.32	1.14	0.855	0.78	18.92	2.12	0.41	3.50
LSD Value		0.99	0.96	2.63	2.27	1.71	1.56	37.80	4.24	0.81	6.99
CV (%)		0.61	0.44	1.6	4.01	14.03	3.68	14.65	3.49	2.16	21.11

Different letters in the same column indicated statistically significant differences at 5% level of probability following LSD test. Here, DFF = Days to 50% flowering, DM = Days to maturity, PH = Plant height (cm), FLL = Flag leaf length (cm), ETH = Number of effective tillers hill^{-1}, PL= Panicle length (cm), NGP= Number of grains panicle^{-1}, SF= Spikelet fertility, TGW= Thousand grains weight (g) and YH= Yield hill^{-1}(g).

Table 4. Estimation of genetic parameters for yield contributing traits.

Traits	Genotypic variance (σ^2_g)	Phenotypic variance (σ^2_p)	GCV(%)	PCV(%)	Heritability (%h^2_b)	GA	GA (%)
DFF	21.21	21.57	4.63	4.67	98.29	9.41	9.46
DM	25.57	25.91	3.8	3.82	98.65	10.35	7.78
PH	56.53	59.14	7.44	7.61	95.6	15.14	14.99
FLL	15.28	17.21	11.27	11.96	88.77	7.59	21.88
ETH	1.37	2.47	15.69	21.06	55.56	1.80	24.09
PL	4.52	5.44	8.16	8.96	83.09	3.99	15.33
NGP	712.51	1249.48	16.88	22.35	57.02	41.52	26.25
SF	61.99	68.75	10.56	11.12	90.17	15.40	20.66
TGW	2.54	2.79	6.95	7.28	91.17	3.13	13.68
YH	27.06	45.46	25.61	33.2	59.53	8.27	40.71

Here, GCV = Genotypic co-efficient of variation, PCV = phenotypic Co-efficient of variation, GA = genetic advance, = GA (%) = Genetic Advance as percent of mean, DFF = Days to 50% flowering, DM = Days to maturity, PH = Plant height (cm), FLL = Flag leaf length (cm), ETH = Number of effective tillers hill^{-1}, PL= Panicle length (cm), NGP= Number of grains panicle^{-1}, SF= Spikelet fertility, TGW= Thousand grains weight (g) and YH= Yield hill^{-1}(g).

The high phenotypic coefficient of variation and genotypic coefficient of variation were noted for yield hill^{-1} (33.2% and 25.61%, respectively). High phenotypic coefficient of variation and moderate genotypic coefficient of variation were recorded for number of grains panicle^{-1} (22.35 and 16.88%, respectively) and the number of effective tillers hill^{-1} (21.06 and 33.69%, respectively). Moderate phenotypic and genotypic coefficient of variation were recorded for flag leaf length (11.96 and 11.27%, respectively) and spikelet fertility (11.12 and 10.56%, respectively). The low phenotypic and genotypic coefficient of variation were recorded for rest of the traits (Table 3). In general, high broad-sense heritability (>60%) was recorded for maximum studied traits. Importantly, high heritability (>60%) united with high genetic advance as percentage of mean (>20%) was documented for the traits flag leaf length (21.88%) and spikelet fertility (20.66%). Moderate heritability (31-60%%) coupled with high genetic advance as percentage of mean (>20%) was recorded for the traits number of effective tillers hill^{-1} (24.09%), number of grains panicle^{-1} (26.25%) and yield hill^{-1} (40.71%).

Phenotypic Correlation Co-efficient

Days to 50% flowering exhibited significant positive correlation with days to maturity (0.94**), plant height (0.28**), flag leaf length (0.36**) whereas it showed a significant negative correlation with thousand grains weight (-0.37**) (Table 4). Days to maturity showed significant positive correlation with plant height (0.29**), flag leaf length (0.32**), whereas it showed a significant negative correlation with thousand grain weight (-0.37**). Plant height exhibited significant positive correlation with flag leaf length (0.42**) and panicle length (0.51**) showed positive correlation with flag leaf length (0.31**) and negative with number of effective tillers hill^{-1} (-0.33**). Number of effective tillers hill^{-1} developed significant negative correlation with thousand grains weight (-0.28**) and positive correlation with yield hill^{-1} (0.52**). Number of grains panicle^{-1} exhibited significant positive correlation with spikelet fertility (0.46**) and yield hill^{-1} (0.72**). Spikelet

fertility positively correlated with thousand grains weight (0.23**) and yield hill^{-1} (0.69**). Importantly yield hill^{-1} showed significant positive correlation with number of effective tillers hill^{-1} (0.52**), number of grains panicle^{-1} (0.72**) and spikelet fertility (0.69**).

Principal Component Analysis

Principal component analysis (PCA) was steered on morphological traits of thirty-three rice genotypes to discover their variability and associations. The analysis revealed three principal components (PCs) that collectively explained 70.54% of the total variance (Table 6). PC1 was the most significant, explaining 26.94% of the variance, followed by PC2 (24.48%) and PC3

Table 5. Phenotypic correlation co-efficient of yield and yield contributing traits.

	DFF	DM	PH	PL	ETH	FLL	NGP	SF	TGW
DM	0.94**								
PH	0.28**	0.29**							
PL	0.03	0.10	0.51**						
ETH	0.05	0.02	-0.13	-0.33**					
FLL	0.36**	0.32**	0.42**	0.31**	0.04				
NGP	0.02	-0.03	0.10	0.09	-0.06	-0.03			
SF	-0.11	-0.15	0.163	0.17	0.09	-0.03	0.46**		
TGW	-0.37**	-0.37**	0.08	0.06	-0.28**	0.09	0.03	0.29**	
YH	-0.06	-0.17	0.07	-0.05	0.52**	0.01	0.72**	0.69**	0.13

*, ** and *** indicate significant at 5%, 1% and 0.1% level of probability, respectively. Here, DFF = Days to 50% flowering, DM = Days to maturity, PH = Plant height (cm), FLL = Flag leaf length (cm), ETH = Number of effective tillers hill^{-1}, PL= Panicle length (cm), NGP= Number of grains panicle^{-1}, SF= Spikelet fertility, TGW= Thousand grains weight (g) and YH= Yield hill^{-1}(g).

Table 6. Principal components (PCs) for yield and yield-related from PCA with Eigenvectors (loadings) of the first three PCs.

Traits	PC_1	PC_2	PC_3
DFF	0.786	0.361	0.36
DM	0.824	0.319	0.297
PH	0.362	0.627	-0.388
FLL	0.241	0.447	-0.63
ETH	-0.133	0.084	0.779
PL	0.484	0.441	-0.178
NGP	-0.38	0.649	0.106
SF	-0.547	0.704	0.045
TGW	-0.425	0.111	-0.581
YH	-0.577	0.701	0.395
Eigen value	2.69	2.45	1.91
Variance (%)	26.94	24.48	19.11
Cumulative variance (%)	26.94	51.42	70.53

Here, DFF = Days to 50% flowering, DM = Days to maturity, PH = Plant height (cm), FLL = Flag leaf length (cm), ETH = Number of effective tillers hill^{-1}, PL= Panicle length (cm), NGP= Number of grains panicle^{-1}, SF= Spikelet fertility, TGW= Thousand grains weight (g) and YH= Yield hill^{-1}(g).

(19.11%). Ladings on PC1 indicated strong associations with days to 50% flowering, days to maturity, plant height flag leaf length, and panicle length. days to maturity, plant height flag leaf length, number of effective tillers plan^{-1}, panicle length, number of grains panicle^{-1}, spikelet fertility, thousand grain weight and yield hill^{-1}. PC3 exposed positive correlations with days to 50% flowering, days to maturity, number of effective tillers plan^{-1}, number of grains panicle^{-1}, spikelet fertility and yield hill^{-1}. The eigen values confirmed the importance of PC1 in capturing the most variation, followed by PC2 and PC3.

Cluster Analysis

The thirty-three rice genotypes were grouped into four distinct clusters under this study based on Euclidean distance following Ward's method (Table 7 & Fig. 1). On the basis of D^2-values, the genotypes were grouped into four clusters. The distribution pattern revealed that cluster II was the largest cluster containing 17 genotypes, while cluster I contained only one genotype. But both cluster III and cluster IV contained seven genotypes.

Table 7. Cluster pattern of thirty-three rice genotypes by Euclidean distance method.

Cluster no.	Total no. of genotypes	Genotype (Code name)
I	2	G-30, G-31
II	17	G-1, G-2, G-3, G-4, G-6, G-7, G-9, G-10, G-12, G-13, G-14, G-25, G-26, G-27, G-28, G-33
III	7	G-17, G-18, G-19, G-20, G-21, G-23, G-24
IV	7	G-5, G-11, G-25, G-16, G-22, G-29, G-32

Intra- and -Inter Cluster Distances

According to Fig. 4, cluster II had the largest intra-cluster distance, measuring 3.58. Cluster IV, had the lowest intra-cluster distances (2.65), whereas cluster I and cluster III had intra-cluster distances of 3.43 and 3.06, respectively (Fig. 2). We found that the inter-cluster distance ranged from 4.55 to 5.45. In contrast to the minimum clusters I and II (4.55), followed by clusters II and III (4.70), clusters I and IV (4.86), clusters I and III (4.90), clusters III and IV (5.07) and clusters II and IV (5.45).

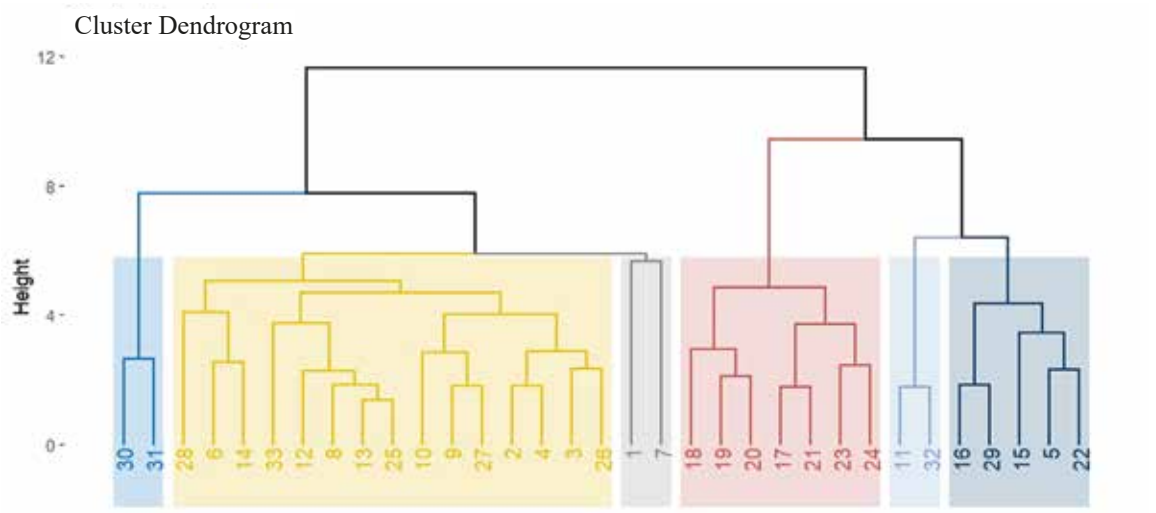

Fig. 1. Hierarchical Wards method dendrogram of thirty three rice genotypes displaying various cluster groups. Legend:1=IR146173-B-B-268-22-45(G-1), 2=IR146173-B-B-268-68-44(G-2), 3=IR146173-B-B-268-94-4(G-3), 4=IR146173-B-B-529-134-4(G-4), 5=IR146173-B-B-529-178-4(G-5), 6=IR146173-B-B-527-90-44(G-6), 7=IR146154-B-B-430-188-46(G-7), 8=IR146154-B-B-430-209-8(G-8), 9=IR146154-B-B-141-10-1(G-9), 10=IR146154-B-B-141-174-42(G-10), 11=IR146154-B-B-547-168-40(G-11), 12=IR146154-B-B-793-7-30(G-12), 13=IR146172-B-B-21-86-5(G-13), 14=IR146172-B-B-136-81-17(G-14), 15=IR146172-B-B-236-87-40(G-15), 16=IR146172-B-B-596-8-10(G-16), 17=IR146164-B-B-54-9-54(G-17), 18=IR146164-B-B-54-52-41(G-18), 19=IR146164-B-B-191-15-40(G-19), 20=IR146164-B-B-191-47-3(G-20), 21=IR146164-B-B-191-86-4(G-21), 22=IR146164-B-B-44-122-4(G-22), 23=IR146164-B-B-543-5-7(G-23), 24=IR146164-B-B-543-165-47(G-24), 25=IR146168-B-B-317-122-6(G-25), 26=IR146168-B-B-15-2-2(G-26), 27=IR146168-B-B-89-41-4(G-27), 28=IR146168-B-B-214-81-38(G-28), 29=IR146151-B-B-439-83-7(G-29), 30=IR146151-B-B-584-44-3(G-30), 31=IR146151-B-B-584-82-40(G-31), 32=IR146151-B-B-1253-16-3(G-32), 33=IR146151-B-B-1266-13-9(G-33).

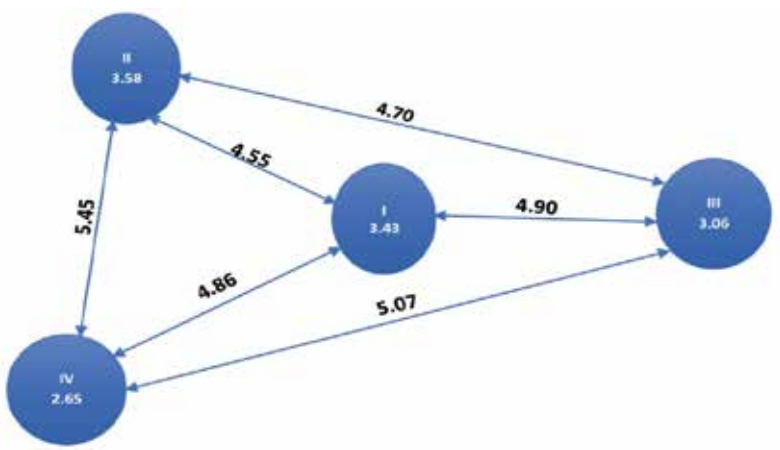

Fig. 2. Cluster diagram showing average intra and inter cluster distance (D=√D2 Values) of the rice genotypes. The values among the lines indicate inter cluster distance and values in the circle indicate intra cluster distance.

DISCUSSION

This study revealed significant genetic variability among the 33 rice genotypes, indicating substantial potential for genetic improvement. Similar results were also observed by many other researchers for plant height (Sumanth *et al.*, 2017; Haque *et al.*, 2014; Sarkar, 2014); for days to 50% flowering (Saha *et al.*, 2022; Shahriar, 2014); for days to maturity (Patnaik and mohanty, 2006); for number of effective tillers hill^{-1} (Saha, 2018, Hoque, 2013); for grain yield hill^{-1} (Ema *et al.*, 2021; Ranawake *et al.*, 2013). The variations observed in days to 50% flowering and days to maturity suggest differences in flowering and maturity patterns, which are crucial for selecting genotypes suitable for specific agro-climatic conditions. IR146173-B-B-527-90-44(G-6), IR146154-B-B-141-10-1(G-9), IR146154-B-B-141-174-42(G-10), IR146154-B-B-547-168-40(G-11), IR146154-B-B-793-7-30(G-12), IR146172-B-B-21-86-5(G-13), IR146172-B-B-136-81-17(G-14), IR146172-B-B-236-87-40(G-15), IR146168-B-B-317-122-6(G-25), IR146168-B-B-89-41-4(G-27), IR146168-B-B-214-81-38(G-28) exhibited the earliest flowering, likely due to genetic factors favoring early reproductive transitions, while IR146164-B-B-54-9-54(G-17) had the longest duration to first flowering, possibly indicating a late-maturing trait beneficial for prolonged seed filling and yield stability. This variation in flowering time could have significant implications for crop management and the synchronization of planting schedules. When considering days to maturity, the study identified genotype IR146168-B-B-214-81-38(G-28) demonstrating early maturity, while IR146164-B-B-54-9-54 G-17) requiring the longest time for maturity to be harvested (Table 3). Plant architecture, as indicated by plant height and number of tillers plant^{-1}, also showed significant diversity among genotypes. Taller plants, such as IR146151-B-B-584-44-3(G-30), IR146151-B-B-584-82-40(G-31), IR146172-B-B-236-87-40(G-15) may offer advantages in terms of light interception and overall productivity, while genotypes with more tillers like, IR146154-B-B-793-7-30(G-12), IR146151-B-B-1266-13-9(G-33), IR146154-B-B-430-209-8(G-8), IR146164-B-B-191-47-3(G-20) could contribute to increased panicle production and yield potential. The flag leaf, the topmost leaf on a rice plant, is decisive for grain yield. It plays a leading role in photosynthesis, providing the majority of carbohydrates for grain filling. Its size, health, and photosynthetic efficiency are closely linked to yield potential. Long flag leaf bearing genotypes like, IR146164-B-B-543-165-47(G-24), IR146164-B-B-191-47-3(G-20), IR146164-B-B-54-52-41(G-18) may offer advantages in terms of chlorophyll interception resulting more carbohydrate production and ultimately higher yield production. Panicle characteristics such as panicle length and number of grains panicle^{-1} are crucial factors influencing yield. Genotypes like IR146164-B-B-44-122-4(G-22) and IR146151-B-B-584-82-40(G-31) exhibited longer panicle, whereas IR146172-B-B-136-81-17(G-14) had shorter panicle. On the other hand, genotypes IR146154-B-B-430-188-46(G-7) and IR146173-B-B-268-22-45(G-1) exhibited maximum number of grains panicle^{-1} whereas IR146151-B-B-1253-16-3(G-32) and IR146154-B-B-547-168-40(G-11) had minimum number of grains panicle^{-1} (Table 3). The study also evaluated thousand grains weight and yield hill^{-1}, providing insights into the genetic potential for grain production and overall crop productivity. Genotypes like IR146151-B-B-584-44-3 (G-30) demonstrated superior grains weight and highest yield hill^{-1}, highlighting their suitability for commercial cultivation with potential contributions to food security and economic prosperity.

Genetic parameter analysis indicated high genotypic and phenotypic variances for days to 50% flowering, days to maturity, plant height, flag leaf length, number of grains panicle^{-1}, spikelet fertility and yield hill^{-1}, highlighting their importance in breeding programs. High broad-sense heritability coupled with high

genetic advance was recorded for flag leaf length, spikelet fertility and moderate heritability coupled with high genetic advance was recorded for the number of effective tillers hill^{-1}, number of grains panicle^{-1} and yield hill^{-1} (Table 3), suggesting that these traits are primarily controlled by additive gene action, making them suitable for direct selection. Similar trend of high heritability with high GA for different traits in rice was also reported earlier (Subbaiah *et al.*, 2011). The higher phenotypic coefficient of variation compared to genotypic coefficient of variation across all traits emphasizes the role of environmental issues in inducing trait expression. This aligns with previous studies highlighting the pivotal role of environmental conditions in modulating plant phenotypes (Dey *et al.*, 2021; Umamaheswar, 2024). However, the small phenotypic coefficient of variation and genotypic coefficient of variation differences for days to 50% flowering, days to maturity, spikelet fertility and thousand grain weight proposed strong genetic control, making them consistent targets for selection (Table 4). Additionally, the assessment of genetic advance provides valuable insights into the potential for improvement through selection in breeding programs. From this study, traits with higher genetic advance, such as flag leaf length, the number of effective tillers hill^{-1}, number of grains panicle^{-1}, spikelet fertility and yield hill^{-1} indicate greater scope for improvement through breeding programs. Conversely, traits with lower genetic advance, like days to 50% flowering and days to maturity may present challenges for improvement through selection due to limited genetic variability. Lastly, traits like yield hill^{-1} and number of grains panicle^{-1} showed the highest genetic advance as a percentage of the mean, suggesting substantial genetic variability and potential for improvement through selection. Traits having high heritability (h^2b) accompanied by high GA might be more advantageous in predicting gain than heritability alone. So the findings of this study might be useful in order to find out the expected traits for crop improvement programmes.

The correlation analysis among various phenotypic traits of rice genotypes revealed intricate relationships that offer valuable insights into the plant's growth and development (Shrestha *et al.*, 2021). Yield hill^{-1} exhibited a strong positive correlation with number of effective tillers hill^{-1}, number of grains panicle^{-1} and spikelet fertility emphasizing the importance of these traits in yield enhancement (Table 4). Similar kind of association was also revealed in the works of other researchers (Islam, 2022; Sameera *et al.*, 2016) Days to 50% flowering showed a significant positive correlation with days to maturity, plant height, flag leaf length but had a negative association with thousand grain weight suggesting that early flowering genotypes tend to produce unfilled and partial filled grains (Table 5). This result was in parallel with (Sadimantara *et al.*, 2021). Days to maturity exhibited a negative correlation with thousand grains weight indicating long duration genotypes may produce more tendinous grains than short duration genotypes. Plant height showed positive correlation with panicle length and flag leaf length suggesting long plant may produce long flag leaf that is important for glucose production ultimately yield production. Additionally, the panicle length positively correlated with flag leaf length and developed a negative correlation with number of effective tillers hill^{-1} that indicating flag leaf length may contribute in panicle development and less tiller hill^{-1} may produce long panicle.

Principal component analysis (PCA) is a powerful statistical technique used to uncover patterns in data by reducing the dimensionality of the dataset while retaining most of the original variability. The results revealed several insights into the relationships between these traits and the contribution of each variable to the principal components (PCs). The Eigen values associated with each principal component indicate the amount of variance explained by that component. Principal component analysis (PCA) identified three principal components explaining 70.53% of total variation, with PC1

contributing the most 26.94%, followed by PC2 with 24.48%. Traits like days to 50% flowering, days to maturity, plant height, flag leaf length, panicle length, had high loadings on PC1, reinforcing their role in yield determination (Table 6). These results indicate that PC1 and PC2 are particularly important for capturing the major patterns of variation in the data, while PC3 also contributes significantly to explaining additional aspects of variability. Therefore, the information provided by these principal components can effectively summarize the multidimensional nature of the dataset, facilitating data interpretation and visualization in subsequent analyses (Lin *et al.*, 2025; Shi *et al.*, 2021). This result is similar with SaiVenkat, *et al.*, (2024).

Any effective plant breeding effort must start with appropriate parent selection. Higher genetic gains via selection are predicted for parents with greater genetic variety. Genetic divergence analysis was used in this work to ascertain the genotypes' genetic relationships and choose the best genotypes for a future breeding effort. Four clusters were formed from the genotypes based on the D^2-value (Table 7 & Fig. 2). Cluster II had the greatest number of genotypes (17), according to the distribution pattern, while cluster I had the fewest number of genotypes (2), indicating that there is greater diversity among the genotypes in cluster IV than in clusters I, which are more closely related. These results were parallel with the results of (Thang, 2022; Singh *et al.*, 2021; Sathyaraj *et al.*, 2024). The analysis of intra-and inter-cluster distances, as shown in Figure 4, further supported these findings. The maximum inter cluster distance was observed between clusters II and IV (5.45), followed by clusters III and I (5.07), suggesting that genotypes from these clusters are highly divergent. This indicates that hybridization between genotypes from these clusters may result in heterotic progeny with broad genetic variability in the subsequent generations. While cluster II contained the highest number of genotypes, its intra-cluster distance was also the largest, signifying considerable genetic variation within this group. This suggests that genotypes within Cluster II hold strong potential for trait enhancement and breeding improvement in rice cultivars. The intra-cluster distances ranged from 2.65 to 3.58, demonstrating that genotypes within the same cluster share close genetic relationships. This finding is related with previous studies (Pandey, 2019). This insight is particularly valuable for plant breeders in selecting parental lines for crossing programs, ensuring the combination of diverse genetic backgrounds to enhance yield potential and overall genetic improvement. Hybridization between distantly related genotypes is expected to introduce novel variations, contributing to the development of superior high-yielding varieties with enhanced adaptability and resilience.

CONCLUSION

This study highlighted substantial genetic variation among rice genotypes. Traits such as flag leaf length, number of effective tillers hill^{-1}, number of grains panicle^{-1}, spikelet fertility and yield hill^{-1} exhibited moderate to high heritability and high genetic advance, making them promising for selection in breeding programs. Yield hill^{-1} showed significant positive correlations with number of effective tillers hill^{-1}, number of grains panicle^{-1} and spikelet fertility. Principal component analysis accounted for 70.53% of the total variation, and cluster analysis grouped the 33 genotypes into four clusters, with Cluster II showing the highest diversity. The high-yielding genotypes IR146151-B-B-584-44-3(G-30), IR146154-B-B-430-188-46(G-7) and IR146173-B-B-268-94-4 (G-3) were identified as potential candidates for further breeding. To confirm the stability of high-yielding genotypes, multi-location trials are recommended for varietal development.

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