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EXPLORING GENETIC DIVERGENCE AND SUPERIOR GENOTYPES IN RICE (*ORYZA SATIVA* L.) THROUGH D² STATISTICS AND PRINCIPAL COMPONENT ANALYSIS

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ABSTRACT

The present study was undertaken during the Kharif season of 2023 to evaluate 72 diverse rice genotypes for yield and quality-related traits under field conditions. The experiment followed a Randomized Complete Block Design (RCBD) with three replications. Principal Component Analysis (PCA) was employed to assess genetic variability and identify key traits contributing to overall divergence. Out of 29 principal components extracted, the first ten with eigenvalues greater than one were retained, collectively explaining 83.13% of the total variation. Among these, PC1 alone accounted for 19.75% of the variation and was primarily associated with important yield attributes including biological yield per plant, panicle weight per plant, grain yield per plant, 1000-grain weight, days to 50% flowering, and panicle length indicating its significance for selection in yield improvement. The remaining components (PC2 to PC10) accounted for 3.34% to 12.93% of the variability and were associated with traits such as harvest index, grain length, decorticated grain L/B ratio, sterile spikelet percentage, milling quality, and days to maturity. High PCA scores identified superior genotypes such as GNV 2076, RP 6771, CSR HZR-5, RP 6771-IRRI-147, and NVSR 649, which exhibited desirable combinations of yield and quality traits and are considered potential donors for future breeding efforts. Genetic divergence estimated using Mahalanobis' D² statistics revealed maximum inter-cluster distances between Clusters XVI and V (2853.06), XV and II (2783.51), and XII and II (2777.20), indicating substantial genetic variability. Crosses between genotypes from these distant clusters are likely to produce transgressive segregants and broaden the genetic base of rice. These findings offer valuable insights for designing effective selection and hybridization strategies in rice improvement programs.

Keywords **:** Rice, PCA, Mahalanobis' D² statistics, genetic variability, transgressive segregants.

Introduction

Rice (*Oryza sativa* L., 2n=24), a self-pollinated, semi-aquatic annual grass, is one of the most important cereal crops globally, serving as the primary food source for over half of the world's population. Belonging to the family *Poaceae* (Gramineae) and the genus *Oryza*, the rice gene pool comprises two cultivated species. *O. sativa* (Asian rice) and *O. glaberrima* (African rice) alongside 22 wild species. Of these wild relatives, 14 are diploid (2n=2x=24) and 8 are tetraploid (2n=4x=48). While *O. sativa* is widely cultivated across the globe, *O. glaberrima* remains confined to limited regions in West Africa. Archaeological evidence suggests that wild rice was domesticated approximately 9,000 years ago, with early cultivation likely influenced by climatic challenges during the Neothermal age in East and Northern India.

Taxonomically, the wild *Oryza* species are classified into four distinct complexes *O. sativa*, *O. officinalis*, *O. meyeriana*, and *O. ridleyi* based on their interspecific crossing compatibility. In India, rice is a staple crop with the second-highest production after wheat. The country has the largest rice-growing area globally, covering approximately 46 million hectares and producing about 132 million tonnes of milled rice annually, with an average productivity of 4560 kg/ha (USDA, 2020). Madhya Pradesh is a key rice-

producing state, contributing 133.08 lakh metric tonnes from 38.50 lakh hectares, with an average yield of 3462 kg/ha (Anonymous, 2023–24). Major rice-growing districts in the state include Balaghat, Hoshangabad, Narsinghpur, Sagar, and Raisen, which benefit from favorable climatic conditions and diverse soil types.

Globally, enhancing both grain yield and nutritional quality has become a primary focus of rice breeding programs. Malnutrition, particularly in Sub-Saharan Africa and South and Southeast Asia, remains a pressing concern (Reddy *et al*., 2005). Biofortification the process of increasing the micronutrient content of staple crops through genetic improvement offers a sustainable solution to address deficiencies in iron, zinc, and vitamin A. Given the significance of rice, wheat, and maize in global diets, improving their nutritional value is critical to combating micronutrient malnutrition.

Identifying genetically diverse parental lines is fundamental to the success of any crop improvement program. Genetic divergence plays a key role in generating variability and achieving transgressive segregants in breeding populations. The Mahalanobis D² statistic is a robust multivariate tool for assessing genetic diversity, enabling the identification of promising parents by quantifying both intra- and inter-cluster divergence. It also reveals the relative contribution of various traits to total divergence, facilitating informed parental selection.

However, analyzing multiple traits often results in complex data sets that can obscure key patterns. Principal Component Analysis (PCA), introduced by Pearson (1901) and formalized by Hotelling (1933), addresses this challenge by reducing data dimensionality. PCA transforms correlated variables into uncorrelated principal components that explain most of the variability in the dataset (Anderson, 1972; Morrison, 1982). This helps identify the traits most responsible for genetic variability and assists in ranking genotypes based on their component scores.

The integration of D² statistics and PCA provides a comprehensive approach for evaluating genetic diversity and trait interrelationships. This study aims to characterize 72 bio fortified rice lines using both methods to identify genetically divergent and agronomically superior genotypes, thereby facilitating their use in future rice improvement programs.

Materials and Methods

The present investigation was carried out during the Kharif season of 2023 to evaluate 72 rice genotypes under field conditions. The experiment was laid out in a Randomized Complete Block Design (RCBD) with three replications at the designated experimental site. Twenty-day-old seedlings were transplanted into the main field, with each genotype sown in 12 rows of 5 meters in length. Planting was done at a spacing of 15–20 cm between hills, maintaining one seedling per hill. Missing hills were promptly gap-filled within a week after transplanting to ensure a uniform plant stand.

The crop was fertilized with 100 kg N, 60 kg P_2O_5, and 40 kg K_2O per hectare. A full dose of phosphorus and potassium, along with half of the nitrogen, was applied as a basal dose during the final land preparation. The remaining nitrogen was split into two equal applications: one during the active tillering stage and the other at the grain-filling stage, following standard agronomic practices.

Data collection adhered to the Distinctness, Uniformity, and Stability (DUS) test guidelines for rice. Observations were recorded on various yield-contributing traits. For each genotype, five competitive plants were randomly selected from the middle rows of each replication. Traits related to panicle characteristics were recorded based on the mean of the largest, average, and smallest panicles from the selected plants.

To assess genetic divergence, Mahalanobis' D² statistics were employed (Mahalanobis, 1936). Genotypic clustering was performed using Tocher's method (Rao, 1952), and a dendrogram was constructed using Ward's method based on Euclidean distance. To explore trait variability and reduce data dimensionality, Principal Component Analysis (PCA) was conducted following the methods of Massy (1965) and Jolliffe (1986). Principal components were extracted and ranked based on their contribution to total phenotypic variation, aiding in the identification of key traits and divergent genotypes for future breeding programs.

Result and Discussion

Genetic Divergence

In the present study, significant genetic divergence was observed among the 72 rice genotypes for various agronomic and grain quality traits. Among the traits analyzed, grain length contributed the highest proportion to total genetic divergence (25.59%), followed by head rice recovery percentage (20.62%), thousand grain weight (20.19%), and sterile spikelets per plant (9.12%). Other notable contributors included fertile spikelets per plant (6.61%), decorticated grain length (5.09%), decorticated grain L/B ratio (2.35%), and panicle weight per plant (2.15%), panicle index

(1.96%), and grain yield per plant (1.78%). Traits such as productive tillers per plant (1.13%), harvest index (0.59%), days to flowering (0.55%), and days to maturity (0.47%) contributed relatively less to the total genetic variation. The least contributing traits were decorticated grain width (0.43%), milling percentage (0.35%), grain width (0.35%), plant height (0.23%), spikelet fertility percentage (0.20%), spikelet density (0.16%), and hulling percentage (0.08%) (Table 1). These results are consistent with the findings of Adhikari *et al.* (2018), highlighting the importance of grain traits in contributing to overall genetic diversity.

Table 1: Percentage (%) contribution of traits towards divergence

S. No.	Character	Time ranked 1st	Percentage (%) contribution of traits towards divergence
1	GL	654	25.59%
2	HRR %	527	20.62%
3	1000 GW	516	20.19%
4	SSPP	233	9.12%
5	FSPP	169	6.61%
6	DGL	130	5.09%
7	DG L/B	60	2.35%
8	PWPP	55	2.15%
9	PI	50	1.96%
10	GYPP	45	1.76%
11	NOPT	29	1.13%
12	HI	15	0.59%
13	DTF	14	0.55%
14	DTM	12	0.47%
15	DGW	11	0.43%
16	M%	9	0.35%
17	GW	9	0.35%
18	PH	6	0.23%
19	F%	5	0.20%
20	SD	4	0.16%
21	H%	2	0.08%

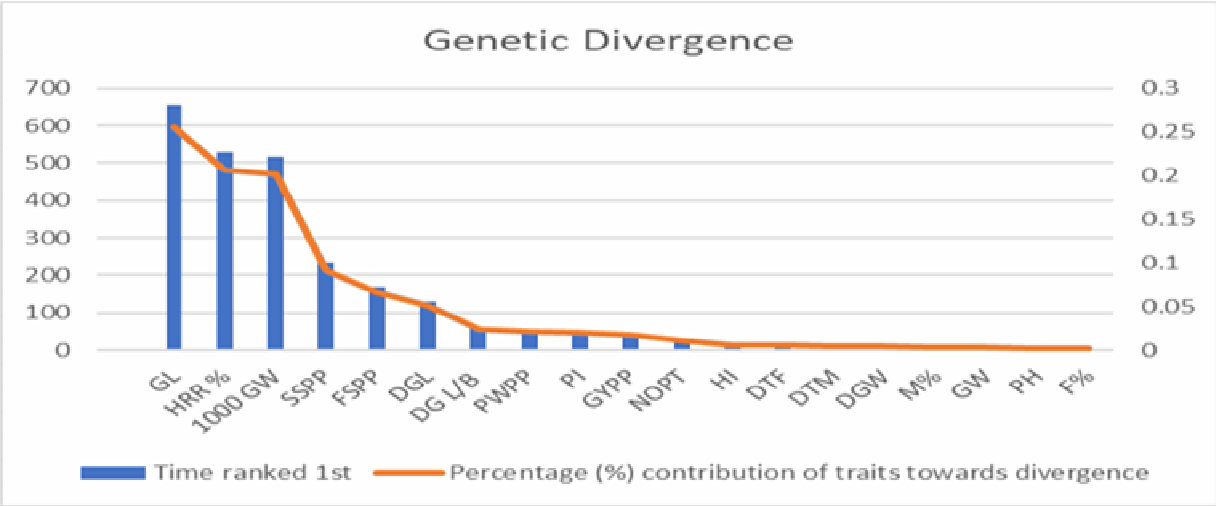

Fig. 1: Contribution of individual characters towards genetic divergence

Using Tocher's method, the genotypes were grouped into 16 distinct clusters based on Mahalanobis' D^2 statistics. Cluster I was the largest, comprising 51 genotypes, indicating a wide genetic base within this group.

Other notable clusters included Cluster IV, which contained 5 genotypes, and Cluster XI, with 2 genotypes. Rest of all clusters are monogenotypic.

Table 2: Grouping of genotypes into various clusters

S. No.	Number of genotypes	Genotypes
Cluster-1	51	CSR-2021-294-164, DRR-48, GNV 2076,CSR HZR-1, R-56, CK-35, RP 6731-BCRK/RIL BCRK-4, HURS 23-8, RNR-34998, RP 6514-IR128768-7-2-2-4, R-RHP-IC-148, ORR 1814, RP 6167-RN-116, RP 6731-BCRK/RIL-BCRK-4-1-P, RP 6615-MK/RIL-FBM1-45-1-5-1,Kalanamak 2020-3, CSR HZR 5, RP 6615-MK/RIL-FBMI-2-1, RP 6731-BCRK/RIL-BCRK-9, DRR-45, SKL 10-15-593-162-25-106-70, NDR 8399-2, IR 124041-B-3-1-1-B,Gurmatiya sel.1, R-RHP-IC-148, RNR 31672, AD 21270, CSR HZR 5, CSR H3R 17-42, R-RHP-IR-142, NVSR 658, RP 6211-PR/RILQ 181, DRR Dhan-45, GNV 2075
Cluster-2	1	DRR Dhan-49
Cluster-3	1	RP 6211-PR/RIL-181
Cluster- 4	5	RP 6771-IRRI-14, Chittimuthyalu, RP 6195-MC/RIL-SM5A-60, AD 21205, NVSR 649
Cluster-5	1	KALANAMAK
Cluster-6	1	UPR 2879-98-105
Cluster-7	1	BPT 5204
Cluster-8	1	HURS-22-3
Cluster-9	1	RP 6458-C1-151
Cluster-10	1	CK 145-3
Cluster-11	2	RP 6615-MK/RIL-FBMI-45-1-5-1,NVSR 787
Cluster-12	1	DRR-48
Cluster13	1	NVSR 787
Cluster 14	1	UPR 4640-11-1-1-1
Cluster 15	1	IR-64
Cluster 16	1	RP Bio 4918-NPS 21

Analysis of intra-cluster divergence revealed that Cluster IV exhibited the highest intra-cluster D² value, suggesting considerable variability among its constituent genotypes. This was followed by Cluster I (479.12) and Cluster XI (433.63). Inter-cluster divergence estimates showed that the maximum genetic distance was observed between Clusters XVI and V (2853.06), indicating substantial genetic divergence between these groups. Other notable high inter-cluster distances included Clusters XV and II (2783.51), XII and II (2777.20), XII and XI (2510.62), and XV and V (2496.03). The lowest inter-cluster divergence was observed between Clusters XII and XV (2252.87).

The distribution pattern of genotypes across clusters suggests a random dispersion, reflecting a broad genetic base within the studied germplasm. High inter-cluster distances indicate substantial genetic divergence among clusters, implying that hybridization between genotypes from these clusters could potentially result in heterotic combinations and enhanced transgressive segregation in segregating populations. Furthermore, substantial intra-cluster divergence observed in poly-genotypic clusters such as Cluster I and Cluster IV also offers opportunities for selecting diverse parents from within these clusters. These findings are in agreement with previous reports by Verma *et al*. (2000) and Chakraborty *et al*. (2010) particularly for traits such as sterile spikelets per panicle, grain yield per plant, biological yield, and productive tillers per plant.

Principal Component Analysis:

In the present study Principal Component Analysis (PCA) was employed to understand the underlying structure of variation among 30 agro-morphological and quality traits and found 10 principal components exhibited eigenvalues greater than 1.0 and cumulatively explained 83.13% of the total variation among the traits studied. The first principal component (PC1) alone accounted for the maximum variance (19.75%), followed by PC2 (12.93%), PC3 (11.07%), PC4 (8.70%), PC5 (6.99%), PC6 (6.16%), PC7 (5.24%), PC8 (4.96%), PC9 (3.95%), and PC10 (3.34%). This pattern of variance distribution is consistent with the findings reported by Haque *et al*. (2014), confirming the robustness of PCA in summarizing trait variability (Table 3). The Eigen value of PC1 was 5.927 indicating a 19.755 percent variability that thereafter decreased progressively as seen in the scree plot (Figure 2).

Table 3: Cumulative variability (more than 1 Eigen value)

Character	PC Value	Eigen value	Variability (%)	Cumulative variability
DTF	PC-1	5.927	19.755	19.755
DTM	PC-2	3.880	12.934	32.689
NOT	PC-3	3.321	11.071	43.760
NOPT	PC-4	2.612	8.705	52.465
SL	PC-5	2.098	6.994	59.459
PL	PC-6	1.848	6.161	65.620
FLL	PC-7	1.573	5.244	70.865
FLW	PC-8	1.489	4.964	75.828
ST	PC-9	1.187	3.956	79.785
SWPP	PC-10	1.004	3.348	83.133
PWPP	PC-11	0.964	3.213	86.346
BYPP	PC-12	0.821	2.735	89.082
FSPP	PC-13	0.631	2.102	91.183
SSPP	PC-14	0.624	2.078	93.262
SF %	PC-15	0.470	1.565	94.827
TSPP	PC-16	0.413	1.376	96.203
SD	PC-17	0.310	1.032	97.235
PI	PC-18	0.227	0.757	97.993
HI	PC-19	0.180	0.601	98.594
GL	PC-20	0.165	0.550	99.144
GW	PC-21	0.103	0.343	99.488
DGL	PC-22	0.079	0.265	99.752
DGW	PC-23	0.028	0.092	99.844
H %	PC-24	0.017	0.057	99.901
M %	PC-25	0.014	0.048	99.949
HRR %	PC-26	0.009	0.028	99.977
TGW	PC-27	0.004	0.013	99.990
DG L/B	PC-28	0.003	0.010	100.000
GYPP	PC-29	0.000	0.000	100.000

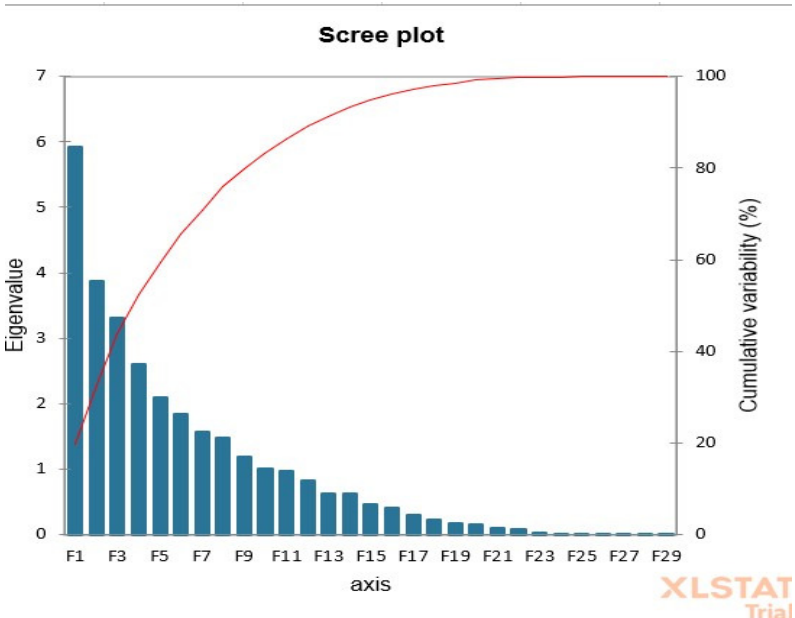

Fig. 2: Scree plot showing the trend in the percentage of Variance for each individual principal component.

The rotated component matrix provided deeper insights into the contribution of individual traits to each principal component. PC1, which captured the highest variability, was predominantly associated with yield-contributing traits such as biological yield per plant, panicle weight per plant, grain yield per plant,

thousand grain weight, days to 50% flowering, and panicle length. PC2 was mainly associated with harvest index, grain length, decorticated grain L/B ratio, decorticated grain length, and spikelet fertility percentage. PC3 captured variation due to spikelet density, total spikelets per plant, fertile spikelets per plant, and stem thickness, while PC4 was influenced by number of tillers and productive tillers per plant. PC5 reflected variation in stem length, flag leaf length, grain width, and plant height (Table 4). The sixth and seventh principal components were primarily influenced by sterile spikelets per panicle and decorticated grain width, findings which support the results of Wattoo *et al*. (2010). PC8 captured hulling percentage and milling percentage, whereas PC9 was defined by head rice recovery percentage, flag leaf width, and straw weight per plant. PC10 was mainly represented by days to maturity, which corroborates the findings of Gour *et al*. (2017).

Table 4 : Interpretation of Rotated Component Matrix for the Traits Having Highest Value in Each PCs.

PC-1	**PC-2**	**PC-3**	**PC-4**	**PC-5**	**PC-6**	**PC-7**	**PC-8**	**PC-9**	**PC-10**
BYPP	HI	SD	NOT	SL	SSPP	DGW	H%	HRR%	DTM
PWPP	GL	TSPP	NOPT	GW			M %	FLW	
GYPP	DGL/B	FSPP		FLL				SWPP	
TGW	DGL	ST		PH					
DTF	F %								
PL									

Table 5 : PC scores of rice lines.

Genotype	PC-1	PC-2	PC-3	PC-4	PC-5	PC-6	PC-7	PC-8	PC-9	PC-10
R-RHP-IC-148	-3.469	1.569	0.395	-1.505	0.154	1.257	-1.066	0.712	-1.199	**0.171**
RNR 31668	-1.892	1.344	-0.474	-1.324	-0.774	0.444	1.656	1.277	-1.808	**0.621**
CSR HZR 1	-0.911	0.599	-0.688	-1.796	1.256	-0.076	0.861	0.290	0.623	**0.448**
AD 21270	-1.958	-1.372	0.225	-1.540	0.193	0.889	1.242	1.053	-0.919	**-1.800**
CK 145-3	-1.868	-0.811	0.776	-1.237	-3.990	-2.929	-0.128	-1.835	-2.075	**0.329**
RP 6731-BCRK/RIL-BCRK-4	0.523	1.731	1.282	-0.173	-0.778	-0.336	-1.783	1.077	0.790	**-0.797**
RP Bio 4918-NPS 21	-0.447	-2.861	1.246	2.196	-2.434	-1.649	1.708	-1.557	-3.594	**1.357**
GNV 2076	-0.447	-2.861	1.246	2.196	-2.434	-1.649	1.708	-1.557	-3.594	**1.357**
CSR HZR 5	1.107	2.562	0.777	-0.840	1.013	-0.616	-1.078	-0.230	-0.648	0.262
RP 6771-IRRI-147	-0.093	3.019	-0.915	2.133	-1.518	-0.701	-1.460	0.169	1.120	1.068
NVSR 649	1.658	0.773	-0.900	-3.444	0.739	0.319	3.853	2.385	0.961	1.204
CR 4225-B-1-1-2	2.007	-2.200	-0.553	-2.331	-2.104	2.549	-0.704	0.647	-0.262	1.589
BPT 5204 (Yield Check)	0.600	-1.511	-0.729	-2.453	2.511	-2.308	-0.478	0.651	-0.311	1.570
RP 6514-IR128768-7-2-2-4	-2.193	-0.827	-0.409	1.323	0.437	-1.516	-1.950	0.984	-0.472	-0.036
RP 6615-MK/RIL-FBMI-2-1	-7.117	-1.689	-0.305	1.258	1.163	1.410	1.177	-2.066	1.472	-0.602
NVSR 787	-1.477	1.091	-0.959	2.273	1.269	0.342	3.115	0.476	0.189	0.282
UPR 4640-11-1-1-1	1.128	0.917	-1.536	0.907	0.293	0.523	1.692	0.001	-1.234	0.763
Gurmatiya sel.1	4.006	4.359	0.110	-0.279	1.927	1.219	-0.648	-2.584	-1.858	0.277
IR 124041-B-3-1-1-B	0.653	1.916	4.537	3.129	2.899	0.528	0.313	0.063	0.599	-1.773
GNV 2075	-3.438	-2.609	0.400	-2.018	1.001	-0.699	-0.150	-1.835	1.237	1.425
RP 6458-C1-151	1.223	1.967	-1.879	-2.505	0.371	-0.158	-0.242	-1.211	-0.941	0.766
IR-64 (Yield Check)	0.813	-0.420	-1.093	-3.249	0.505	-0.073	0.167	-1.215	-1.038	-0.972
HURS 23-10	0.579	1.676	2.182	-0.575	1.158	-0.526	1.119	-0.952	-1.813	-0.651
RNR 31672	1.282	1.291	2.542	-0.513	-0.324	3.919	-0.805	-0.522	-0.561	0.584
RP 6731-BCRK/RIL-BCRK-9	-0.759	3.663	-0.073	-0.382	0.336	-0.266	1.411	1.952	-0.543	-0.888
CK 35-3	0.127	0.470	1.782	-0.400	1.535	-0.924	0.363	-0.790	0.898	-0.210
CSR 2021-294-164	1.789	-0.281	2.750	0.132	-0.087	0.219	0.800	-0.094	-1.001	0.060
AD 21205	-1.453	1.391	-0.206	-1.010	-0.157	-0.343	0.848	-0.312	-0.269	0.591
ORR 1814	0.036	2.491	-0.632	-0.086	-0.763	-0.821	-0.098	1.499	-1.087	-0.920
RP 6195-MC/RIL-SM4A-A57	-0.079	-3.520	1.541	-1.126	3.959	-0.090	-0.525	0.274	-0.692	0.728
CB 21102	4.067	-1.201	-2.395	-1.708	1.526	-0.147	0.011	-0.844	1.014	-0.530
DRR Dhan-45	3.013	-0.070	-0.913	0.882	1.126	-0.026	1.167	-1.518	-1.953	-2.086
SKL 10-15-593-162-25-106-70	1.254	1.496	-1.581	0.412	0.144	1.346	0.232	-0.217	1.473	0.308

RP 6731-BCRK/RIL-BCRK-4-1-P	2.650	1.196	-1.498	-0.024	0.507	0.056	1.600	-0.667	-0.046	-0.096
CR 4107-1-B-4-1-B	3.163	1.047	0.342	1.148	1.365	0.114	1.099	-0.225	0.583	-0.151
R-56	-2.410	0.318	-0.300	0.960	-0.696	1.004	-2.384	-1.814	-1.154	-0.502
R-RHP-IR-142	-2.445	2.122	-0.331	-1.095	-0.811	-0.418	-1.696	1.338	0.352	-0.175
DRR Dhan-48	-4.945	2.690	-3.129	0.789	0.205	0.839	-0.089	-2.874	0.694	0.335
HURS 23-8	2.004	-1.320	1.409	1.217	1.409	-1.312	1.864	-0.101	0.024	0.053
RNR 34998	-1.798	2.856	-1.545	-0.332	-1.071	0.124	-0.507	0.627	-0.627	-1.162
RP 6615-MK/RIL-FBM1-45-1-5-1	0.709	3.449	0.715	-0.344	-0.090	-0.636	-0.730	-0.088	0.823	1.025
RP 6167-RN-116	-2.088	1.864	0.376	-0.017	-1.237	0.527	0.575	-1.147	0.801	-0.307
NVSR 658	-2.118	1.432	-0.451	0.178	-1.787	-0.105	1.485	0.211	1.195	-0.307
CR 4199-2-B-1-2-B-2	-0.680	0.315	-1.560	-1.333	-2.112	-0.871	-0.074	-0.092	0.619	-0.216
Kalanamak 2020-3	-0.002	-1.258	-0.675	0.791	-1.239	-1.919	1.283	-1.425	0.479	-0.996
CSR H3R 17-42	-3.431	1.624	-0.880	2.022	1.278	0.163	-0.484	1.859	-0.187	3.651
RP 6195-MC/RIL-SM5A-60	-1.717	0.327	-0.603	0.221	-0.700	0.383	-0.236	0.657	0.911	-0.035
Chittimuthyalu	1.635	-2.425	-1.011	-0.911	0.708	0.974	-0.077	-0.097	0.415	-0.582
UPR 2879-98-105	-0.344	-5.476	-4.055	-4.022	1.279	-0.593	-1.307	-0.300	-0.166	-1.783
RP 6733-SP-M-KS-57-4-5	0.715	2.085	-0.627	-1.608	-0.397	0.475	-2.408	-2.556	0.905	0.350
NDR 8418-3	4.404	-1.954	1.160	-0.154	0.083	0.022	-1.498	0.560	0.274	1.066
HURS 22-3	4.758	-1.355	1.142	1.263	0.752	0.141	-1.904	-0.360	0.242	0.233
RP 6615-MK / RIL- FBMI 45-1-5-1	-3.906	-3.010	3.655	-0.758	0.888	-2.480	-0.696	0.597	-0.033	0.479
RP 6204-MB/RIL-J159	1.646	-1.387	1.009	1.383	-0.496	0.466	1.481	-2.185	2.169	0.142
Chapti Gurmatiya Mutant-4	3.477	-2.301	0.335	0.335	-1.221	-0.402	-0.807	-0.065	0.716	2.113
RP 6211-PR/RIL-Q181	0.086	-1.235	-0.852	2.832	-1.481	-0.040	0.045	-0.819	1.359	-0.277
NDR 8399-2	4.748	0.030	-2.005	0.014	-1.195	-0.643	-0.486	2.626	-0.041	-1.951
GNV 1922-16	-0.861	1.610	3.367	-0.572	0.631	0.164	-0.201	1.745	0.020	-0.258
Chittimuthyalu	1.465	0.301	4.953	0.273	0.790	-0.729	-1.839	-0.855	0.806	-0.276
RP 6204-MB/RIL-J159	-5.019	-0.754	3.556	0.364	-0.419	-1.697	0.157	1.858	-0.778	-0.565
RP 6615-MK / RIL- FBMI 45-1-5-1	1.524	-2.272	0.246	0.795	-1.687	0.513	2.139	-0.279	0.395	1.250
-(R-RHP-IR-142)	1.606	-2.552	2.283	0.288	-2.772	3.611	0.852	0.140	-1.040	-0.420
RP 6211-PR/RIL-Q181	0.164	-2.081	0.167	0.991	-0.919	0.269	0.685	0.376	1.423	1.141
HURS 22-3	2.014	-0.887	-0.828	0.099	-1.157	-1.161	-0.457	2.078	0.283	-0.499
GNV 1906	1.481	1.821	-2.391	-0.602	-0.519	0.282	-0.131	1.193	1.195	0.461
CSR HZR 5	1.605	0.039	0.247	0.942	-2.044	-3.649	-0.302	-0.190	0.779	0.070
R-RHZ-IR-140	2.228	-0.400	2.621	0.813	0.219	0.288	-0.573	0.730	1.197	-1.037
DRR-45	1.147	-1.375	-0.337	1.039	-3.570	0.698	-0.043	0.291	0.853	-1.795
DRR-48	-0.940	0.046	-0.946	0.859	-0.143	-0.284	-1.869	1.077	0.251	-0.330
DRR-49	-2.401	-2.774	-2.612	2.666	2.538	0.159	0.441	1.177	0.988	-0.575
IR-64	-2.494	-3.353	-0.041	1.145	-0.226	5.397	-1.464	1.545	-1.333	**0.363**

From this analysis, it is evident that most of the key yield-contributing traits were grouped under PC1, PC2, PC3, and PC5. Therefore, genotypes associated with these components may serve as potential donors in yield improvement breeding programs (Table 5). Similarly, for enhancing grain quality, traits clustered under PC4, PC6, and PC7 could be targeted, as these components captured variation associated with quality attributes. The differentiation of traits into specific PCs highlights the efficiency of PCA in identifying components governing yield and quality, thereby offering a strategic basis for genotype selection. Consequently, integrating this information into a breeding program would facilitate the development of high-yielding genotypes with desirable quality traits by selecting superior lines from the appropriate principal components.

Conclusion

The present investigation revealed significant genetic divergence among rice genotypes for yield and quality traits. Grain length, head rice recovery, and 1000-grain weight contributed most to total divergence, indicating their potential in trait-based selection. PCA and D^2 statistics identified highly diverse genotypes such as GNV 2076, RP 6771, CSR HZR-5, and RP 6771-IRRI-147, which showed superior performance for both yield and grain quality. Clusters XVI & V, XV & II, and XII & II exhibited maximum inter-cluster distances, making them ideal

candidates for hybridization to exploit heterosis and obtain transgressive segregants. These findings support the strategic selection of parents from diverse clusters to enhance genetic variability and develop high-yielding, quality-rich rice cultivars through effective breeding programs.

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