PLANT SCIENCE TODAY
ISSN 2348-1900 (online)
Vol 11(1): 64–75
https://doi.org/10.14719/pst.2231

HORIZON
e-Publishing Group
HePG

RESEARCH ARTICLE

Multivariate analysis in rice (*Oryza sativa* L.) germplasms for yield attributing traits

Satya Prakash[1], **S Sumanth Reddy**[2], **Sandeep Chaudhary**[3]*, **SC Vimal**[4] & **Adesh Kumar**[2]*

[1]Division of Genetics and Plant Breeding, Lovely Professional University, Phagwara, Punjab-144411, India
[2]Division of Plant Pathology, Lovely Professional University, Phagwara, Punjab-144411, India
[3]Division of Entomology, Lovely Professional University, Phagwara, Punjab-144411, India
[4]Department of Genetics and Plant Breeding, ANDUAT, Kumarganj, Ayodhaya, Uttar Pradesh- 224229, India

*Email: sandeep.25793@lpu.co.in, adesh.19078@lpu.co.in

ARTICLE HISTORY
Received: 09 November 2022
Accepted: 03 April 2023

Available online
Version 1.0 : 11 October 2023
Version 2.0 : 01 January 2024

Additional information

Peer review: Publisher thanks Sectional Editor and the other anonymous reviewers for their contribution to the peer review of this work.

Indexing: Plant Science Today, published by Horizon e-Publishing Group, is covered by Scopus, Web of Science, BIOSIS Previews, Clarivate Analytics, NAAS, UGC Care, etc
See https://horizonepublishing.com/journals/index.php/PST/indexing_abstracting

CITE THIS ARTICLE
Prakash S, Reddy S S, Chaudhary S, Vimal S C, Kumar A. Multivariate analysis in rice (*Oryza sativa* L.) germplasms for yield attributing traits. Plant Science Today. 2024; 11(1): 64–75. https://doi.org/10.14719/pst.2231

Abstract

A study was conducted to evaluate the genetic diversity and relationships among sixty rice genotypes by assessing eleven morphological yield traits using principal component analysis (PCA) and cluster analysis at ANDUAT, Ayodhya (Uttar Pradesh), India. The results revealed significant variation among the genotypes, with certain genotypes displaying higher values for specific traits, thus confirming the presence of genetic diversity. Cluster analysis revealed that Cluster V had the highest number of genotypes, while Cluster IV exhibited the highest intra-cluster distance, indicating the potential usefulness of these genotypes for rice improvement purposes. Principal component analysis revealed that the first two principal components, along with three other components, accounted for 75.11 percent of the total variability. Days to 50% flowering (DFF), days to maturity (DM), 1000 seed weight (TSW), and panicle length (PL) were identified as the most accurate predictors of variability. The first principal component (PC1) was associated with plant height (PH) and harvest index (HI), while the second principal component (PC2) was linked to DFF and DM. The third principal component (PC3) was associated with TSW and grains/panicle (GP), the fourth principal component (PC4) with panicles bearing per plant (PBP) and biological yield per plant (BY), and the fifth principal component (PC5) with PL and BY. The study identified several promising genotypes for various traits. G.35, G.17, G.30, G.45, and G.46 exhibited short plant height, while G.60, G.40, G.54, G.55, and G.41 displayed high yield potential.

Keywords

Oryza sativa; genetic variability; food security; principal component analysis; multivariate analysis

Introduction

Rice holds a critical position as a staple food source for approximately half of the global population (1). Its wide distribution across continents and subcontinents is a testament to its diverse genetic makeup (2). However, despite efforts made in breeding programs, challenges persist in the production of rice varieties due to genetic and human-induced factors. Ensuring the availability and suitability of suitable crop lines for future advancements necessitates substantial time and expert involvement (3). Genetic variations play a fundamental role in plant breeding strategies, contributing not only to existing germplasm collections but also facilitating the development of new pure lines (4, 5). As most yield-related traits are controlled by multiple genes, accurately assessing the variance across available genotypes becomes crucial for plant breeders (6). Leveraging the natural diversity and divergence of crops has long been recognized and employed in the improvement of crop species since the advent of systematic plant breeding (7). The effectiveness of any breeding program relies on harnessing the existing variability among germplasms, underscoring the need to conserve, evaluate, and utilize genetic diversity for sustainable crop production and to meet the demands of a growing population (8).

In rice crop improvement projects, genetic diversity is a fundamental prerequisite as it promotes the development of more robust recombinants (9). The fastest response to genetic development is often achieved by crossings between parents with substantial genetic potential (10). Therefore, it is essential for plant breeders to have a clear understanding of the level of genetic divergence in order to select the most suitable parents for their breeding programs (8). To assess the degree of genetic divergence among the genotyped rice samples, D2 analysis was employed. The finding provided valuable insights on inter and intra-cluster distance that put light on cluster level variety and recommends that mixing the genetic materials of different clusters may result in heterozygous offspring (11).

In order to evaluate the genetic diversity, heritability, genetic progress, and multivariate analysis among yield and yield-associated variables of sixty rice genotypes, the following experiment was carried out. “Principal component analysis (PCA), a non-parametric, multivariate technique that analyses a data table consisting of intercorrelated quantitative dependent variables, thereby extracting essential information” (12). In hybrid breeding programs, fertility restorer lines play a crucial role in enhancing productivity by exploiting variability. The utilization of diverse fertility restorers in hybridization programs and the identification of elite genotypes within the diverse population were the objectives of this study (13).

Materials and Methods

Experimental site

The experimental work was carried out at two locations: Crop Research Station Masodha, Ayodhya, and Student Instructional Farm of Acharya Narendra Deva University Agriculture & Technology (ANDUAT), Kumarganj, Ayodhya. These locations are geographically positioned between 26.470 N latitude and 82.120 E longitude, at an altitude of approximately 113 m above mean sea level.

Experimental material

The experimental material for this study consisted of 60 genotypes of the local landrace rice (*Oryza sativa* L.) cultivars Type-3, Lalmati, NDR-359, and NDR-2064 from Uttar Pradesh. The germplasms were collected from the Crop Research Station Masodha, Ayodhya, and ANDUAT, Kumarganj, Ayodhya (Table 1).

Table 1. Description of the genotypes used in the study.

Germplasm code	Germplasm	S.N.	Germplasm	S.N.	Germplasm	S.N.	Germplasm
G1 checks	Type 3	G16	Moti farm	G31	Badshah bhog	G46	Singul
G2	Lalmati	G17	Karahani white	G32	Hazaar dana	G47	Chingari
G3	NDR-359	G18	Sona chur	G33	Heera	G48	Ketaki
G4	NDR-2064	G19	Ram bilas	G34	Tinpakani	G49	Sukhawan
G5	Kalamadan	G20	Ram bhog-1	G35	Dudhi	G50	Basahwa
G6	Naina	G21	Sakkar chinni	G36	Binni	G51	Mangla
G7	Ram gandha	G22	Madhuri	G37	Bakain	G52	Hari krishana
G8	Son – kharcha	G23	Rasi	G38	Nankawa	G53	Norin
G9	Karangi	G24	Lal surya	G39	Padhani	G54	TCA-52
G10	Joginiya	G25	Kabira	G40	Mutra	G55	TCA-151
G11	Gujraj	G26	Sapana	G41	Mazeera	G56	IET-16719
G12	Bazaar bang	G27	Bagari Gorakhpur	G42	Aguwari	G57	IET-16717
G13	Parson	G28	Bhadhi black	G43	Ghee bhat	G58	IET-16724
G14	Pahariya	G29	Karahni	G44	Bee	G59	IET-16735
G15	Akatahawa –BBK	G30	Ram kajara	G45	Raj muniya	G60	IET-4673

Nursery raising and transplanting

All the genotypes were sown during the Kharif (autumn) season of 2016 and 2017. Thirty sun-dried seeds of each genotype were utilized to raise the nursery and subsequently one seedling per hill was transplanted into the field. Twenty-five days old rice seedlings were used to transplant (13). A randomized complete block design (RCBD) with three replicates per genotype was employed for the experiment. The spacing between genotypes within each replication was maintained at 15×20 cm. Furthermore, a recommended rate of NPK fertilizer application at 120:60:60 kg/ha was followed (14).

Morphological data collection

For data collection on morphological features, five randomly chosen representative plants from each genotype in each replication were selected. The observations for each character were recorded using the standard evaluation system (15). A total of eleven quantitative traits were measured, including plant height (PH) in centimeters, tillers per plant (TP) in number, panicles bearing per plant (PBP) in number, panicle length (PL) in centimeters, grains per panicle (GP) in number, biological yield per plant (BY) in grams, harvest index (HI) in grams, 1000 seed weight (TSW) in grams, and seed yield per plant (SYP) in grams.

Statistical analysis

The obtained data were analyzed using analysis of variance (ANOVA) through the general linear model (GLM) approach in SAS version 9.2. This analysis aimed to determine the effects of genotypes and their interaction in the randomized complete block design (16). For traits with homogeneous mean squares, variance components were estimated, and a combined analysis of variance was conducted.

The phenotypic and genotypic variances, as well as their coefficients, heritability in the broad sense, and genetic progress, were calculated using the formula proposed by Burton and DeVane in 1953 (17, 18). To assess the genetic diversity among the 60 genotypes along with the four check landraces, a dendrogram was constructed using the Windostat 9.3 software (19).

Results

Analysis of variance (mean squares) for grain yield and quality traits

The analysis of variance (ANOVA) showed highly significant differences among all the traits and an adequate amount of genetic variability among all the genotypes (Table 2 & Fig. 1) which favours selection in the desired direction.

Mean performance of genotypes for various traits

The general mean, range, standard error, and critical difference (CD) for eleven quantitative traits of rice studied during the Kharif season of 2016 & 2017 is represented in (Fig. 2 & 3) that provides crude information on the presence of genetic variability among the genotypes.

The general mean of G.7 to G.9 for DM is 121.16 days, while the mean value of DFF varied from G.9 to G.7 with a range of 77.33 to 109.50 days. Plant height varied from 89.51 (G.54) to 153.00 (G.35), with a mean value of 111.98 cm and the number of tillers per plant varied from 9.63 (G.30) to 21.02 (G.57), with a mean value of 13.69.

One of the important traits in crop improvement is the number of panicles bearing tillers per plant. The mean value of this trait was 9.01, ranging from 7.00 (G.46) to 12.95 (G.3), revealed that the PL had a range of 20.93 cm (G.5) to 28.09 cm (G.36), with an average of 23.26 cm. Biological yield ranged from 37.73 (G.12) to 4673 (G.60) with a grand mean of 74.28 g, harvest Index ranged from 34.93 (G.18) to 42.37 (G.54) with an overall mean of 38.98, and the highest GP was observed from 78.37 (G.57) to 177.47 (G.54) with a mean of 123.10. Seed yield per plant ranged from 14.78 (G.12) to 41.31 (G.60), with a general mean of 28.94 g, while 1000 seed weight ranged from 38.22 (G.21) to 11.90 (G.30), with a mean value of 23.21 g. G.60 had the SYP that was much higher, followed by G.40, G.54, G.55, and G.41. An important factor for increasing crop output is seed yield/plant.

The coefficient of variation (CV) for the studied traits had a mean value of 7.89, ranging from 2.63 to 18.00. The variables related to yield, such as tillers per plant (TP), panicles bearing per plant (PBP), biological yield (BY), and seed yield per plant (SYP), showed high coefficients of variation (20), indicating that the rice genotypes are more variable.

Previous studies by Gomez and Gomez (20) have indicated that the CV is a reliable indicator of the relationship between variables and the consistency of research. They also noted that as the CV values exceed 20, the experimental consistency tends to decrease.

Table 2. Analysis of variance for 11 characters of rice genotypes.

Characters	Source of variation					
	Replicate	Environments	Interactions (df=2)	Overall, Sum	Treatments (df=59)	Error (df=295)
	(df=2)	(df=1)		(df=5)		
DFF	0.23	1.23**	0.03	0.35	189.45**	11.17
DM	8.60	0.47	12.04	8.35	197.82**	10.12
P H	16.07	156.41*	15.86	44.06*	1266.72**	14.39
T P	0.76	5.28**	0.22	1.45	37.15**	6.07
PBP	0.03	36.93**	0.24	7.48*	10.90**	2.20
P L	0.29	10.15**	0.03	2.16	16.07**	1.99
GP	38.65	691.50*	82.74	186.85*	2388.87**	70.77
B Y	1.54	241.31**	3.70	50.36	1507.86**	68.68
H I	1.49	11.14**	0.39	2.98	26.66**	2.29
TSW	0.76	0.80	0.33	0.60	124.46**	0.67
YP	2.19	9.40*	1.57	3.38	233.90 **	10.51

*, ** significant at 5 % and 1 % probability level, respectively, Where, *=significant, **=highly significant.

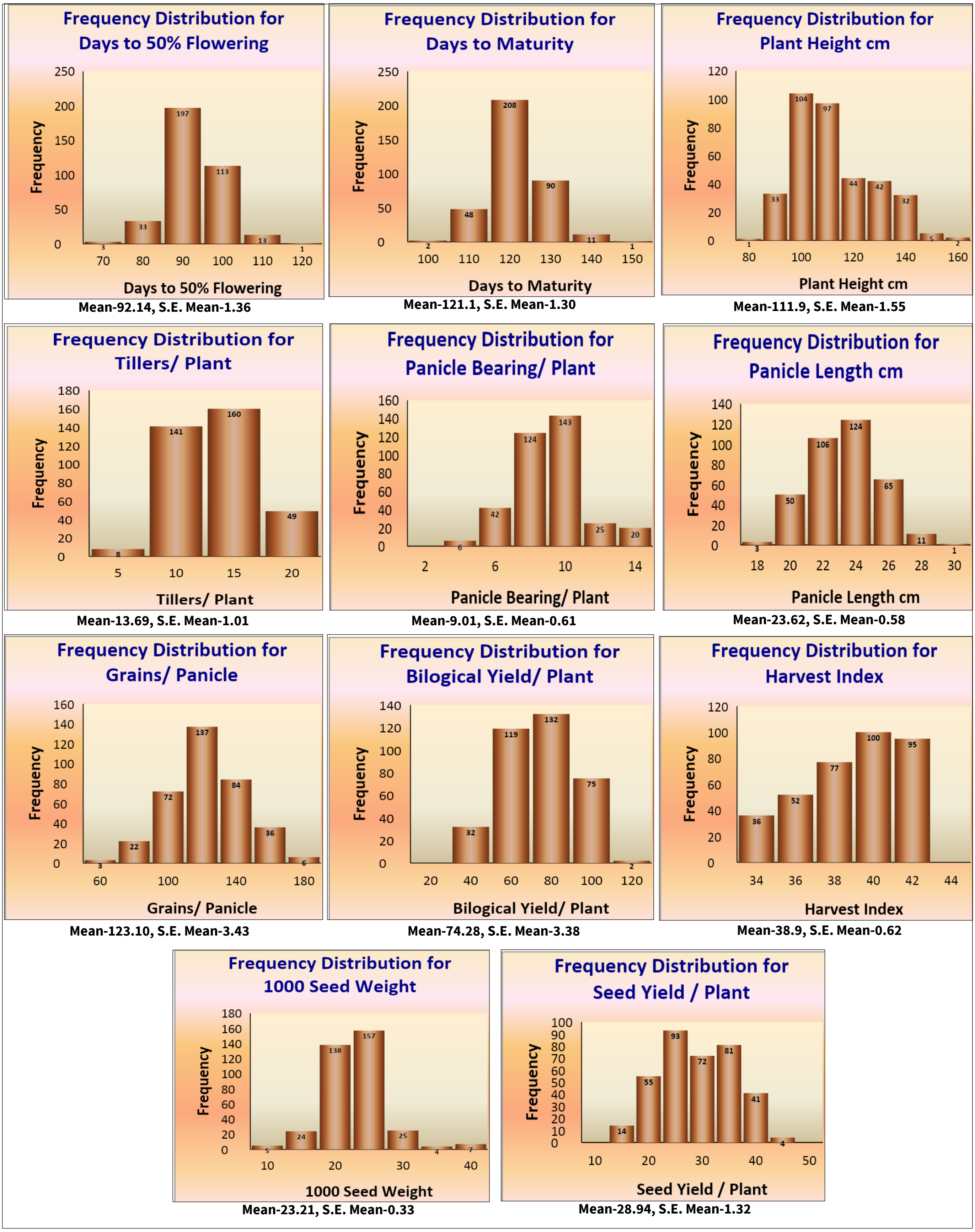


Fig. 1. Frequency distribution of different quantitative traits of rice (*Oryza sativa* L.).

In the present study, the average critical difference (CD) value was 7.89, with a range of 2.63 to 18.00. The high coefficient of variation observed for yield-related traits, TP, PBP, BY, and SYP, indicates substantial variability among the rice genotypes (21).

Determination of genetic variations

Phenotypic and genotypic coefficient of variation

During the two-year periods, TP exhibited the highest estimates of both phenotypic and genotypic coefficients of variation, followed by SYP (g), BY (g) and several PBP.

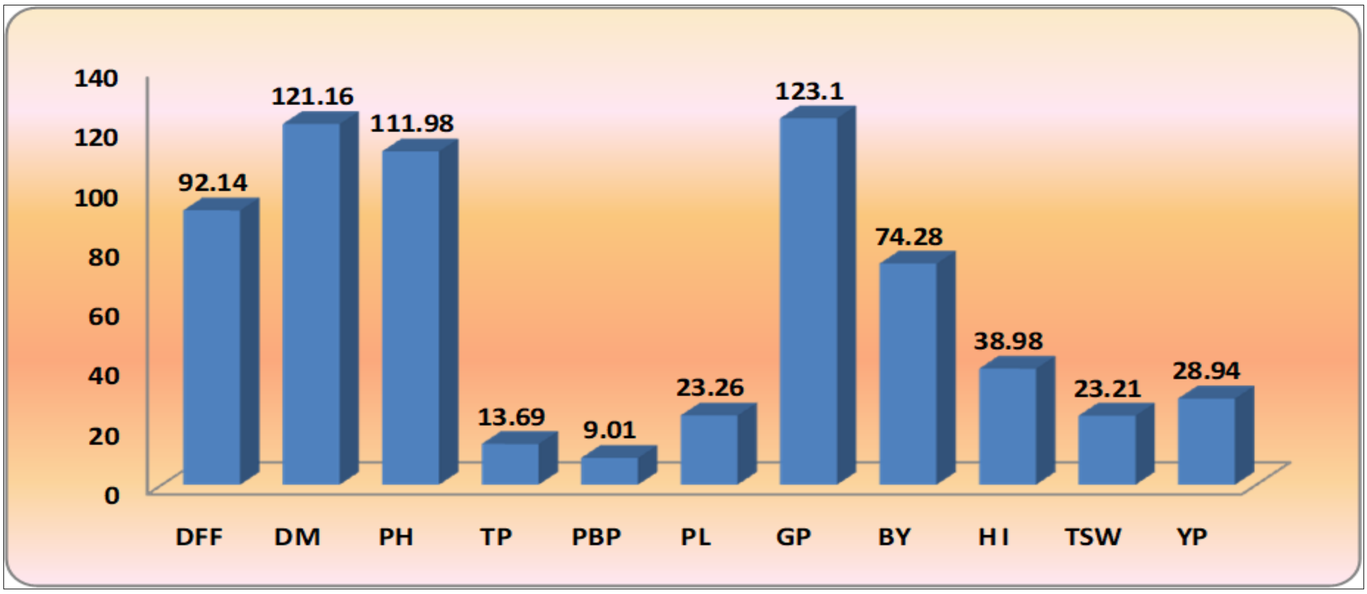


Fig. 2. Graphical representation of the mean performance of sixty rice (*Oryza sativa* L.) genotypes.

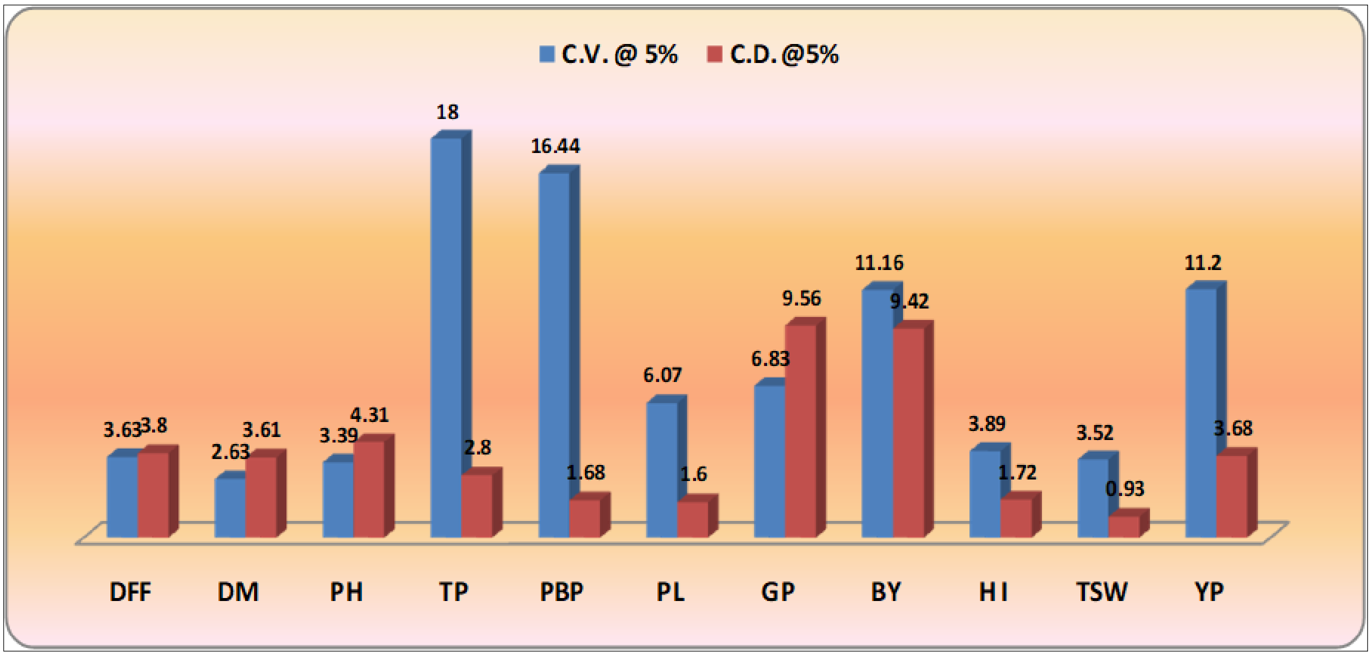


Fig. 3. Graphical representation of CV (%) and CD among sixty rice (*Oryza sativa* L.) genotypes for 11 yield contributing traits (**CV** = Coefficient of variation, **CD** = Critical difference).

The PCV and GCV estimates for these four traits were found to be greater than 20% (Fig. 4), indicating a substantial level of variation within the studied rice genotypes.

When the phenotypic coefficient variation (PCV) value exceeds the genotypic coefficient of variation (GCV), it suggests that observed variation may be influenced by

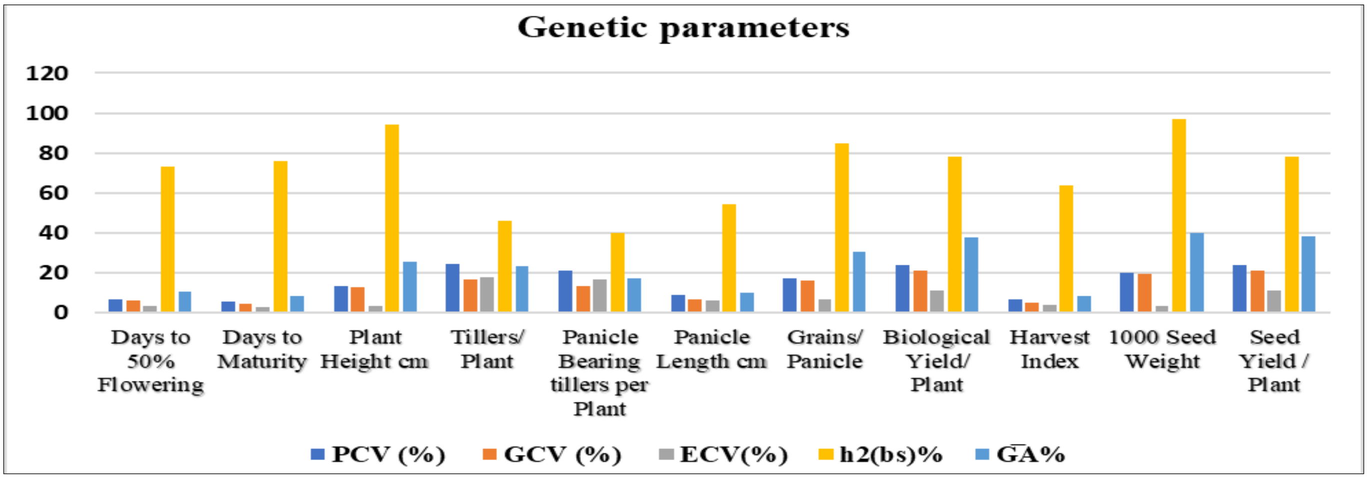


Fig. 4. Graphical representation of heritability and genetic advance as % of mean in rice (*Oryza sativa* L.) genotypes (**PCV** = Phenotypic Coefficient of Variation, **GCV** = Genotypic Coefficient of Variation, and **ECV** = Environmental Coefficient of Variation, **GA**= Genetic advancement %, **h²** = Heritability %).

environmental factors rather than solely by genetic factors. In such cases, the variation observed in the traits may not be solely attributed to genetic differences among the genotypes.

In accordance with previous studies (22 - 23), our findings also showed high estimates of phenotypic and genotypic coefficients of variation for the TP and PBP across both years. Additionally, we observed substantial phenotypic and genotypic variation in BY (g) and SYP (g) throughout the study period.

Heritability and genetic progress

Results from Fig. 4 demonstrated high heritability values and significant genetic progress as a percentage of the mean value for TSW (g), BY (g) and SYP (g) in both the years. These findings indicate that these traits were predominantly controlled by genetic factors and were amenable to selection for improvement.

Traits that exhibit high heritability and significant genetic progress are considered ideal for selection and breeding purposes due to their greater transmissibility and variability and found in synchronization with the studies of Acevedo-Siaca *et al*. and Adhikari *et al*. (24 - 25).

Cluster analysis by Mahalnobis Euclidean^2 Distance method

With nineteen genotypes, cluster V was the largest and exhibited the highest overall genetic similarity, followed by clusters VI (11), Cluster VII (9), Cluster III (8), Cluster I (6), and cluster IV (3). Clusters II and VIII were the smallest, each containing only two genotypes (Fig. 5).

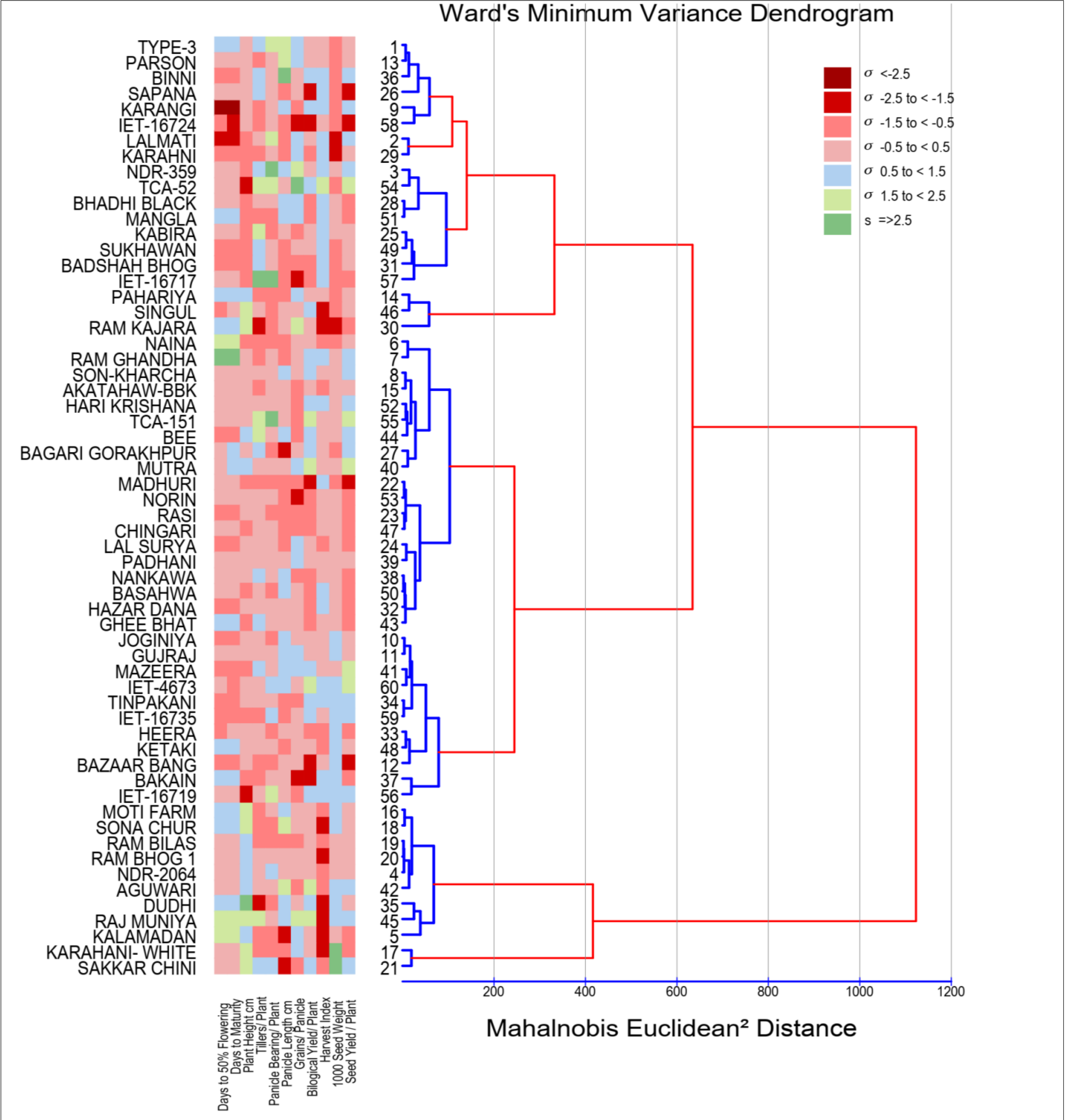


Fig. 5. Clustering patterns of rice genotypes based on Mahalnobis Euclidean^2 Distance method

Intra-Inter cluster distances among eight clusters

Cluster IV had the highest intra-cluster distance, followed by clusters III, I, VI, VII, V, VIII and cluster II, indicating that these genotypes may be amenable to informal feature adjustment for rice improvement (26).

All the cluster combinations showed considerable inter-cluster distances. The largest inter-cluster distance was recorded between clusters II and VIII. On the other side, clusters VI and VIII displayed the smallest cluster distance, followed by clusters VII and VIII, I and V (Fig. 6).

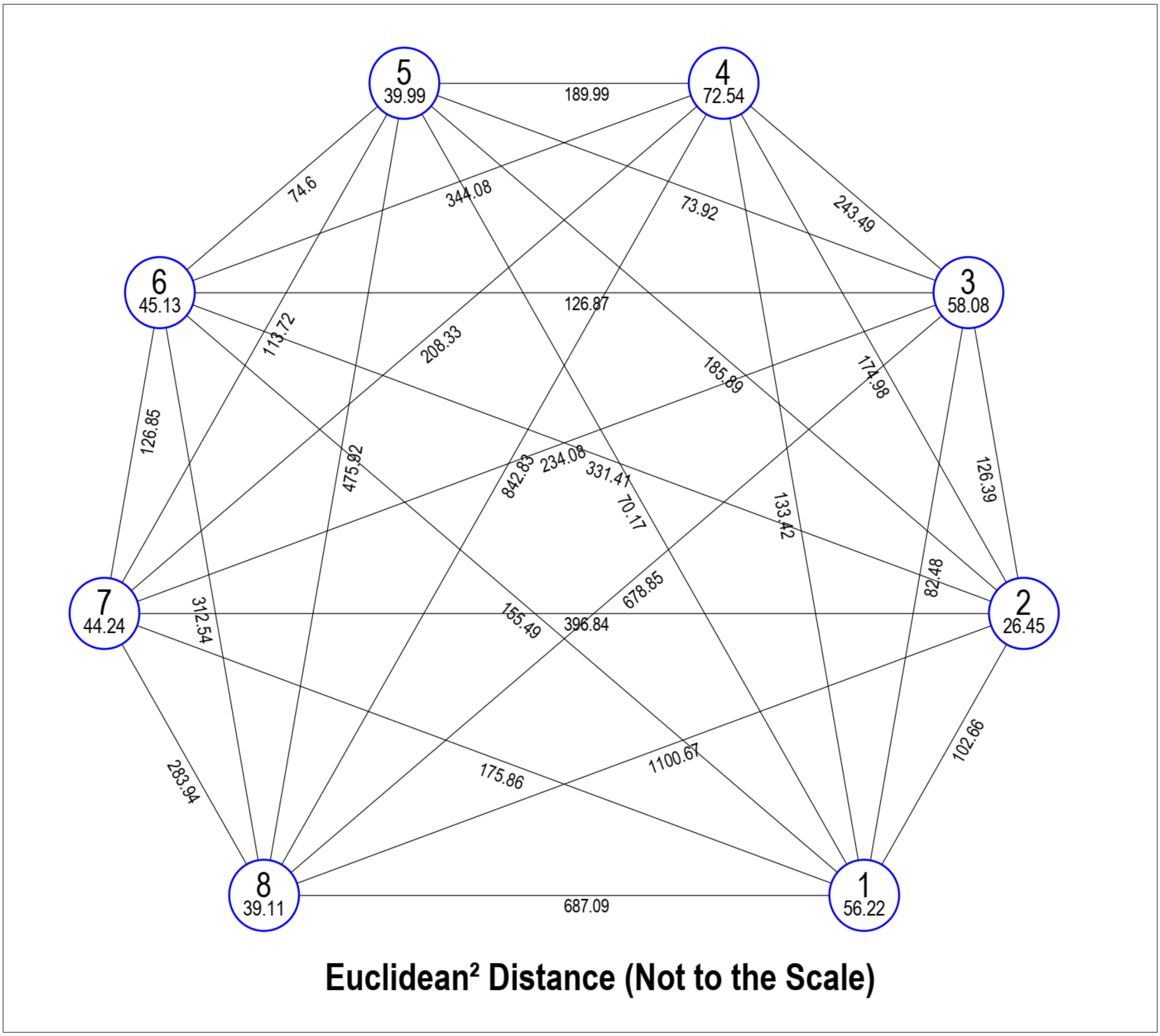


Fig. 6. Graphical representation of intra and inter cluster distances among eight clusters in 60 genotypes of rice (*Oryza sativa* L.).

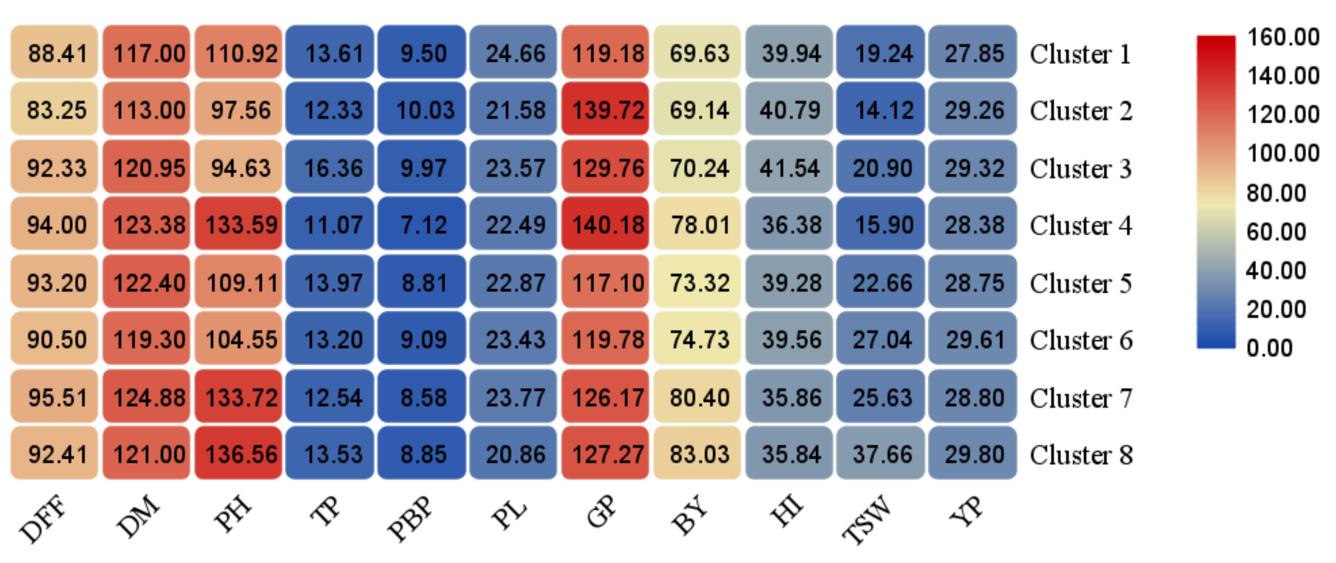
Mean values of eight clusters

There have been calculated variations among all the genotypes for each yield attributing trait. Cluster VII, followed by clusters IV, V, VIII, III, VI, I and II had the highest cluster mean of 95.51 (DFF) and 124.88 (DM) (Fig. 7). Plant height varied between clusters III (94.63) and VIII (136.56), indicating that these clusters might be taken into consideration for improving the PH of rice (*Oryza sativa* L.).

The variations in yield and the contributing traits were observed across different clusters, with TP ranging from cluster IV (11.07) to cluster III (16.36). The key attributes were the number of tillers per plant, and the goals for crop improvement ranged from cluster IV (7.12) to cluster II (12.95). This indicates that the PL ranged from cluster VIII (20.86) to cluster I (24.66), and the highest GP was observed from cluster V (117.10) to cluster IV (140.18). Additionally, the BY ranged from cluster III (70.24) to cluster VIII (83.03), while the HI ranged from cluster VIII (35.84) to cluster III (41.54). The TSW showed a range from cluster II (14.12) to cluster VIII (37.66), and the SYP was measured at 29.80 across these clusters.

Contribution of different characters genetic divergence

Among the studied characters, TSW, PH, GP, BY, and DFF exhibited the highest contributions to the overall genetic divergence among the rice genotypes. These traits played a significant role in contributing to the total diversity observed in the population. On the other hand, characters such as DM and SYP made no substantial contribution to the overall genetic divergence in this study (Fig. 8).



	DFF	DM	PH	TP	PBP	PL	GP	BY	HI	TSW	YP
Cluster 1	88.41	117.00	110.92	13.61	9.50	24.66	119.18	69.63	39.94	19.24	27.85
Cluster 2	83.25	113.00	97.56	12.33	10.03	21.58	139.72	69.14	40.79	14.12	29.26
Cluster 3	92.33	120.95	94.63	16.36	9.97	23.57	129.76	70.24	41.54	20.90	29.32
Cluster 4	94.00	123.38	133.59	11.07	7.12	22.49	140.18	78.01	36.38	15.90	28.38
Cluster 5	93.20	122.40	109.11	13.97	8.81	22.87	117.10	73.32	39.28	22.66	28.75
Cluster 6	90.50	119.30	104.55	13.20	9.09	23.43	119.78	74.73	39.56	27.04	29.61
Cluster 7	95.51	124.88	133.72	12.54	8.58	23.77	126.17	80.40	35.86	25.63	28.80
Cluster 8	92.41	121.00	136.56	13.53	8.85	20.86	127.27	83.03	35.84	37.66	29.80

Fig. 7. Graphical representation of mean values of eight clusters by Tocher's method for 60 genotypes of rice (*Oryza sativa* L.)

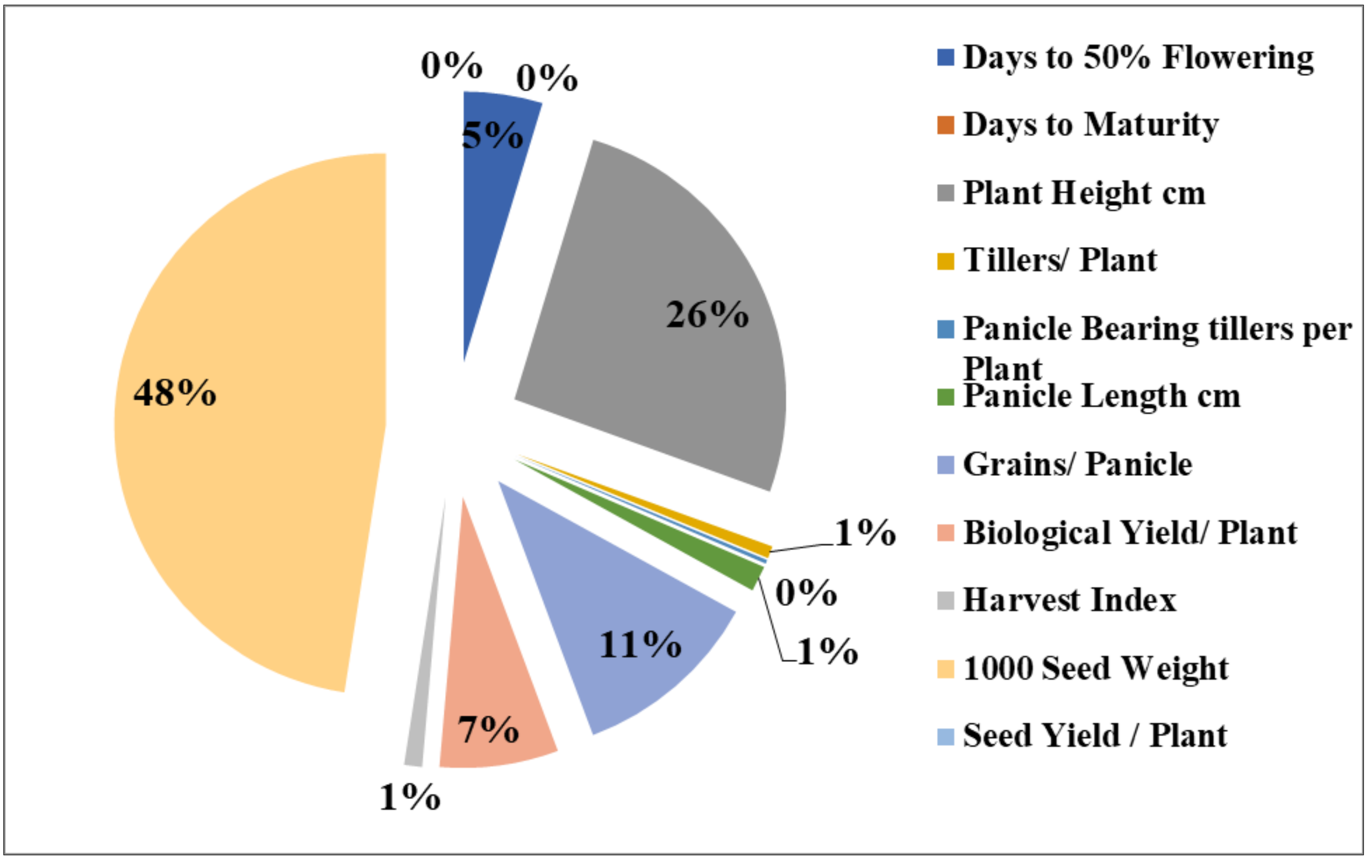


Fig. 8. Graphical representation of the contribution of different characters towards genetic divergence in 60 genotypes of rice (*Oryza sativa* L).

Most promising rice genotypes for different traits

Genotypes, G.35, G.17, G.30, G.45, and G.46 displayed short plant height which may be useful to minimize waterlogging. On the other hand, genotypes with early maturity characteristics were G.9, G.2, G.58, G.44, G.34, and G.31. Genotypes, G.60, G.40, G.54, G.55, and G.41 have had high yield and yield-contributing characters (Fig. 9).

Principal component analysis (PCA)

Since they are responsible for the significant magnitude of variance in the population, principal components with eigenvalues greater than 1 are observed as imperative components of variability. Selecting such elements is essential to plant breeders in order to upsurge the genetic progress. The eigenvalue of PC1 was 3.29, indicating that this component was very variable. Principle component 1 (29.90) had a higher percent variability followed by PC2 (18.43) (Table 3).

The canonical analysis revealed that DFF, followed by DM, TSW and PL, were the most accurate predictor of variability. The HI and PH were measured by PC1; DFF and DM were measured by PC2. GP is measured by PC3. PC5 was a measure of PL, whereas PC4 measures PBP and BY.

An increase in Plant height (PH) and a decrease in HI and SYP (g) contributed to the rise of PC1. An increase in DFF and DM, as well as the traits TP, GP and SYP contributed to the increase in PC2. PC3 showed a notable increase with an increase in TSW (g) and a decrease in GP. PC4 exhibited a substantial increase with an increase in PBP and BY (g), while PC5 showed a significant increase with an increase in PL (cm) and a decrease in BY (g) (Fig. 10).

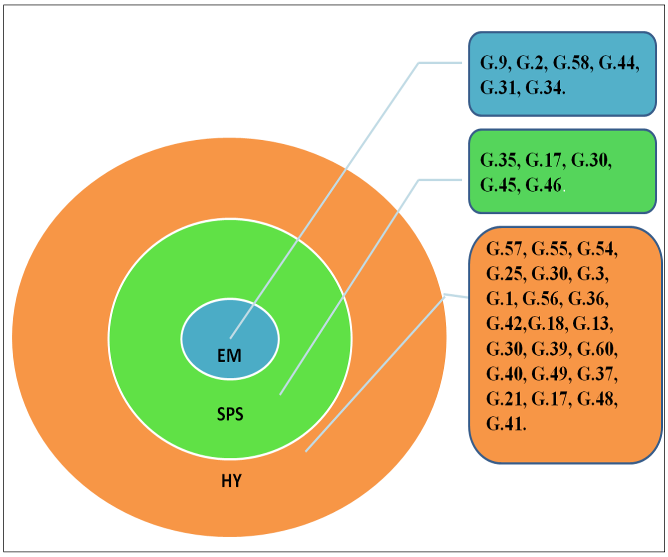


Fig. 9. Graphical representation of identification of most promising rice (*Oryza sativa* L.) genotypes (**EM**- Early maturity, **SPS**- Short plant stature, **HY**- High yield).

Table 3. Eigenvectors and Eigenvalues of the first five principal components of 11 traits of rice (*Oryza sativa* L.).

PCs	PC1	PC2	PC3	PC4	PC5
Eigenvalue	3.28	2.03	1.56	1.36	0.92
Variation %	29.89	18.53	14.26	12.41	8.40
Cumulative %	29.89	48.43	62.69	75.10	83.51
DFF	0.25	**0.55**	0.23	0.11	0.11
DM	0.25	**0.57**	0.19	0.02	-0.05
PH	**0.48**	-0.07	-0.18	-0.04	-0.23
TP	-0.33	0.30	**0.31**	0.27	0.03
TBP	-0.07	-0.15	-0.19	**0.58**	0.16
PL	0.15	0.04	-0.33	0.23	**0.73**
GP	0.14	**0.31**	-0.49	0.03	0.03
BY	0.07	0.04	-0.26	**0.56**	-0.59
HI	-0.50	0.05	0.11	0.22	0.04
TSW	0.28	-0.22	**0.43**	0.39	0.04
SYP	-0.40	**0.31**	-0.37	-0.09	-0.13

Discussion

Genetic analysis of quantitative traits is essential in plant breeding programs to formulate effective breeding strategies (27). The present study demonstrated significant variations in all traits, except for GP, BY, and SYP, among sixty genotypes. This indicates the presence of substantial diversity for crucial traits. These findings align with a previous study on rice trait data, which also reported significant results for all the traits (28).

The varieties G.9 and G.7 exhibited significant variability in certain traits, making them valuable for crop improvement programs. Specifically, these varieties showed potential for the development of short-duration rice varieties (29). Additionally, they have high mean values for the days to 50% blooming and maturity, indicating their potential for early maturation and shorter growth cycles.

The variety G.54 had the minimum plant height (PH) value, while G.35 had the maximum value, indicating significant fluctuation in this trait. This information can be utilized in the development of rice varieties with a short shelf life (30). Furthermore, among the ten rice varieties mentioned (G.30, G.57, G.46, G.3, G.5, G.36, G.12, G.60, G.18, and G.21), significant variation was observed in terms of yield and related characteristics.

The analysis of genotypic and phenotypic coefficients of variation (GCV and PCV) revealed that the PCV values were higher than the GCV values for all traits, indicating the influence of environmental factors on these traits. The magnitude of the differences between GCV and PCV can serve as an indicator of the extent of environmental effects. When the differences are large, it suggests that environmental factors have a substantial impact on trait variation, whereas smaller differences indicate a higher genetic influence. Based on the information provided, all the characteristics examined in the study align with this description (31).

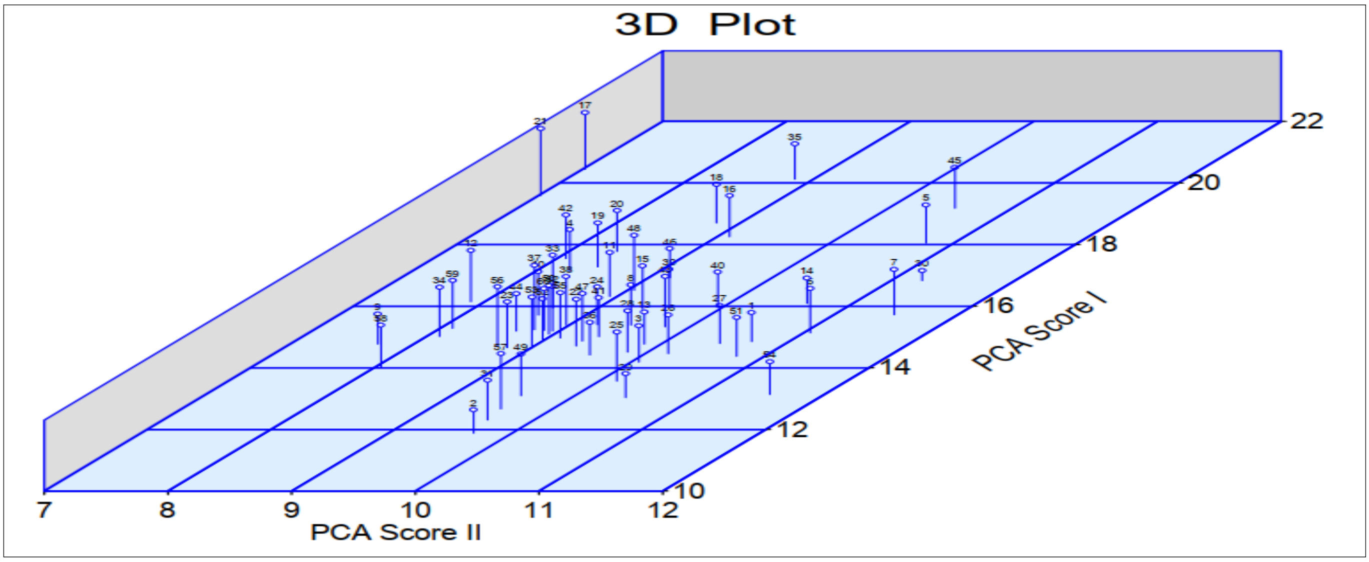


Fig. 10. Graphical representation of a three-dimensional graph of 60 promising germplasm in rice (*Oryza sativa* L.).

The small differences between PCV and GCV for traits such as DFF, DM, PH, PL, GP, HI, and TSW suggest that these traits are less influenced by environmental factors and are more genetically determined. This implies that the observed variations in these traits are primarily due to genetic differences among the studied individuals rather than environmental conditions. Furthermore, the study suggests that individuals showing desirable traits with low environmental influence can be selected and utilized in crossing programs that lead to future yield enhancement. All among the yield attributing traits TP, BY and SYP had the highest PCV and GCV (32-36). The heritability values of the traits varied across the moderate to low range, with certain traits such as DFF, DM, BY, HI, and SYP demonstrating high heritability values.

Broad sense heritability accounts for total genetic variance that includes additive, dominance and, epistatic variance. These were less influenced by environmental factors (37). The presence of high genetic advance values for certain traits such as plant height (PH), tillers per plant (TP), grains per panicle (GP), biological yield (BY), 1000 seed weight (TSW), and seed yield per plant (SYP) suggests that these traits were primarily controlled by additive genes and were amenable to improvement through selection. The findings of this study were consistent with the results reported by Panse and Sukhatme (38).

Clusters of rice germplasm (Clusters II and VIII, Clusters IV and VIII, and Clusters I and VIII) have a high cluster distance which can be beneficial for developing high-yielding, short-lived and, early-maturing breeding lines. Latest research findings from 2020 highlight the diverse nature of rice germplasm and its potential to create such breeding lines (39).

Clusters (II and VII) were better suited for creating early maturity segregates while other clusters (I and VIII) have genotypes that can be used to develop transgressive breeding lines for high yield. Clusters III and VIII were important for the development of semi-dwarf lines due to their high cluster mean values. The findings of this study were consistent with the previous study (40).

The similarity in inter-cluster distance between Cluster VIII and Clusters I, II, and IV suggests that genotypes G.17 and G.21 in Cluster VIII share similar characteristics and genetic divergence with the genotypes in the other clusters. This indicates that these genotypes can be included in a hybridization program with the genotypes from other clusters. The yield and yield contributing features such as TSW, GP, BY and, SYP play a significant role in the divergence of these clusters. The sources (41-43) which indicate that these features contribute significantly to the divergence and these changes can bring improvement to the breeding lines.

The Principal Component Analysis (PCA) conducted in this study revealed that a small number of eigenvectors were sufficient to capture the significant morphological variations among the genotypes. The first principal component (PC1), which had an eigenvalue of 3.29, explained 83.51% of the total variation based on the morphological parameters that resulted in early maturity and semi-dwarf plant height.

Principal Components with eigenvalues of 2.03, 1.56, and 1.36 resulted in variance of 18.53%, 14.26%, and 12.41% respectively seem helpful in developing selection criteria and selecting superior lines from a variety of breeding populations. Majid *et al*. and Akhtar *et al*. (44-46) also reported similar findings.

The potential for developing hybrid rice varieties is promising, especially in countries with well-established seed production, certification, and distribution programs that offer affordable hybrid seeds. However, it is important to consider the potential risks associated with the loss of genetic diversity in crops, such as increased vulnerability to diseases, insect pests, climate change, and changes in agricultural practices. Therefore, breeding programs must prioritize the maintenance of agricultural genetic diversity.

Conclusion

The analysis of variance (ANOVA) conducted on the experiments showed significant variations among the sixty rice genotypes. Among them, genotypes G.60, G.40, G.54, G.55, and G.41 exhibited the highest likelihood of achieving high seed yields. These genotypes also displayed consistently high mean performance across other traits related to yield. This indicates their potential for being effective lines in terms of overall yield and other yield-contributing characteristics. The selected genotypes demonstrated not only high mean performance but also showed promising performance across various pathways that contribute to yield. Genotypes G.9, G.2, G.44, G.58, and G.31 for earliest DFF, G.9, G.2, G.58, G.44, and G.31 for earliest DM, G.35, G.17, G.30, G.45, G.46 for minimum PH and, G.60, G.40, G.54, G.55 and G.41 for SYP. The superior lines identified for yield and other traits may be used as male parents in the hybridization program for the characters to which they showed high mean performance. High estimates of PCV and GCV were observed for BY and SYP during both the years of analysis while the PCV was only estimated maximum for the number of TP and PBP in the pooled analysis. At the point of intra and inter-cluster distance, cluster II showed minimum intra-cluster distance during both the years of analysis however, maximum intra-cluster distance was shown by cluster IV during both the years of analysis. The greatest inter-cluster distance was found between cluster II and VIII in pooled analysis while, the poorest inter-cluster distance was found among cluster I and V in pooled analysis. The percent contribution to genetic divergence of rice was reported in TSW, PH, GP, BY and DFF showing maximum per cent contribution to the overall genetic divergence. The first PC, PC1 was responsible for early maturity so, this can be used for the development of early maturity variety and rest three PCs (PC2, PC3 & PC4) were responsible for yield enhancement and can be used for yield improvement. Indeed, the genetic diversity observed among the rice genotypes serves as a valuable foundation for the development of new varieties with improved traits. Recognizing and understanding this diversity highlights the need to employ various statistical tools and techniques to effectively exploit the diverse genetic properties present in the genotypes. By utilizing these tools in breeding programs, breeders can strategically harness the genetic potential of different genotypes to develop superior rice varieties. Lastly, the identification and exploitation of specific principal components that contribute to early maturity and yield enhancement can be applied in the development of new rice varieties with desired traits ultimately improving crop yield and profitability of the farmers will be a true contribution to the society.

Acknowledgements

The authors are highly thankful to the Vice-chancellor and Director of Research, ANDUAT, Kumarganj, Ayodhya for providing all the necessary facilities for conducting the Ph.D. research work experiment, and acknowledge the field experimentation centre, Crop Research Station, Masodha, Ayodhya, for their support.

Authors contributions

SP carried out the studies and drafted the manuscript. AK edited and communicated the manuscript. SSR did analysis of the data. SC helped in statistical analysis using R-Studio. SCV helped designing the research and finalizing objectives. All authors read and approved the final manuscript.

Compliance with ethical standards

Conflict of interest: Authors do not have any conflict of interests to declare.

Ethical issues: None.

References

1. Fukagawa NK, Ziska LH. Rice: Importance for global nutrition. J Nutr Sci and Vitaminology. 2019;65(Supplement): S2-S3. https://doi.org/10.3177/jnsv.65.S2
2. Naaz S, Pandey V, Yadav HK. Evaluation of genetic diversity in rice (*Oryza sativa* L. sp. *indica*) accessions using SSR marker. Vegetos. 2022;1-8. https://doi.org/10.1007/s42535-022-00378-3
3. Mia S, Ahmed NU, Islam MZ, Rashad MM, Islam MM, Zaman AM. Genetic diversity and yield performance among T. Aman rice (*Oryza sativa* L.) landraces in Barishal region of Bangladesh. J Cro Sci and Biotech. 2022;25:123-32. https://doi.org/10.1007/s12892-021-00117-1
4. Hasan S, Furtado A, Henry R. Analysis of domestication loci in wild rice populations. Plants. 2023;12(3):489. https://doi.org/10.3390/plants12030489
5. Roy B, Sundarrao GS. Morphological depiction of seeds of landraces of rice (*Oryza sativa* L.). Int J Envi and Climate Change. 2022;12(11):3010-25. https://doi.org/10.9734/ijecc%2F2022%2Fv12i111347
6. Kumari N, Kumar R, Kumar A. Genetic variability and association of traits in mutant lines of rice (*Oryza sativa* L.) for submergence tolerance. Curr J Appl Sci. Tech. 2019;33(2):1-7. https://doi.org/10.9734/cjast/2019/v33i230062
7. Fu YB. Understanding crop genetic diversity under modern plant breeding. Th Appl Gen. 2015;128(11):2131-42. https://doi.org/10.1007/s00122-015-2585-y
8. Govindaraj M, Vetriventhan M, Srinivasan M. Importance of genetic diversity assessment in crop plants and its recent advances: An overview of its analytical perspectives. Gen Res International. 2015;Article ID 431487:1-14. https://doi.org/10.1155/2015/431487
9. Kapoor C, Avasthe RK, Chettri PK, Gopi R, Kalita H. On-farm status and collection of rice (*Oryza sativa* L.) genetic resources of Sikkim Himalayas. Indi J Pl Gen Res. 2017;30(1):48-54. https://doi.org/10.5958/0976-1926.2017.00005.5
10. Sellamuthu R, Liu GF, Ranganathan CB, Serraj R. Genetic analysis and validation of quantitative trait loci associated with reproductive-growth traits and grain yield under drought stress in a doubled haploid line population of rice (*Oryza sativa* L.). Field Crops Research. 2011;124(1):46-58. https://doi.org/10.1016/j.fcr.2011.06.002
11. Mahalanobis PC. On the generalized distance in statistics. Nati Insti Sci Indi. 1936;2:49-55.
12. Jegadeeswaran M, Manivannan A, Mohan S, Pavithradevi G, Salini AP, Anandakumar CR, Maheswaran M. Characterization of rice (*Oryza sativa* L.) landraces and cultivars using agro morphological traits. ORYZA-An Int J on Rice. 2017;54(1): 89-96.
13. Shah ML, Yadav R. Response of rice varieties to age of seedlings and transplanting dates. Nepal Agric Res J. 2001:14-17. https://doi.org/10.3126/narj.v4i0.4858
14. Debsharma SK, Syed M, Ali M, Maniruzzaman S, Roy PR, Brestic M, Gaber A, Hossain A. Harnessing on genetic variability and diversity of rice (*Oryza sativa* L.) genotypes based on quantitative and qualitative traits for desirable crossing materials. Genes. 2023;14(1):10. https://doi.org/10.3390/genes14010010
15. Shiragudikar SK, Bharamagoudar G, Manohara KK, Malati SY. Insight analysis of deep learning and a conventional standardized evaluation system for assessing rice crop's susceptibility to salt stress during the seedling stage. SN Comp Sci. 2023;4(3):262. https://doi.org/10.1007/s42979-022-01656-2
16. Spector P. An introduction to the SAS system. Berkeley. Archived from the original on October. 2013;12.
17. Burton GW, Devane DE. Estimating heritability in tall fescue (*Festuca arundinacea*) from replicated clonal material 1. Agro J. 1953 Oct;45(10):478-81. https://doi.org/10.2134/agronj1953.00021962004500100005x
18. Faysal AS, Ali L, Azam MG, Sarker U, Ercisli S, Golokhvast KS, Marc RA. Genetic variability, character association and path coefficient analysis in transplant Aman rice genotypes. Plants. 2022;11(21):2952. https://doi.org/10.3390/plants11212952
19. Singh SK, Singh P, Korada M, Khaire AR, Singh DK, Habde SV, Majhi PK, Naik R. Character association and path-coefficient analysis for yield and yield-related traits in 112 genotypes of rice (*Oryza sativa* L.). Cur J App Sci Tech. 2020;39:545-56. https://doi.org/10.9734/cjast/2020/v39i4831275
20. Gomez KA, Gomez AA. Statistical procedures for agricultural research. John Wiley and Sons; 1984;17.
21. Kumar M, Kumar RR. Genetic variability parameters for yield and yield related traits in rice (*Oryza sativa* L.) under irrigated and drought stress condition. Int J Curr Microbiol App Sci. 2020;9(2):1137-43. https://doi.org/10.20546/ijcmas.2020.902.133
22. Dhakal K, Yadaw RB, Baral BR, Pokhrel KR, Rasaily S. Agromorphological and genotypic diversity among rice germplasms under rainfed lowland condition. AGRIVITA- J Agri Sci. 2021;43(3):466-78. http://doi.org/10.17503/agrivita.v43i3.3026

23. Deepthi KP, Mohan YC, Hemalatha V, Yamini KN, Singh TV. Genetic variability and character association studies for yield and yield related, floral and quality traits in maintainer lines of rice (*Oryza sativa* L.). The Pha Inno J. 2022;11(2):191-97.

24. Acevedo-Siaca LG, Coe R, Quick WP, Long SP. Evaluating natural variation, heritability and genetic advance of photosynthetic traits in rice (*Oryza sativa*). Plant Breed. 2021;140:P. 745-57. https://doi.org/10.1111/pbr.12965

25. Adhikari BN, Joshi BP, Shrestha J, Bhatta NR. Genetic variability, heritability, genetic advance and correlation among yield and yield components of rice (*Oryza sativa* L.). J Agri and Natu Reso. 2018;1(1):149-60. https://doi.org/10.3126/janr.v1i1.22230

26. Shrestha J, Subedi S, Kushwaha UK, Maharjan B. Evaluation of rice genotypes for growth, yield and yield components. J Agri and Natu Reso. 2021 Sep;4(2):339-46. https://doi.org/10.3126/janr.v4i2.33967

27. Kumari S, Singh PK, Bisen P, Loitongbam B, Rai VP, Sinha B. Genetic diversity analysis of rice (*Oryza sativa* L.) germplasm through morphological markers. Inter J Agri Envir and Biores. 2018:953-57.

28. Bernardo R. Reinventing quantitative genetics for plant breeding: Something old, something new, something borrowed, something blue. The Genetics Society. 2020;125: P. 375-85. https://doi.org/10.1038/s41437-020-0312-1

29. Abebrese SO, Mustapha SA, Alex OK. Genetic diversity and evaluation of assembled rice (*Oryza sativa* L.) germplasm for breeding purposes in Northern Ghana. Int JPla and Soil Sci. 2022:2;34 (23)1548-64. https://doi.org/10.9734/ijpss/2022/v34i232573

30. Naik M, Pillai MA, Saravanan S. Genetic diversity analysis for yield associated and quality traits in promising rice varieties of Tamil Nadu. IJBSM. 2021;12(4):361-69. DOI: https://doi.org/10.23910/1.2021.2300.

31. Rahman AK, Islam MM, Nadim MK, Akter SE, Alim SA, Noor MM. Genetic variability analysis of different yield contributing characters of cultivated T. Aman rice (*Oryza sativa*) varieties. J Biosci Agric Res. 2021;27(01):2258-66. https://doi.org/10.18801/jbar.270121.275

32. Srivastava N, Babu GS, Singh ON, Verma R, Pathak SK, Behra M, Jena D, Chanda M. Genetic variation, heritability and diversity analysis of exotic upland rice (*Oryza sativa* L.) germplasms based on quantitative traits. The Pharma Innova J. 2017;6 (12):316-20.

33. Sarankumar C, Dhasarathan M, Kavithamani D, Vanniarajan C, Kokiladevi E, Ravikesavan R, Senthil N. Assessment of genetic variability, heritability and genetic advance in backcross population of BC1F1, BC2F1 and BC2F2 in maize. Ele J Pla Bre. 2019;10(2):576-84. https://doi.org/10.5958/0975-928X.2019.00073.5

34. Rasel M, Hassan L, Hoque MI, Saha SR. Estimation of genetic variability, correlation and path coefficient analysis in local landraces of rice (*Oryza sativa* L.) for the improvement of salinity tolerance. J of the Bangladesh Agri Uni. 2018;16(1):41-46. https://doi.org/10.3329/jbau.v16i1.36479

35. Islam MA, Raffi SA, Hossain MA, Hasan AK. Analysis of genetic variability, heritability and genetic advance for yield and yield associated traits in some promising advanced lines of rice. Progressive Agri. 2015;26(1):26-31. https://doi.org/10.3329/pa.v26i1.24511

36. Dey S, Kumar R, Battan KR, Chhabra AK, Reddy AL. Study of coefficient of variation, heritability and genetic advance for different traits of rice genotypes grown under aerobic condition. Int J of Bio-reso and Stre Manag. 2021;12(5):426-30. http://dx.doi.org/10.23910/1.2021.2290a

37. Alam MS, Hassan L, Islam MM, Begum SN, Islam SN. Evaluation of habitual rice (*Oryza sativa* L.) landraces of Bangladesh through different genetic parameters. Int J of Inno and Sci Rese. 2014;11(2):494-502.

38. Tiwari DN, Tripathi SR, Tripathi MP, Khatri N, Bastola BR. Genetic variability and correlation coefficients of major traits in early maturing rice under rainfed lowland environments of Nepal. Adva in Agri. 2019;Article ID 5975901:1-9. https://doi.org/10.1155/2019/5975901

39. Asins MJ. Present and future of quantitative trait locus analysis in plant breeding. Plant Breeding. 2002;121(4):281-91. https://doi.org/10.1046/j.1439-0523.2002.730285.x

40. Palaniyappan S, Arunachalam P, Banumathy S, Mini ML, Muthuramu S. Genetic divergence and clustering studies in advanced breeding lines of rice (*Oryza sativa* L.). Ele J Pla Bre. 2020;11 (02):499-504. https://doi.org/10.37992/2020.1102.084

41. Mishra A, Shahani M, Bijarania S. Genetic divergence studies of submergence tolerant rice genotypes. Int J Envi and Clima Chan. 2023;13(3):195-99. https://doi.org/10.9734/ijecc/2023/v13i31697

42. Singh SK, Pandey V, Mounika K, Singh DK, Khaire AR, Habde S, Majhi PK. Study of genetic divergence in rice (*Oryza sativa* L.) genotypes with high grain zinc using Mahalanobis' D2 analysis. Electro J of Pl Breed. 2020;11(02):367-72. https://doi.org/10.37992/2020.1102.065

43. Perween S, Kumar A, Prasad BD, Choudhary M. Assessment of genetic diversity in rice (*Oryza sativa* L.) under irrigated and drought stress condition. Curr J Appl Sci and Tech. 2020;39 (1):112-25. https://doi.org/10.9734/cjast/2020/v39i130487

44. Verma SP, Pathak VN, Verma OP. Interrelationship between yield and its contributing traits in wheat (*Triticum aestivum* L.). Int J Curr Microbiol App Sci. 2019;8(2):3209-15. https://doi.org/10.20546/ijcmas.2019.802.375

45. Mazid MS, Rafii MY, Hanafi MM, Rahim HA, Shabanimofrad M, Latif MA. Agro-morphological characterization and assessment of variability, heritability, genetic advance and divergence in bacterial blight resistant rice genotypes. South Afri J Bot. 2013;86:15-22. https://doi.org/10.1016/j.sajb.2013.01.004

46. Akhtar AR, Iqbal A, Dasgupta T. (). Genetic diversity analysis of aromatic rice (*Oryza sativa* L.) germplasm based on agro-morphological characterization. *Oryza*. 2022;59(2): 141-149. https://doi.org/10.35709/ory.2022.59.2.1