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Genetic diversity analysis in rice genotypes suitable for aerobic cultivation

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Abstract

A total of 48 rice genotypes were evaluated for 23 morpho-physiological and quality traits at Rice Research Station, Kaul, CCSHAU, Hisar, to assess genetic diversity using Mahalanobis D² statistics and principal component analysis (PCA). Cluster analysis grouped the genotypes into six clusters, with Cluster II being the largest (17 genotypes) and Cluster III the smallest with one genotype. The highest inter-cluster distance was observed between Clusters I and VI, while the lowest was between Clusters I and V. Desirable mean values for traits like grain yield, 1000-grain weight, harvest index, panicle length and number of grains per panicle and root characteristics were observed in Clusters I and VI, suggesting their potential for genetic improvement under aerobic conditions. PCA revealed that the first seven principal components explained 78.20 % of the total variability, with PC1 contributing the most (23.10 %). Genotypes HKR16-1-IR14L521, CRR 4118-1-1-2-2-1, RCPR 79-IR 84899-B-185-8-1-1-1, CSR-88, CSR YET-78, CSR-87 and BRR 0180-IR 14L 157 exhibited significant diversity and could be utilized in crossing programs for generating genetic variability.

Keywords: Rice, aerobic cultivation, cluster analysis, principal component analysis, genetic diversity and Mahalanobis D² analysis

INTRODUCTION

Rice (*Oryza sativa*) is the world's leading staple food crop, playing a crucial role in food security and supporting the livelihoods of over half the global population (Bendi *et al*., 2018). It provides essential nutritional benefits, being high in carbohydrates and rich in minerals, proteins, vitamins and calories (Mousa *et al*., 2024). In Asia, nearly 90 % of the population depends on rice as a staple, often referred to as the 'grain of life'. The reduction in water resources, caused by both natural and human-induced factors, is likely to severely impact water-intensive crops like rice (Farooq *et al*., 2023). Water scarcity threatens the productivity of irrigated rice ecosystems, making it essential to explore water-saving technologies that conserve water while maintaining rice yields. Aerobic rice cultivation is an innovative strategy aimed at reducing water usage and improving water-use efficiency. It has gained significant attention in recent years (Sheeba and Mohan, 2025) for its potential to reduce water consumption and enhance agricultural sustainability (Ramanjaneyulu *et al*., 2014). This technique involves cultivating rice in non-flooded conditions, utilizing supplemental irrigation and fertilizers to achieve optimal yields (Pavankumar *et al*., 2022; Das *et al*., 2024). However, this system is prone to moisture stress at various growth stages, leading to yield reductions ranging from 15 to 40 %, which is considered unacceptable (Kumari *et al*., 2016). The lack of varieties with stable yields under aerobic systems is a major limitation in achieving maximum yield potential under water-limited conditions (Sandhu *et al*., 2019). Aerobic rice exhibits enhanced tolerance to adverse weather conditions including droughts and floods, which are occurring frequently as a result of climate change. Therefore, to develop a suitable cultivar for aerobic cultivation, identifying superior genotypes with desirable traits is important (Salunkhe *et al*., 2024).

Additionally, genetic improvement efforts for rice in aerobic environments have received less attention compared to breeding for lowland production systems (Mall *et al*., 2013) and are generally restricted to screening existing varieties (Kahani and Hittalmani, 2015). Although several aerobic rice varieties have been developed, their yields are 20-30 % lower than those obtained with varieties grown under flooded conditions (Prasad, 2011). Currently, only a few

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successful aerobic rice cultivars with high yield potential and broad tolerance to biotic and abiotic stresses are grown (Maliha *et al*., 2020). However, there remains a need to develop more varieties that experience less yield penalty in aerobic environments.

It is essential to measure genetic diversity among genotypes to identify elite parents for hybridization programs, as it plays a crucial role in enhancing heterosis in hybrids (Meena *et al*., 2022) and aids in the development of superior recombinants for more resilient and higher-yielding varieties (Islam *et al*., 2012). In this context, multivariate analysis tools such as principal component analysis (PCA) and cluster analysis are effective in evaluating phenotypic diversity. PCA is a multivariate technique that processes data and transforms it into a set of orthogonal variables, known as principal components, by linearly combining the variables that account for the majority of the variance in the original data (Srinivas *et al*., 2025). Cluster analysis is a key method for determining relationships among accessions and measuring genetic distance. Divergence analysis using PCA and cluster analysis has proven effective in identifying potential genotypes for hybridization. Considering the importance of PCA and cluster analysis, this study aimed to identify morpho-physiological and quality traits responsible for yield differences among rice genotypes under aerobic conditions. The information obtained will be valuable for identifying diverse rice genotypes and developing an effective rice breeding program.

MATERIALS AND METHODS

The study was conducted at the Rice Research Station, Kaul, CCS Haryana Agricultural University, Hisar, during *Kharif* 2022. The experiment was laid out in a Randomized Block Design with three replications, evaluating 48 rice genotypes (**Table 1**). The plot size consisted of a single row of 5-meter in length with a spacing of 20 x 15 cm sown under dry direct seeded conditions. The recommended cultural operations and plant protection measures were followed for raising a healthy crop stand and the observations were recorded for 23 traits, including growth, yield and grain quality parameters. Genetic diversity was assessed using Mahalanobis D^2 statistics and cluster analysis was performed using the Ward method (Ward, 1963). Principal component analysis (PCA) was conducted to identify the major traits contributing to the variation. The PCA and cluster analysis was done using R packages and General R-shiny based Analysis Platform Empowered by Statistics (GRAPES 1.1.0).

Table 1. List of rice genotypes evaluated in the study

S. No.	Genotype	S. No.	Genotype
1	HKR16-1-IR14L521	25	RP 6326-278-14-1
2	CR 9583-53-1-2-1-2	26	CR 4317-2-IR 97034-21-2-1-3
3	IR 95780-43-1-1-1	27	CR 3918-109-5-6-4-1
4	HKR 16-35	28	CRR 821-21-2-1-3
5	HKR 17-35	29	RP 6324-123-14-4-1
6	HKR 2018-24	30	TRC 2020-14
7	HKR 2018-39	31	CR 3985-1-3-1-2-1
8	HKR 2018-32	32	CRR 4118-1-1-2-2-1
9	HKR 2018-63	33	CRR 780 B-B-14-1
10	HKR 2018-33	34	RCPR 79-IR 84899-B-185-8-1-1-1
11	HKR 2018-54	35	CSR PET-27
12	HKR 2018-40	36	BRR 0180-IR 14L 157
13	CSR-88	37	BRR 2137
14	RCPR 71-IR93827-29-2-1-3	38	CRR 842-IR 14L 159
15	TRC 2020-3	39	RCPR 80-IR 14L 157
16	CRR 756-21	40	CSR YET-78
17	RP 6326-124-54-1	41	NVSR- 726
18	HURS 18-2-IR9876-20-1-2-2	42	BRR 2185
19	CRR 822-20-1-2-2	43	CRR 790-69
20	RCPR-70-IR 84899-B-184-16-1-1-1	44	CSR-87
21	CR 4161-5-6-IR 14L572	45	CR Dhan-201(National check)
22	R 2272-515-2-287-1	46	CR Dhan-202(Zonal check)
23	CSR-57	47	HKR-48 (Local check)
24	RCPR 63-IR 97034-21-2-1-3	48	HKR-47

RESULTS AND DISCUSSION

Assessment of genetic divergence

Genetic diversity is fundamental in plant breeding as it facilitates the selection of genetically distinct parents, enhancing heterosis in hybridization programs (Shinde *et al*., 2015). A greater genetic gap between parental lines increases variability in the resulting segregating generations (Sarma *et al*., 2015). The Mahalanobis D^2 statistic (Mahalanobis, 1936) is widely employed to assess genetic divergence. In this study, 48 rice genotypes were classified into six clusters based on D^2 values (**Fig. 1**). Cluster II contained the highest number of genotypes (17), followed by Cluster IV with 12, while Clusters I, V and VI included 9, 5, and 4 genotypes, respectively. Cluster III was unique in being mono-genotypic, with only one genotype (**Table 2**). Similar results were reported by Sheeba and Mohan in drought tolerant rice genotypes (2025). Genetic variability was observed to be greater among clusters than within them, indicating substantial genetic heterogeneity. Further, the clustering pattern did not correspond to the geographical origin of the genotypes, aligning with previous observations by Sravan *et al*. in upland rice germplasm (2013).

A greater inter-cluster distance indicates a higher level of genetic diversity among genotypes. **Table 3** presents the inter- and intra-cluster distances for the 48 evaluated genotypes. The inter-cluster distances ranged from 46.39 (Cluster I and Cluster V) to 76.17 (Cluster III and Cluster VI), with the greatest genetic divergence observed between Clusters III and VI (76.17), followed by Cluster II and VI (75.59) and Cluster IV and VI (73.90). Other

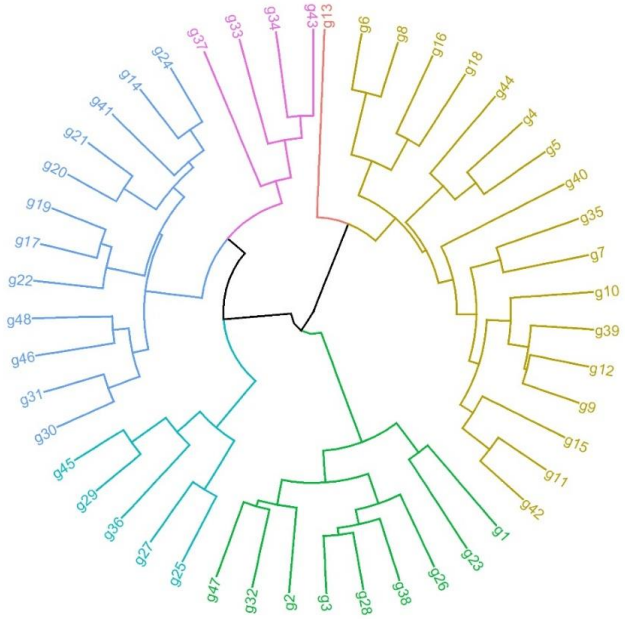

Fig. 1. Dendrogram depicting clustering pattern of rice genotypes under aerobic conditions
(Note: For genotype names refer Table 1)

Table 2. Clustering pattern of genotypes under aerobic conditions

Clusters	Number of genotypes	Name of genotypes
Cluster I	9	HKR 16-1-IR14L521, CR 9583-5-3-1-2-1-2, CR 95780 43-1-1-1, CSR -57, CR 4317-2-IR-97034-21-2, CRR 821-21-2-1-3, CRR 4118-1-1-2-2-1, CRR 842 IR 14 L 159, HKR 48
Cluster II	17	HKR 2018-33, HKR 2018-54, HKR 2118-40, TRC-2020-3, CRR-756-21, HURS 18-2-IR9876-20-1-2-2, CSR PET-27, RCPR 80-IR 146 157, CSR YET- 78, HKR 16-35, BRR-2185, CSR-87, HKR 17-35, HKR 2018-24, HKR-2018-39, HKR-2018-32, HKR-2018-63
Cluster III	1	CSR-88
Cluster IV	12	RCPR 71-IR93827-29-2-1-3, RP 6326-124-54-1, CRR 822-20-1-2-2, RCPR-70-IR 84899-B-184-16-1-1-1, CR 4161-5-6-IR 14L572, R 2272-515-2-287-1, RCPR 63-IR 97034-21-2-1-3, TRC 2020-14, CR 3985-1-3-1-2-1, NVSR-726, CR Dhan-202, HKR- 47
Cluster V	5	RP 6326-278-14-1, CR 3918-109-5-6-4-1, RP 6324-123-14-4-1, BRR 0180-IR 14L157, CR Dhan-201
Cluster VI	4	CRR 780-B-B-14-1, RCPR 79-IR 84899-B-185-8-1-1-1, BRR 2137, CRR 790-69

Table 3. Average inter- and inter-cluster distance among rice genotypes under aerobic conditions

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI
Cluster I	31.21	60.29	64.75	56.66	46.39	48.21
Cluster II		38.98	54.25	63.01	48.71	75.59
Cluster III			0.00	64.30	57.19	76.17
Cluster IV				44.63	50.87	73.90
Cluster V					33.08	54.60
Cluster VI						40.19

notable distances included 64.75 (Cluster I and Cluster III), 63.01 (Cluster II and Cluster IV) and 60.29 (Cluster I and Cluster II), indicating substantial genetic variability across these groups (Haque *et al*., 2014). These results suggest that genotypes within a given cluster exhibit genetic similarity, whereas those in separate clusters display significant divergence. Consequently, the genomic composition of genotypes in one cluster is distinct from those in another, supporting the potential for hybridization between distantly related groups. Crosses between highly divergent clusters may enhance genetic recombination and lead to a more diverse segregating population (Sravan *et al*., 2013). The intra-cluster D^2 values varied from 0.00 (Cluster III) to 44.63 (Cluster IV), indicating differences in genetic homogeneity within clusters. The highest intra-cluster distance was recorded in Cluster IV (44.63), followed by Cluster VI (40.19), Cluster II (38.98), Cluster V (33.08) and Cluster I (31.21). Since genotypes within a cluster are genetically similar, selecting parents from the same cluster may result in limited genetic variability. To maintain a broader genetic base and reduce the risk of excessive homozygosity, selection should prioritize genetically diverse parents from different clusters (Soharu *et al*., 2021)

Cluster mean analysis helps in evaluating the average performance of genotypes within each cluster, enabling the identification of potential parents for hybridization programs. **Table 4** presents the cluster mean values for various traits. The analysis showed that Cluster I had the highest mean values for grain yield per plant (28.59 g), 1000-grain weight (25.50 g), harvest index (49.69 %), root fresh weight per plant (30.71 g), root dry weight per plant (10.10 g) and root volume per plant (28.41 cm^3). However, it exhibited the lowest milling percentage (65.55 %). Cluster II recorded the longest days to 50% flowering (89.71) but had the lowest values for plant height (99.97 cm), flag leaf length (36.31 cm), panicle length (22.94 cm) and biological yield per plant (47.17 g). Cluster III exhibited the highest mean values for days to maturity (122.33), number of effective tillers per plant (12.67), root fresh and dry weight ratio (6.06), kernel length (7.57 mm) and kernel length-to-breadth ratio (4.53). Conversely, it had the lowest mean values for grain yield per plant (17.85 g), number of grains per panicle (80.07), harvest index (35.26%), root fresh weight per plant (19.40 g), root dry weight per plant (3.36 g), root volume per plant (19.22 cm^3), hulling percentage (74.55 %), head rice recovery percentage (52.65 %) and kernel breadth (1.68 mm). Cluster V had the highest milling percentage (69.16 %) but recorded the lowest values for days to 50% flowering (84.27), days to maturity (115.40), flag leaf width (1.03 cm), number of effective tillers per plant (9.99) and root length (14.63 cm). Cluster VI, consisting of four genotypes, had the highest mean values for plant height (127.68 cm), flag leaf width (1.30 cm), flag leaf length (43.28 cm), panicle length (24.89 cm), number of grains per panicle (124.96), biological yield per plant (59.35 g), root length (17.48 cm), hulling percentage (79.71 %), head rice recovery (59.26%) and kernel breadth (2.19 mm). However, it exhibited the lowest values for 1000-grain weight (21.39 g), kernel length (6.07 mm) and kernel length-to-breadth ratio (2.79). These findings indicate that no single cluster contained all desirable traits, reinforcing the need for hybridization among genotypes from different clusters to achieve superior recombinants. Similar clustering trends and their significance in breeding programs have been reported by Chuchert *et al*., 2018, Kumari *et al*., 2016, Toshimenla *et al*., 2016, Tripathi *et al*., 2017 and Soharu *et al*., 2021 in rice genotypes.

Principal component analysis

Principal component analysis (PCA) is a widely used multivariate statistical technique that quantifies the contribution of various traits to overall genetic variability, aiding in the identification of key selection traits. This non-parametric approach reduces complex datasets into a smaller number of principal components while preserving essential information (Kumari *et al*., 2024; Sasipriya *et al*., 2022). PCA assists in ranking genotypes and identification of economically important traits that contribute to genetic diversity, which is critical for developing high-yielding hybrids in rice (Janghel *et al*., 2020). By utilizing indexing through PCA-identified traits could enhance the reliability of the selection process (Umamaheswar *et al*., 2024). In this study, PCA was employed to determine the key traits influencing yield variations among rice genotypes under aerobic conditions. Following the criteria outlined by Brejda *et al*. (2000), only principal components (PCs) with eigenvalues greater than one and accounting for at least 5% of the total variation were considered for further interpretation in the present study. The first seven PCs, each meeting these criteria, collectively accounted for 78.20 % of the total phenotypic variation across 23

Table 4. Cluster mean values for various trait groups under aerobic conditions

S.No.	Characters	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI
1	Grain yield per plant (g)	28.59	22.31	17.85	24.76	23.44	24.84
2	Days to 50% flowering	87.63	89.71	89.33	88.72	84.27	89.33
3	Days to maturity	118.85	122.18	122.33	120.64	115.40	122.08
4	Plant height (cm)	112.35	99.97	105.97	110.56	111.97	127.68
5	Flag leaf width (cm)	1.16	1.13	1.16	1.14	1.03	1.30
6	Flag leaf length (cm)	39.40	36.31	42.17	39.69	36.72	43.28
7	Panicle length (cm)	24.84	22.94	23.25	23.78	23.72	24.89
8	Number of grains per panicle	123.03	100.11	80.07	112.29	113.95	124.96
9	Number of effective tillers per plant	12.36	11.28	12.67	11.08	9.99	11.93
10	1000-grain weight (g)	25.50	22.88	23.01	22.97	21.86	21.39
11	Biological yield per plant (g)	57.75	47.17	50.42	54.53	47.62	59.35
12	Harvest index (%)	49.69	47.27	35.26	45.66	49.25	42.03
13	Root fresh weight per plant (g)	30.71	23.53	19.40	23.58	24.05	24.45
14	Root dry weight per plant (g)	10.10	8.09	3.36	8.04	7.30	8.23
15	Root fresh-to-dry weight ratio	3.04	2.96	6.06	2.96	3.52	2.79
16	Root volume per plant (cm^3)	28.41	23.10	19.22	22.26	22.89	24.36
17	Root length per plant (cm)	16.95	16.20	15.77	15.38	14.63	17.48
18	Hulling (%)	75.51	77.44	74.55	76.81	79.28	79.71
19	Milling (%)	65.55	67.53	66.55	67.09	69.16	68.92
20	Head rice recovery (%)	57.61	58.58	52.65	54.30	56.88	59.26
21	Kernel length (mm)	6.84	6.90	7.57	6.34	6.37	6.07
22	Kernel breadth (mm)	2.07	1.96	1.68	2.18	2.02	2.19
23	Kernel length-to-breadth ratio	3.31	3.55	4.53	2.92	3.16	2.79

morpho-physiological and quality traits influencing grain yield. The contribution of each PC is detailed in **Table 5**, with PC1 explaining the largest proportion of variability (23.10 %), followed by PC2 (13.87 %), PC3 (11.20 %), PC4 (9.55 %), PC5 (8.31 %), PC6 (6.38 %) and PC7 (5.79 %). The scree plot (**Fig. 2**) illustrates the cumulative variance explained by the first ten PCs, highlighting PC1 as the most influential, with an eigenvalue of 5.313. PC2 and PC3 followed with eigenvalues of 3.190 and 2.575, respectively. These results indicate that traits associated with PC1 contributed the most to overall genetic variation. The predominance of the first two principal components in explaining genotype variability aligns with findings reported by Mousa *et al*. (2024) in rice genotypes under aerobic conditions and Janghel *et al*. (2020) in chickpea genotypes.

The correlation of individual traits with principal components is presented in **Table 6** and illustrated in **Fig. 3.** The results indicate that the first principal component (PC1) was predominantly associated with traits influencing grain yield, including grain yield per plant (0.862), root fresh weight per plant (0.774), biological yield per plant (0.740), root volume per plant (0.737), number of grains per panicle (0.71), root dry weight per plant (0.698), plant height (0.473), number of effective tillers per plant (0.463), kernel breadth (0.434), panicle length (0.432), root length per plant (0.429) and 1000-grain weight (0.420). These traits collectively accounted for the highest variation in the dataset. PC2 was primarily influenced by kernel length-to-breadth ratio (0.782), kernel length (0.74), root fresh weight per plant (0.402), root dry weight per plant (0.392) and root volume per plant (0.349). PC3 exhibited positive correlations with days to maturity (0.863), days to 50 % flowering (0.836), flag leaf width (0.698), root length per plant (0.331) and biological yield per plant (0.299). PC4 showed significant contributions from root fresh-to-dry weight ratio (0.55), flag leaf length (0.545), panicle length (0.463), plant height (0.401), kernel length-to-breadth ratio (0.352) and flag leaf width (0.324). PC5 was positively associated with head rice recovery percentage (0.711), milling percentage (0.591), root length per plant (0.427), hulling percentage (0.384) and 1000-grain weight (0.317). PC6 had strong contributions from 1000-grain weight (0.538), harvest index percentage (0.456), number of effective tillers per plant (0.349) and grain yield per plant (0.329). Finally, PC7 was positively correlated with the number of effective tillers per plant (0.458), root length per plant (0.422), hulling percentage (0.421) and root fresh-to-dry weight ratio (0.375). These results highlight the key traits contributing to genetic variability, providing useful insights

Table 5. Eigenvalue, contribution of variability and factor loading for the principal component in rice

	PC1	PC2	PC3	PC4	PC5	PC6	PC7
Eigne value	5.313	3.190	2.575	2.195	1.911	1.467	1.332
Proportion	23.100	13.870	11.198	9.547	8.312	6.382	5.792
Cumulative variability	23.100	36.971	48.170	57.717	66.030	72.412	78.205

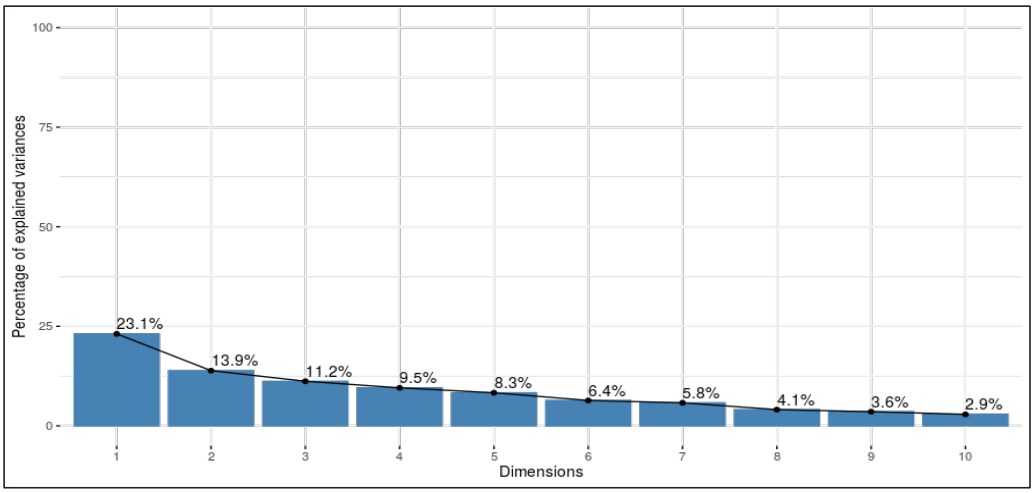

Fig. 2. Scree plot illustrating the percentage of explained variation by each principal component

Table 6. Correlations of the variables with the first seven principal components

S.No.	Traits	PC1	PC2	PC3	PC4	PC5	PC6	PC7
1	Grain yield per plant	0.862	0.077	-0.081	-0.006	-0.175	0.329	-0.011
2	Days to 50% flowering	-0.174	0.208	0.836	-0.260	-0.195	-0.018	-0.047
3	Days to maturity	-0.261	0.175	0.863	-0.206	-0.167	-0.003	-0.076
4	Plant height	0.473	-0.483	0.053	0.401	0.179	-0.196	-0.266
5	Flag leaf width	0.132	-0.062	0.698	0.324	0.294	0.203	-0.287
6	Flag leaf length	0.321	-0.197	0.252	0.545	0.220	0.073	0.179
7	Panicle length	0.432	-0.099	-0.123	0.463	0.209	-0.398	-0.217
8	Number of grains per panicle	0.710	-0.331	-0.143	0.168	-0.058	-0.066	-0.175
9	Number of effective tillers per plant	0.463	0.296	0.005	0.112	-0.325	0.349	0.458
10	1000-grain weight	0.420	0.252	-0.077	-0.016	0.317	0.538	-0.298
11	Biological yield per plant	0.740	-0.071	0.299	0.298	-0.252	-0.022	0.161
12	Harvest index	0.247	0.148	-0.467	-0.410	0.085	0.456	-0.229
13	Root fresh weight per plant	0.774	0.402	-0.051	-0.201	0.065	-0.260	0.160
14	Root dry weight per plant	0.698	0.392	0.024	-0.420	0.078	-0.347	-0.075
15	Root fresh-to-dry weight ratio	-0.299	0.017	-0.148	0.550	-0.065	0.293	0.375
16	Root volume per plant	0.737	0.349	-0.004	-0.234	0.164	-0.272	0.183
17	Root length per plant	0.429	0.263	0.331	0.064	0.427	0.142	0.422
18	Hulling per cent	-0.080	-0.457	-0.003	-0.288	0.384	-0.125	0.421
19	Milling per cent	-0.352	-0.446	-0.071	-0.202	0.591	-0.012	0.259
20	Head rice recovery	-0.042	0.110	0.178	-0.175	0.711	0.164	-0.069
21	Kernel length	-0.230	0.740	-0.083	0.251	0.267	0.037	-0.190
22	Kernel breadth	0.434	-0.672	0.163	-0.302	-0.047	0.242	-0.121
23	Kernel length-to-breadth ratio	-0.399	0.782	-0.134	0.352	0.161	-0.141	-0.031

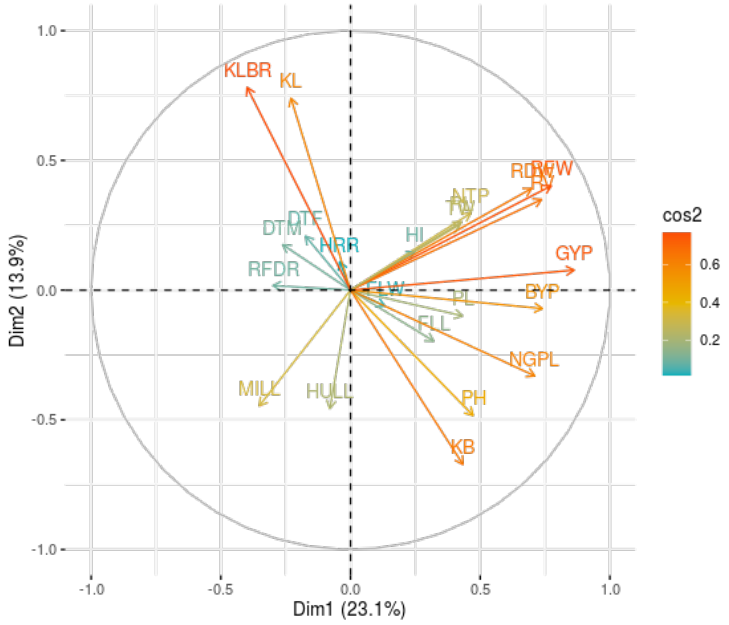

Fig. 3. PCA plot for various morpho-physiological and quality traits under study

GYP: Grain yield per plant , DTF: Days to 50% flowering, DTM: Days to maturity, PH: Plant height , FLW: Flag leaf width, FLL: Flag leaf length , PL: Panicle length , NGP: Number of grains per panicle, NTP: Number of effective tillers per plant, TW: 1000-grain weight, BYP: Biological yield per plant , HI: Harvest index , RFW: Root fresh weight per plant , RDW: Root dry weight per plant , RFDR: Root fresh-to-dry weight ratio, RV: Root volume per plant , RL: Root length per plant , HULL: Hulling per cent, MILL: Milling per cent, HRR: Head rice recovery , KL: Kernel length , KB: Kernel breadth, KLBR: Kernel length-to-breadth ratio

for breeding strategies aimed at improving rice yield under aerobic conditions. The present findings align with the previous studies by Mushtaq and Kumar (2022) and Shanmugam *et al*. (2023) in rice genotypes, Janghel *et al*. (2020) in chickpea genotypes and Kumari *et al*. (2024) in foxtail millet accessions.

The correlation circle **(Fig. 3**) for the first two principal components (PC1 and PC2) categorized the studied traits into four distinct groups. The first group included root fresh weight per plant, root dry weight per plant, root volume per plant, number of effective tillers per plant, harvest index percentage and grain yield per plant, all of which were positively correlated with both PCs. The second group consisted of traits negatively correlated with PC1 but positively correlated with PC2, such as kernel length-to-breadth ratio, kernel length, days to 50% flowering, days to maturity, head rice recovery percentage and root fresh-to-dry weight ratio. The third group included biological yield per plant, panicle length, number of grains per panicle, plant height, kernel breadth, flag leaf length and flag leaf width, which exhibited positive correlations with PC1 but negative correlations with PC2.

The fourth group, comprising milling percentage and hulling percentage, was negatively correlated with both principal components. In the correlation circle, vector length represents the relative contribution of each trait to overall variation, with longer vectors indicating greater influence. Grain yield per plant contributed the most (13.997 %) to PC1, while the kernel length-to-breadth ratio was the dominant trait in PC2 (19.146 %) (**Table 7**). Traits aligned along the X-axis were more strongly associated with PC1, whereas those aligned along the Y-axis had a higher correlation with PC2. The cosine of the angle between vectors reflects trait relationships, with smaller angles (<90°) indicating strong positive correlations and wider angles (>90°) representing negative correlations. A perpendicular orientation suggests independence between traits was also reported by Kalagare *et al*. (2022) in parental lines and land races of pearl millet. Among the observed traits, positive correlations were noted for harvest index, number of effective tillers per plant, root dry weight per plant, root fresh weight per plant, root volume per plant, biological yield per plant, 1000-grain weight, number of grains per panicle, panicle length, root volume, root length and grain yield per plant. Conversely, negative associations were found between grain yield per plant and milling percentage, hulling percentage, kernel length, days to 50% flowering and days to maturity, as indicated by their placement in opposite quadrants.

The biplot diagram (**Fig. 4**) of PC1 and PC2 illustrates the dispersion of genotypes, capturing a substantial degree of genetic variability. PC1 and PC2, represented on the X- and Y-axes, respectively, accounted for significant variation among the studied genotypes. These results align with

Table 7. Contribution (%) of each trait to PCs

S.No.	Traits	PC1	PC2	PC3	PC4	PC5	PC6	PC7
1	Days to 50% flowering	0.568	1.355	27.136	3.068	1.996	0.023	0.168
2	Days to maturity	1.286	0.960	28.926	1.924	1.451	0.001	0.439
3	Plant height	4.209	7.325	0.109	7.316	1.676	2.617	5.330
4	Flag leaf width	0.328	0.119	18.908	4.790	4.524	2.818	6.166
5	Flag leaf length	1.936	1.213	2.463	13.538	2.535	0.359	2.413
6	Panicle length	3.518	0.309	0.589	9.779	2.286	10.803	3.549
7	Number of grains per panicle	9.501	3.432	0.790	1.282	0.178	0.299	2.306
8	Number of effective tillers per plant	4.038	2.753	0.001	0.572	5.509	8.283	15.727
9	1000-grain weight	3.328	1.994	0.229	0.011	5.254	19.735	6.650
10	Biological yield per plant	10.312	0.159	3.482	4.057	3.332	0.032	1.937
11	Harvest index	1.148	0.691	8.466	7.638	0.376	14.189	3.920
12	Grain yield per plant	13.997	0.187	0.256	0.002	1.600	7.384	0.009
13	Root fresh weight	11.281	5.074	0.102	1.831	0.218	4.606	1.916
14	Root dry weight	9.173	4.812	0.022	8.028	0.316	8.225	0.424
15	Root fresh-to-dry weight ratio	1.684	0.009	0.850	13.788	0.223	5.852	10.547
16	Root volume	10.218	3.827	0.001	2.489	1.403	5.030	2.524
17	Root length	3.456	2.173	4.247	0.189	9.541	1.378	13.395
18	Hulling per cent	0.120	6.540	0.000	3.784	7.728	1.070	13.300
19	Milling per cent	2.334	6.242	0.195	1.851	18.251	0.009	5.044
20	Head rice recovery	0.033	0.376	1.234	1.399	26.411	1.835	0.354
21	Kernel length	0.993	17.149	0.267	2.875	3.722	0.091	2.704
22	Kernel breadth	3.541	14.156	1.030	4.159	0.116	4.003	1.105
23	Kernel length-to-breadth ratio	2.998	19.146	0.697	5.630	1.354	1.356	0.072

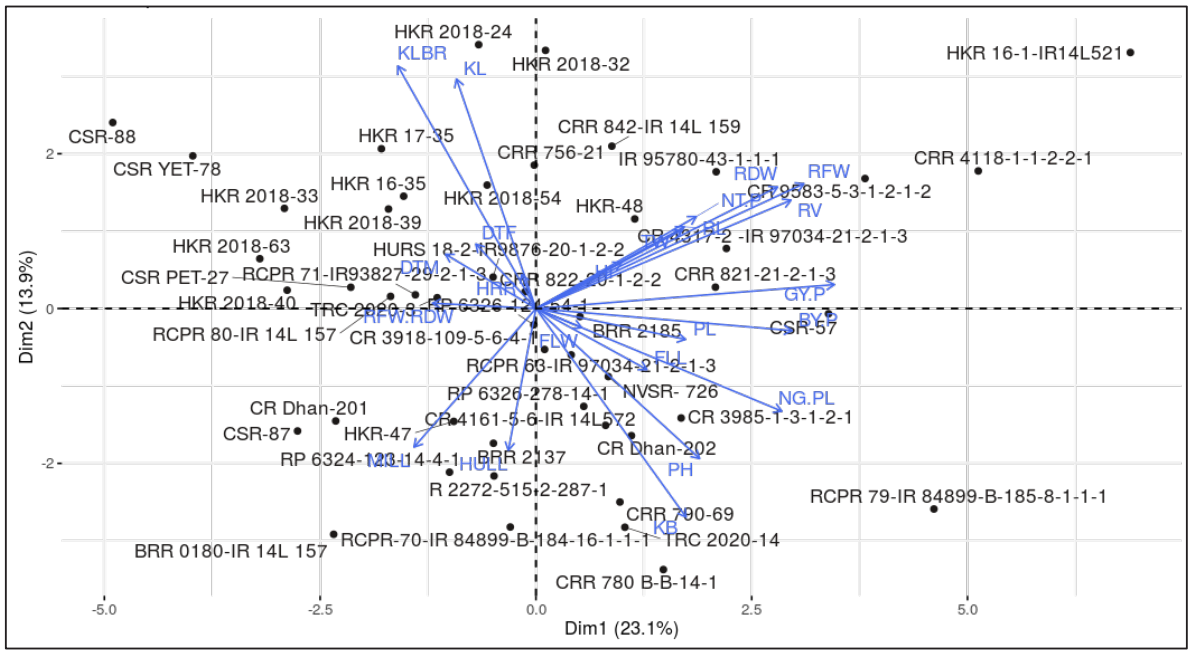

Fig. 4 PCA biplot graph representing genotypes in two main principal components for various morpho-physiological and quality traits

Table 8. Genotypes selected based on PC score (value more than one)

Principal components	Number of genotypes	Genotypes with PC score >1
PC1	13	HKR 16-1-IR14L52, CRR 4118-1-1-2-2-1, RCPR 79-IR 84899-B-185-8-1-1-1, CR 9583-5-3-1-2-1-2, CSR-57, CR 4317-2 -IR 97034-21-2-1-3, IR 95780-43-1-1-1, CRR 821-21-2-1-3, CR 3985-1-3-1-2-1, CRR 780 B-B-14-1, HKR-48, CR Dhan-202, TRC 2020-14
PC2	16	HKR 2018-24, HKR 2018-32, HKR 16-1-IR14L521, CSR-88, CRR 842-IR 14L 159, HKR 17-35, CSR YET-78, CRR 756-21, CRR 4118-1-1-2-2-1, IR 95780-43-1-1-1, CR 9583-5-3-1-2-1-2, HKR 2018-54, HKR 16-35, HKR 2018-33, HKR 2018-39, HKR-48
PC3	10	BRR 2137, CR Dhan-202, HKR 17-35, HKR-47, HKR 2018-39, HKR 16-35, CSR-87, CR 9583-5-3-1-2-1-2, CRR 780 B-B-14-1, NVSR- 726
PC4	9	CSR-88, CSR YET-78, BRR 2137, CR 9583-5-3-1-2-1-2, CR 3985-1-3-1-2-1, CRR 780 B-B-14-1, BRR 0180-IR 14L 157, CRR 842-IR 14L 159, CR 4161-5-6-IR 14L572
PC5	9	HKR 2018-39, CSR PET-27, CRR 780 B-B-14-1, CSR YET-78, HKR 16-1-IR14L521, CSR-5, HKR 2018-54, BRR 2185, BRR 2137
PC6	13	BRR 0180-IR 14L 157, NVSR- 726, BRR 2185, CRR 821-21-2-1-3, HKR 2018-40, RCPR 71-IR93827-29-2-1-3, CRR 756-21, CSR-87, CR 4161-5-6-IR 14L572, CRR 842-IR 14L 159, RCPR-70-IR 84899-B-184-16-1-1-1, IR 95780-43-1-1-1, HKR 16-35
PC7	6	TRC 2020-3, RCPR 79-IR 84899-B-185-8-1-1-1, CSR-88, CRR 790-69, BRR 0180-IR 14L 157, HKR 16-1-IR14L521

findings from Sheela *et al*. (2020). Genotypes positioned near the origin contributed minimally to total variability, whereas those located farther from the origin exhibited greater genetic divergence. Such extreme genotypes are particularly valuable for breeding programs, as they offer a broader genetic base for hybridization (Kiprotich *et al*., 2015). The genotypes HKR16-1-IR14L521, CRR 4118-1-1-2-2-1, RCPR 79-IR 84899-B-185-8-1-1-1, CSR-88, CSR YET-78, CSR-87 and BRR 0180-IR 14L 157 were the most distant from the biplot origin, indicating their significant contribution to genetic variability across principal components. These genotypes hold potential for use in future breeding programs to enhance yield-related and agronomic traits. Genotypes aligned toward the far right of the X-axis exhibited superior performance in grain yield per plant, 1000-grain weight, harvest index, number of effective tillers per plant, root fresh weight per plant and root dry weight per plant. In contrast, those positioned to the far left had lower values for these traits. Overall, PCA-based biplot analysis effectively identifies genetically diverse genotypes and key agronomic traits contributing to variation. These results emphasize the utility of PCA in genotype selection for breeding programs aimed at crop improvement.

The selection of rice genotypes in this study was based on their principal component (PC) scores across multiple PCs (**Table 8**). In PC1, positive scores ranged from 6.82 (HKR 16-1-IR14L521) to 1.02 (TRC 2020-14). For PC2, values varied from 3.37 (HKR 2018-24) to 1.15 (HKR-48). In PC3, the range extended from 6.19 (BRR 2137) to 1.09 (NVSR-726), while PC4 scores ranged from 5.43 (CSR-88) to 1.12 (CR 4161-5-6-IR 14L572). In PC5, positive component values were between 3.42 (HKR 2018-39) and 1.04 (BRR 2137). PC6 scores spanned from 2.22 (BRR 0180-IR 14L 157) to 1.09 (HKR 16-35) and PC7 exhibited values between 2.82 (TRC 2020-3) and 1.41 (HKR 16-1-IR14L521). These results indicate a considerable degree of genetic diversity, which can be effectively utilized in breeding programs. Principal component scores provide a valuable basis for constructing selection indices, with their effectiveness depending on the variability captured by each PC. Genotypes with high PC scores for specific principal components demonstrate superior performance in the corresponding traits. Moreover, genotypes that exhibit strong scores across multiple PCs indicate greater adaptability and genetic potential, making them ideal candidates for breeding programs. These selected genotypes can contribute to the development of heterotic hybrids with enhanced yield and quality traits, further advancing rice improvement efforts.

This study highlights the significant genetic variability among 48 rice genotypes evaluated under aerobic conditions. Cluster analysis revealed that genotypes in Clusters I and VI exhibited superior traits, including higher grain yield, 1000-grain weight and root characteristics, making them ideal for breeding programs. Principal Component Analysis (PCA) confirmed substantial genetic divergence, with the first seven PCs explaining 78.20 % of total variability. Key traits contributing to genetic variation included grain yield per plant, root traits and yield components. Biplot analysis identified diverse genotypes such as HKR16-1-IR14L521, CRR 4118-1-1-2-2-1 and CSR-88, which hold potential for hybridization programs. Overall, integrating PCA and cluster analysis effectively identifies genetically diverse genotypes, providing a foundation for developing high-yielding, stress-resilient aerobic rice varieties.

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