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Original Article

Genetic Variability and Multivariate Analysis of Agro-Morphological Traits in Selected Rice Germplasm (*Oryza sativa* L.) of India

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Abstract

Thirty-six valuable rice germplasm accessions were collected from different regions of West Bengal and evaluated at the experimental farms of The Neotia University, located in the coastal saline zone of West Bengal, India. The mini-core collection is maintained at the university through periodic seed multiplication during the rainy (kharif) season. The accessions were evaluated for twenty-four agro-morphological traits over two consecutive years (2022 and 2023) during the kharif season. The study revealed that two traits—number of tillers (84.488%) and panicles per plant (84.478%)—exhibited the highest heritability, followed by 1000-grain weight (77.627%), days to 50% flowering (74.938%), and panicle length (72.623%). High genotypic coefficient of variation was observed for total yield (42.969%), chaffy grains per panicle (32.656%), leaf area (31.278%), number of tillers per plant (28.621%), 1000-grain weight (27.525%), and filled grains per panicle (27.523%). The highest genetic advance was recorded for total grain number per panicle (68.471%), followed by filled grains per panicle (54.431%). Principal component analysis of the twenty-four traits resulted in eight components with eigenvalues greater than 1. These eight components together accounted for 84.78% of the cumulative variance of the population. The first principal component explained the highest proportion of variance (20.09%), followed by the second (16.67%), third (12.96%), and fourth (10.48%) components. The germplasm bank represents unique traits such as low-input rice, aromatic and non-aromatic fine-grained rice, and micronutrient-rich landraces. This collection, with its diverse and distinctive characteristics, represents a climate-smart gene pool encompassing a broad range of life cycles, enabling adaptation and resilience under unpredictable climatic adversities. The present study successfully identified, integrated, and conserved elite genetic resources that are important for future rice improvement programs.

Keywords: *Agro-Morphological Traits; Food Security; Genetic Advance; Multivariate Analysis; Rice Mini Core Collection*

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Introduction

Landraces and local cultivars represent a vital gene pool of cultivated crop plants, conserving the potential for crop improvement and maintaining the adaptive balance of species under dynamic ecological and environmental pressures. Traditional germplasm harbors a rich allelic repository that is beneficial for climate-resilient breeding strategies, enhanced nutritional performance, and adaptive advantages in localized environments. The allelic combinations present in landraces integrate early domestication signals that enabled the wild progenitors of cultivated crops to overcome barriers of low agronomic performance, ultimately leading to varietal development. Chance mutations, rapid hybridization between landraces and wild relatives of cultivated crops, along with demand-based breeding practices, have generated numerous extant rice varieties. Farming communities in China, India, and Southeast Asian countries have played an instrumental role for generations in the domestication and development of new cultivars and varieties from indica rice germplasm (Jing *et al*., 2023).

Landraces are heterozygous and heterogeneous entities that conserve favorable combinations of alleles and ensure moderate yields, which are selected and maintained by farmers to meet local consumer needs. Landraces can safeguard species survival by enabling adaptation to disasters and by helping to overcome yield thresholds in selective breeding experiments. Rapid industrialization of agriculture has promoted monocropping, leading to drastic erosion of plant biodiversity. In contrast, traditional farming systems preserve wild and local germplasm pools and indirectly support the maintenance and restoration of intraspecific heterozygosity and heterogeneity. The long history of cereal crop cultivation has caused genetic erosion affecting more than 75% of agricultural crop species, including major dietary contributors such as wheat, rice, maize, and potato (Khoury *et al*., 2022). Yield-centric breeding objectives during the colonial period of Indian agriculture, followed by the Green Revolution, resulted in a drastic reduction of rice cultivars from 400,000 to 30,000, accompanied by a narrowing of the genetic base (Azeez *et al*., 2018; Cai *et al*., 2025).

The global population is increasing at an alarming rate, and to feed this growing number of people, the demand for rice is rising proportionately. Half of the global population, along with one-third of the world's poor, resides in Asia. Fortunately, India and China, the two leading economies in Asia, have shown an 85.25% and 67.28% increase in rice production, respectively, due to the yield effect. This increase was attributed to the interaction between yield and area (Mahajan *et al*., 2023). India accounts for 20% of the world’s total rice production annually and holds the second position after China. Approximately 1.2 billion domestic consumers in India and 150 countries worldwide directly depend on Indian rice farmers. In 2021-22, the country contributed 127.93 million tonnes (MT) of rice, with 85% of this production relying on kharif rice (Maiti *et al*., 2024).

The erratic climatic shifts occurring worldwide are compelling scientists to innovate novel techniques for the continued cultivation of cereals, in order to cope with frequent climatic challenges. In this context, landraces could support both scientists and farmers in sustaining rice breeding strategies. Indica rice varieties and landraces possess several agro-morphological traits valuable for genotypic marking (Mohanty *et al*., 2024). The consistency of these traits over long periods of cultivation suggests a perfect balance between homozygous and heterozygous combinations of diverse genes. The widespread cultivation of High Yielding Varieties (HYVs) has led to a dramatic decline in the cultivation of traditional rice landraces. This dwindling rice diversity threatens the existence of one of the world's most important crops. Cultivating diverse landraces and showcasing their potential to urban consumers could help preserve the remaining indica rice landraces from total extinction on the global scale. In this study, thirty-six indica rice landraces were evaluated based on twenty-four agro-morphological parameters to determine the main contributors to phenotypic diversity in the mini-collection and to dissect the genetic and environmental components of the studied parameters.

Material and Methods

Collection of Landraces and Experimental Set-Up

Plant Materials

Rice landraces were collected from farmers' fields in different parts of West Bengal in 2022. The genetic purity of the landraces was maintained through periodic rouging of the "off-type" plants within the lines. The details of the plant materials used in the experiment are provided in Table 1.

Experimental Site

The experiment was conducted during the kharif season in small plots at the experimental farm of the School of Agriculture & Allied Sciences, The Neotia University, using the asynchrony flowering technique for two consecutive years (2022 and 2023). A plot size of 3m x 1m was maintained for each landrace, with a plant-to-plant spacing of 20 cm and a row-to-row spacing of 25 cm.

Cultural Practices

The crop was supplied with 10 ton well decomposed farmyard manure ha-1 along with 60-30-30 kg NPK ha-1. Half N+ Full P2O5, K2O and farmyard manure were applied as basal dose during final land preparation and rest of the nitrogen was equally splitted at 25 and 45 days after transplanting. Manual hand weeding was done at 20 and 40 days after transplanting.

Data Collection

Field data were recorded from five randomly selected plants within the plots. The vegetative and reproductive traits were measured following the standard evaluation system for rice as outlined by Kumar *et al*., 2023.

Statistical Analysis

Analysis of variance was conducted for all the characters using a Randomized Block Design, as described by Ozturk *et al*., 2024. Since the error mean squares for both years were homogeneous, as confirmed by Bartlett's Chi-square test (Jagadeesh *et al*., 2024), the mean values from both years were used for further statistical analysis. The estimation of phenotypic and genotypic coefficients of variation was performed using the formulas suggested by Singh *et al*., 2024. Genotypic and phenotypic correlations, along with path coefficient analysis, were calculated using the formulas suggested by Sarkar *et al*., 2024, and Salunkhe *et al*., 2024.

Table 1: *Inventory of Rice Landraces Reported in the Experiments*

Sl. No.	**Name of Landraces**	**Sl. No.**	**Name of Landraces**	**Sl. No.**	**Name of Landraces**	**Serial No.**	**Name of Landraces**
1	Aduisen	10	Deheradun Mathura	19	Koushalya	28	Prabhat
2	Altaluti	11	Dhiren	20	Mahasugandha	29	Radhunipagol
3	Amala	12	Dhruba	21	Malabati	30	Sampriti
4	Badshabhog	13	Dinesh	22	Marichshal	31	Sohini2
5	Bankut	14	Gandheswari	23	Motibas	32	Sugandha
6	Bishnubhog	15	Harmanina	24	Narayan Kamini	33	Sujala
7	Chamalmoni	16	Hawai	25	Neela	34	Talmagur
8	Chapakushi	17	Heera	26	Pakuri	35	Talmarhi
9	Dudsal	18	Kalopatnai	27	Para mannya	36	ThupiKejurChari

Analysis of Data

The data collected over two consecutive years were pooled after Bartlett's X^2 test of homogeneity for each trait, and the mean values were used for analysis of variance. The estimation of various genetic parameters such as variability, heritability, and genetic advance, including the genotypic correlation matrix, was performed using SPSS (2009), version 28 software. Principal component analysis of the quantitative parameters and hierarchical cluster analysis were conducted using Minitab (2025) software.

Results

The landraces included in this experiment were collected from different parts of West Bengal, as well as from the Nalhati Research Station and Rice Gene Bank, representing a rice mini-core collection of landraces and varieties grown by farmers. This mini-core collection is maintained at the Genetics and Plant Breeding Department of the School of Agriculture & Allied Sciences at The Neotia University for the rice improvement program. The selected germplasm exhibited unique characteristics, and most of them are ideal for cultivation in the coastal saline region of India.

Table 2: *Unique Characteristics of The Selected Thirty-Six Landraces and Cultivars of Rice Included in the Mini-Core Collection*

Landraces	Special Characteristics	Area Of Cultivation
Aduisen	Salinity tolerance coastal landrace	Sundarbans areas, W.B.
Altaluti	Salinity tolerance coastal landrace	Sundarbans areas, W.B.
Amala	Short grain, soft and short duration	Indo-gangetic plains
Badshabhog	Soft, digestive, Long duration late maturing	Dry farming region, Purulia, West Bengal
Bankut	Short grain, soft and short duration	Indo-gangetic plains
Bishnubhog	Aromatic, short grained, intermediate amylose content	Madhya Pradesh, Chhattisgarh, Odisha
Chamalmoni	Fine grained, soft, withstand salinity and water logging	South Bengal
Chapakushi	Iron and zinc rich	Indo-gangetic plains
Dudshal	Short grain, high protein %, late maturing, salinity tolerant	West Bengal, Odisha
Dehradun Mathura	Fine grained, aromatic	Mathura, Uttar Pradesh
Dhiren	Short, bold grain, late duration high yielding	Bankura, West Bengal
Dhruba	Short, bold grain, moderately resistance to leaf blast	Hooghly,West Bengal
Dinesh	Short grained, medium duration	Hooghly, West Bengal
Gandhaswari	Scented rice	Birbhum, West Bengal
Harmanina	Vitamin B and iron rich, submergence tolerant	Birbhum,West Bengal
Hawai	Salt and submergence tolerant	Odisha, India
Heera	Boro hybrid	Mednipur, West Bengal
Kalopatnai	Fine grained	Bihar,India
Kaushalya	Moderately submergence tolerance	Eastern coast of India
Mahasugandha	Hybrid aromatic basmati	Northern India
Malaboti	Long period of submergence tolerant	Coastal Bengal
Marichshal	submergence tolerant	Coastal Bengal
Motibas	Aromatic folk rice	Murshidabad,West Bengal
Narayan Kamini	Fine grain, submergence tolerant	North 24 Parganas
Neela	Short height, medium duration	Murshidabad
Pakuri	Short grained	Jharkhand, India
Paramanna	Fine grained, Aromatic	Cooch Behar, India
Prabhat	Early maturing type	Red lateritic zone, W.B.
Radhunipagal	Small grained, non-basmati, scented	Raiganj, North Bengal
Sampriti	Late duration high yielding	Rain-fed areas, W.B.
Shohini	Aromatic, tall	Bihar, West Bengal
Sugandha	Aromatic, short grained	Jharkhand, India
Sujala	Salt sensitive local variety	South Bengal
Talmagur	Red grained, salt tolerant	Birbhum, West Bengal
Talmahi	Low input rice	Jharkhand, India
Thupi Khejur Chari	Multiple spikelets from one pedicel	South Bengal

The number of tillers and the number of panicles per plant showed very high estimates of heritability, followed by 1000-grain weight, days to 50% flowering, and panicle length. It was observed that these five traits were the most highly heritable out of the twenty-four agro-morphological traits considered in this experiment.

The number of tillers and panicles per plant, along with the number of primary branches per panicle and seed weight, reflected higher Genotypic Coefficient of Variation (GCV). These traits are important for evaluating the overall performance of the selected landraces. Seed weight, panicle number per plant, and total yield showed relatively high Genetic Advance (GA). The parameters with higher GCV and GA values could be used for direct selection of varieties or landraces for hybridization or breeding programs, as the environmental influence on those traits will be minimal. The genetic analysis of these diverse traits aligns with the findings of previous rice researchers (Faysal *et al*., 2022).

Table 3*: Estimation of Genetic Components for Agro-Morphological Traits Related to Performance of Rice Landraces*

Characters	**Abbreviation used**	**Trait Type**	**Heritability (%)**	**Genotypic Coefficient of Variations (GCV)**	**Phenotypic Coefficient of Variations (PCV)**	**Genetic Advance (GA)**	**Genetic Advance value % means**	**Standard Deviation**
1.	GL	Grain length (cm)	39.826	11.07	17.542	0.119	14.392	0.112
2.	GW	Grain width(cm)	41.588	15.107	23.425	0.135	20.069	0.12
3.	CKL	Cooked Kernel length (cm)	34.525	9.339	15.893	0.081	11.304	0.092
4.	CKB	Cooked Kernel breadth(cm)	65.507	20.605	25.458	0.217	34.355	0.094
5.	SW	1000 grain weight (gm)	77.627	27.525	31.241	6.737	49.958	1.993
6.	DGL	Decorticated grain/ kernel length (cm)	24.017	11.176	22.804	0.057	11.282	0.1
7.	DGB	Decorticated grain/ kernel width (cm)	53.695	22.059	30.104	0.133	33.298	0.082
8.	PH	Plant height (cm)	61.173	9.804	12.535	24.073	15.796	11.904
9.	DOF	Days to 50% flower	74.938	15.396	17.785	22.388	27.455	7.26
10.	SD	Stem diameter (cm)	63.559	12.827	16.090	2.221	21.067	1.024
11.	PL	Panicle Length(cm)	72.623	14.438	16.942	7.251	25.346	2.536
12.	PN	Panicle number per plant	84.478	32.081	34.904	9.992	60.742	2.262
13.	DTM	Time of maturity(Days)	41.094	8.071	12.591	11.271	10.658	10.219
14.	DSW	Decorticated 1000 seed weight(gm)	64.727	21.114	26.244	5.689	34.993	2.534
15.	NPB	Number of primary branch per panicle	69.218	23.873	28.695	5.45	40.916	2.12
16.	NSB	Number of secondary branch per primary branch per panicle	50.095	21.636	30.569	1.157	31.546	0.792
17.	NSPB	Number of seed on primary branch per panicle	45.596	21.668	32.089	4.86	30.141	3.817
18.	NSSB	Number of seed on secondary branch per primary branch per panicle	7.29	6.998	25.92	0.15	3.892	0.964
19.	FG	Filled grain per panicle	53.264	27.523	37.712	54.431	41.379	33.913
20.	CG	Chaffy grain per panicle	57.862	32.656	42.93	22.885	51.171	12.463
21.	TG	Total grain number per panicle	56.689	25.113	33.354	68.471	38.95	38.587
22.	LA	Leaf area (cm2)	61.386	31.278	39.921	29.71	50.482	14.6
23.	TN	Tiller number per plant	84.488	28.621	31.138	10.124	54.194	2.291
24.	TY	Total yield per plant(gm)	62.962	42.969	54.152	20.264	70.236	9.508

Genotypic Correlation of Traits

The genotypic correlation matrix reveals both positive and negative associations between paired traits. Vegetative traits, such as the number of panicles, are influenced by the number of tillers. The date of flowering and time of maturity have a positive influence on seed production in secondary branches. The number of seeds in primary and secondary branches regulates the recovery of unfilled (chaffy) grains, while the total grain count is correlated with the number of secondary branches. Grain weight is highly correlated with cooked kernel length, grain width is correlated with seed weight, and decorticated grain length is correlated with cooked kernel length. Decorticated seed weight and decorticated grain length show a positive correlation. The time of plant maturity is negatively associated with cooked kernel length, the number of seeds in primary and secondary branches, and decorticated grain length, all of which show strong negative associations. The biological yield of the landraces shows a highly significant positive correlation with leaf area, panicle number, tiller number, seed production in primary branches, seed weight, and the number of total as well as filled grains. The vegetative traits—plant height, stem diameter, number of branches in the stem, and date of maturity—show no significant correlation with the ultimate yield of the rice landraces.

Principle Component Analysis

The principal component analysis of twenty-four traits resulted in eight components with eigen values more than 1 as shown in Figure 1. These eight components contributed 84.78 % of the cumulative variance. The first component accounted the highest variance (20.09%) with second, third and fourth components covered 16.67%, 12.96% and 10.48% respectively shown in Table 3. Figure 2 showed the outlier plot, score plot, loading plot and biplot obtained from first two vectors of Principle Component Analysis (PCA). The outlier plot constructed using Mahalanobis distance showed the distance of the data point and centroid of the multivariate space. In this experiment all the variables were found below the reference line and no outliers were detected in the graph. The outlier plot provides information on fidelity of field experiments. In the score plot the first and the second components showed a random distribution around zero following a normal distribution, but one outlier point is identified in the graph at PC1 (0.736) and PC2 (-0.566). The loading plot was utilized for fast interpretation of the relative weight of each variable in the components. The variables with coefficient close to zero were considered weak in interpretation of the components. The angle between different variables determines the level of correlation between variables. The biplot loads PC scores and the loading values in the same graph and provides a trend for understanding the clustering of variables with identification of outliers (Figure 1).

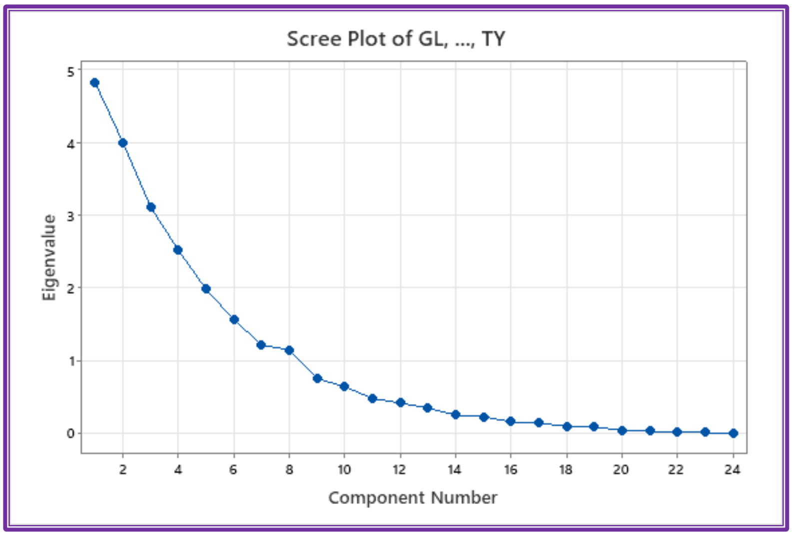

Figure 1: *Scree Plot Analysis of Twenty-Four Parameters in PCA Analysis of Thirty-Six Rice Landraces*

In our study, the number of primary and secondary branches, the number of seeds in primary branches, the total number of grains, the total number of filled grains, and total yield contributed more positively to the explanation of the first principal component (PC1). In contrast, tiller number, panicle number, seed production in secondary branches, chaffy (unfilled) grains, and leaf area contributed moderately to PC1. On the other hand, plant height, date of flowering, cooked kernel breadth, decorticated kernel breadth, stem diameter, and decorticated seed weight negatively contributed to component 1 (PC1). Interestingly, Component 2 (PC2) was mainly explained by agronomic traits, including plant height, date of flowering, time of maturity (days), number of seeds produced in primary branches, and tiller number per plant, all showing positive correlations. Grain length, cooked kernel length, decorticated grain length, decorticated seed weight, and the number of primary branches, as well as leaf area, showed negative associations with PC2. Cooked kernel length, seed weight, panicle number, leaf area, and tiller number exhibited positive associations with component 3 (PC3). PC4 showed a high negative association with important yield traits, such as grain weight and decorticated seed weight. The first four components explain about 60% of the total variation.

Table 4: *Contribution of Different Agro-Morphological Traits Towards Different Components of PCA*

Variable	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8
GL	0.068	-0.395	-0.142	-0.208	0.033	-0.063	0.093	-0.071
GW	-0.067	0.005	-0.050	-0.454	-0.091	-0.028	-0.471	-0.154
CKL	0.011	-0.378	-0.144	-0.079	-0.063	-0.163	-0.211	0.019
CKB	-0.160	-0.002	0.305	-0.196	-0.269	-0.313	0.094	0.321
SW	-0.003	-0.112	0.284	-0.351	-0.274	0.209	-0.179	0.206
DGL	-0.066	-0.374	-0.036	-0.163	0.219	-0.098	0.327	-0.051
DGB	-0.290	0.148	0.043	-0.302	0.001	0.112	0.283	0.127
PH	-0.151	0.228	-0.240	-0.235	-0.020	0.001	0.014	-0.277
DOF	-0.166	0.295	-0.128	-0.153	-0.007	-0.404	0.040	0.035
SD	-0.103	-0.049	-0.075	0.120	-0.516	-0.166	0.034	-0.203
PL	0.064	-0.106	-0.118	0.104	-0.476	-0.186	0.076	-0.377
PN	0.136	0.133	0.432	-0.047	0.144	-0.257	0.005	-0.287
DTM	-0.099	0.345	-0.142	-0.161	-0.091	0.124	0.158	-0.133
DSW	-0.174	-0.178	-0.126	-0.336	0.282	0.022	-0.007	-0.336
NPB	0.228	-0.155	-0.054	0.011	-0.028	-0.383	0.383	0.077
NSB	0.329	0.021	-0.184	0.004	-0.036	-0.149	-0.401	-0.049
NSPB	0.299	0.228	-0.014	0.039	-0.031	0.253	0.162	-0.295
NSSB	0.187	0.167	-0.132	0.029	0.279	-0.305	-0.255	0.241
FG	0.383	0.046	-0.091	-0.169	-0.149	0.140	0.151	0.131
CG	0.234	0.065	-0.222	-0.265	0.156	-0.083	0.154	0.055
TG	0.383	0.058	-0.163	-0.196	-0.094	0.070	0.126	0.104
LA	0.106	-0.270	0.249	0.038	0.101	0.224	-0.020	-0.223
TN	0.115	0.137	0.419	-0.059	0.158	-0.288	0.010	-0.311
TY	0.309	0.019	0.297	-0.276	-0.130	0.083	0.018	0.039

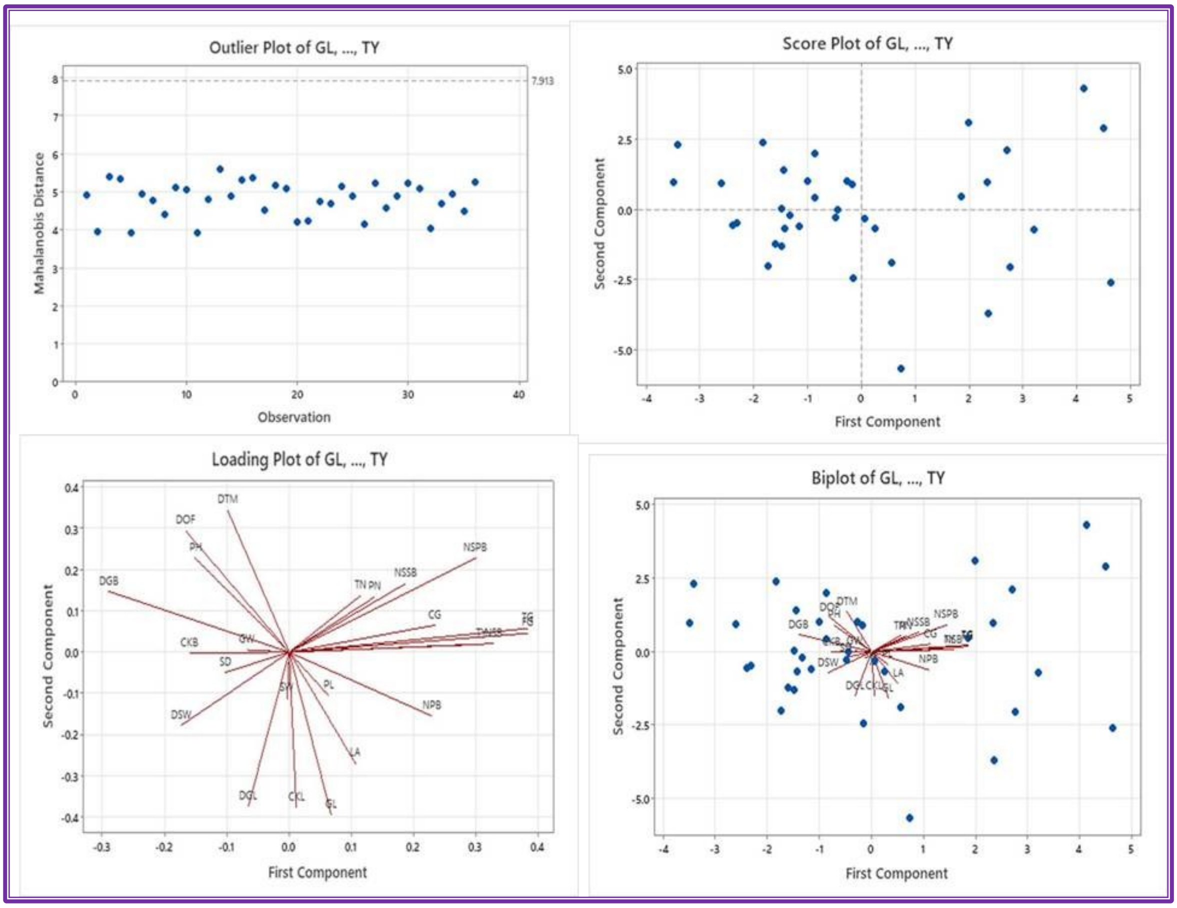

Figure 2: *The Relationship of Twenty-Four Agro-Morphological Traits of Thirty-Six Rice Germplasms Are Exhibited in Outlier Plot, Score Plot, Loading Plot and Biplot*

Discussion

Rice is the most important cereal crop, feeding one-third of the global population. Several scientists are conducting rigorous experiments to improve this miracle cereal. A fascinating study conducted in Assam involving twelve photo-insensitive mutants of fragrant joha rice and two local checks revealed that gamma irradiation could be used to design improved varieties with better agronomic qualities while preserving the unique aroma and cooking attributes (Bhogal *et al.*, 2025). The assessment of the mutants and their progenitor genotypes on sixteen agro-morphological traits identified eight traits as major contributors to the overall genotypic variation. In that study, principal component analysis (PCA) identified spike fertility, harvest index, grain yield per hectare, average panicle weight, filled grains per panicle, and panicle length as key components belonging to PC1, with the greatest contribution to the variation. The first three principal components accounted for 85.16% of the genotypic variation (Table 4). Among the dozen mutants, types JKOJM 250-22-17-120 and JKOJM 250-22-17-40 outperformed one of their parents, Disang, in direct yield-related traits. This study exemplified that agro-morphological traits could play a pivotal role in the selection of superior genotypes in rice.

In a recent study, the agro-morphological variation of 60 traditional landraces from ANDUAT, Kumarganj, and the Ayodhya region of Uttar Pradesh was analyzed using 11 quantitative traits. Principal component analysis showed that the first two components, along with three other component axes with eigenvalues greater than one, accounted for more than 75.11% of the cumulative variance. The study identified days to 50% flowering (DFF), days to maturity (DM), 1000-seed weight, and panicle length as the most effective traits for assessing total variability. Plant height and harvest index were linked to the first principal component (PC1), while DFF and DM made important contributions to PC2. The research confirmed five genotypes out of nineteen varieties with stable mean performance across several yield-related traits, particularly demonstrating high consistency in seed yield per plant (Prakash *et al*., 2024).

In a study conducted with Indonesian pigmented rice accessions using 20 morpho-agronomic characteristics, researchers were able to separate the pigmented genotypes into two distinct clusters (Table 3). The research included 22 accessions, encompassing black, brown, red, and white rice genotypes. One group included all pigmented rice, while the second group contained only two black rice genotypes: one traditional Wojaloka landrace and the other, a black rice variety, IR Ngawi Hitam. PCA analysis revealed that the first two principal components, PC1 and PC2, accounted for 35.93% of the total variability. Tiller color and number, along with leaf color, significantly contributed to the diversity. The second component was primarily influenced by tiller color and the number of total filled grains. The white-grained rice accession Rojolele, with the highest plant height and flag leaf, along with the black genotype Melik from this core collection, produced the highest number of total grains, which is considered the most significant economic parameter. The study also highlighted that Indonesian black rice was more productive than white rice, with a higher panicle number and better plant height. Another striking observation was the distance between two brown rice accessions, Sigupai and HMS 700, which occupied different clusters in the dendrogram. The authors suggested that spontaneous mutation might have played a role in the genetic difference in their origin and trait development. The mini-core collection of pigmented rice included short-duration germplasm such as Sigupai and long-duration types like Berlian. The research underscored the significance of conserving and maintaining germplasm core collections for contemporary rice breeding initiatives, including climate-resilient crop production (Husnah *et al*., 2024).

An interesting study on the agro-morphological and physio-chemical parameters of ninety-eight indigenous aromatic landraces of India highlighted significant variation among the accessions. The study identified panicle length as a major determinant of yield, with a significant positive correlation to pre-cooking kernel length and the length/width ratio of the kernel. Gel consistency of the rice varieties showed a positive association with pre-cooking kernel length but a negative correlation with apparent amylose content. The integration of cooking parameters in varietal analysis directly enriched the research objectives, addressing both industrial needs and consumer acceptability. In our study, we also emphasized several attributes of pre-cooked and post-cooked grains to interpret the performance of the mini-core collection of 36 rice germplasm from West Bengal, India (Dixit *et al*., 2022).

Mulsanti *et al*., 2021 investigated the agro-morphological variation of 103 Indonesian local germplasms using 20 related traits. Principal component analysis showed that the first five component axes, with eigenvalues greater than one, accounted for more than 80% of the cumulative variance (Figure 1). The study highlighted tiller number and vegetative tiller number as important traits, contributing 32.54% of the total variability. The research identified plant height, culm length and diameter, flag leaf width, and panicle length as major contributors to the description of variability. In our study, the contribution of different traits to the analysis of variance showed moderate contributions from several quantitative traits. The number of filled grains, total grains, and the number of primary and secondary branches were important parameters related to variance. Agronomic parameters such as the date of flowering and time of maturity of the rice germplasm also emerged as determining traits.

Rice is the most widely grown and highly consumed staple food in the world. Multiple research studies have highlighted the use of agro-morphological parameters for analyzing rice in various countries around the world (Table 2). A recent study on the variability analysis of rice with agro-morphological characteristics was conducted using an F3 segregating population of rice by Laghari *et al*. (2025), which included 26 distinct rice genotypes. Additionally, the assessment of hybridization-based low methane-emitting genotype development was attempted by another group of researchers (Jin *et al*., 2025). Other notable research includes breeding for thermo-sensitive stress-tolerant lines using CRISPR-Cas9 (Chen *et al*., 2025), augmentation of biotic stress resistance in rice genotypes (Senthilvel *et al*., 2025), performance estimation of upland rice (Izhar & Zakaria, 2025), and the development of highly fragrant rice germplasm (Li *et al*., 2025). Studies on the export potential of rice (Harshitha *et al*., 2023), comparison of aromatic and non-aromatic rice (Aekram *et al*., 2025), alkalinity tolerance at the seedling stage of rice (Ganapati *et al*., 2025), anthocyanin production in black rice (Thilavech *et al*., 2025), and marker-assisted backcross breeding for bacterial blight and blast (Duppala *et al*., 2025) are also significant contributions to the field. Additional research includes screening for salinity tolerance (Anwar *et al*., 2025), performance evaluation of hybrid rice (Fritsche-Neto *et al*., 2023), marker-assisted breeding for submergence tolerance (Anumalla *et al*., 2025), investigation of grain micronutrient content (Moulick *et al*., 2022), analysis of glutinous varieties (Tran *et al*., 2025), biochemical parameters of red rice (Ribeiro-Filho *et al*., 2024), and analysis of indica landraces based on in-vitro digestion and glycemic indices, including cooking variables (Govindaraju *et al*., 2025). These are some of the distinct research studies conducted in the last four years.

Conclusion

In our study, the 36 rice germplasms exhibited several distinct qualities, but above all, they performed well in the low-lying coastal saline region of West Bengal. This mini-core collection of diverse gene-pools is an important asset for rice improvement programs. The aromatic landraces, along with the non-aromatic accessions, could meet diverse consumer demands as well as farmers' needs to overcome challenging situations. In resource-scarce regions, low-input rice could be grown by marginal farmers, while short-duration germplasm could help save fertilizer inputs and water in ideal saline zones and potentially avoid the devastation caused by erratic super-cyclones. Our core collection includes landraces with multiple spikelets, a fascinating trait that could be directly utilized to increase rice yield. The examination of the performance of short, medium, and long-duration rice germplasm in coastal areas could assist farmers in selecting suitable landraces for year-round cultivation. The mini-core collection of rice germplasm maintained at the university is a powerful tool for future rice crop improvement programs.

Conflict of Interest

The authors declare they have no conflict of interest.

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References

Aekram, S., Klinsuk, J., Budtri, N., Sunongbua, P., Somphong, C., & Lertsiriyothin, W. (2025). Differentiation of white rice Khao Dawk Mali 105 (KDML105) from other Thai white rice using FTIR microscope-attenuated total reflectance-focal plane array detector. *Food Research, 9*(1), 282-287. https://doi.org/10.26656/fr.2017.9(1).571

Anumalla, M., Khanna, A., Catolos, M., Ramos, J., Sta. Cruz, M. T., Venkateshwarlu, C., ... & Hussain, W. (2025). Future flooding tolerant rice germplasm: Resilience afforded beyond Sub1A gene. *The Plant Genome, 18*(2), e70040. https://doi.org/10.1002/tpg2.70040

Anwar, A., Tabassum, J., Ahmad, S., Ashfaq, M., Hussain, A., Ullah, M. A., ... & Javed, M. A. (2025). Screening and assessment of genetic diversity of rice (*Oryza sativa* L.) germplasm in response to soil salinity stress at germination stage. *Agronomy, 15*(2), 376. https://doi.org/10.3390/agronomy15020376

Azeez, M. A., Adubi, A. O., & Durodola, F. A. (2018). Landraces and crop genetic improvement. In *Rediscovery of Landraces as a Resource for the Future*. IntechOpen. https://doi.org/10.5772/intechopen.75944

Bhogal, A. S., Sharma, G., Das, B. K., Das, R., Deka, S. D., Sharma, K. K., & Sarma, D. (2025). Morpho-agronomic variability in photoperiod insensitive aromatic Joha rice mutants under late Sali situation in Assam. *Vegetos*, 1-13. https://doi.org/10.1007/s42535-025-01236-8

Cai, X., He, W., Qian, Q., & Shang, L. (2025). Genetic resource utilization in wild rice species: Genomes and gene bank. New Crops, 2, 100065. https://doi.org/10.1016/j.ncrops.2025.100065

Chen, T., Pu, N., Ni, M., Xie, H., Zhao, Z., Hu, J., ... & Wang, H. (2025). Development of Fragrant Thermosensitive Genic Male Sterile Line Rice Using CRISPR/Cas9. *Agronomy*, 15(2), 411. https://doi.org/10.3390/agronomy15020411

Dixit, D., Siddiqui, N., Bollinedi, H., Krishnan, G., Malik, A., Bhowmick, P. K., ... & Singh, A. K. (2022). Assessment of agro-morphological traits, grain physical and physico-chemical properties in the Indian aromatic rice (*Oryza sativa*) germplasm. *Indian Journal of Agricultural Sciences*, 92(9), 1157-1161. https://doi.org/10.56093/ijas.v92i9.124304

Duppala, M. K., Srinivas, T., LV, S. R., Suneetha, Y., Sundaram, R. M., Satyanaryana, P. V., ... & Singh, G. (2025). (2025) Marker-assisted backcross breeding for bacterial blight, blast and tolerance to low soil phosphorus in rice (*Oryza sativa* L.). PREPRINT (Version 1) available at Research Square. https://doi.org/10.21203/rs.3.rs-6286636/v1

Faysal, A. S. M., Ali, L., Azam, M. G., Sarker, U., Ercisli, S., Golokhvast, K. S., & Marc, R. A. (2022). Genetic variability, character association, and path coefficient analysis in transplant Aman rice genotypes. *Plants*, 11(21), 2952. https://doi.org/10.3390/plants11212952

Fritsche-Neto, R., Ali, J., De Asis, E. J., Allahgholipour, M., & Labroo, M. R. (2024). Improving hybrid rice breeding programs via stochastic simulations: number of parents, number of hybrids, tester update, and genomic prediction of hybrid performance. *Theoretical and Applied Genetics*, 137(1), 3. https://doi.org/10.1007/s00122-023-04508-6

Ganapati, R. K., Chen, K., Zhao, X., Zheng, T., Zhang, F., Zhai, L., & Xu, J. (2025). Genome-Wide Association Study and Haplotype Analysis Jointly Identify New Candidate Genes for Alkaline Tolerance at Seedling Stage in Rice. *Rice Science*, 32(4), 537-548. https://doi.org/10.1016/j.rsci.2025.04.006

Govindaraju, I., Das, A. R., Chakraborty, I., Mal, S. S., Sarmah, B., Baruah, V. J., & Mazumder, N. (2025). Investigation of the physicochemical factors affecting the in vitro digestion and glycemic indices of indigenous indica rice cultivars. *Scientific Reports*, 15(1), 2336. https://doi.org/10.1038/s41598-025-85660-5

Harshitha, P., Jeyaprakash, P., Geetha, K., Selvam, S., & Vanniarajan, C. (2023). Genetic analysis of quality traits in non-aromatic rice varieties for export potential. *Electronic Journal of Plant Breeding*, 14(3), 1174-1184. https://doi.org/10.37992/2023.1403.139

Salunkhe, H., Kumar, A., Janeja, H. S., Krishna, B., Talekar, N., Mehandi, S., & Pawar, P. (2024) Genetic variability, correlation and path-coefficient analysis for yield and yield attributing traits in aerobic rice (*Oryza sativa* L.). *Electronic Journal of Plant Breeding*, 15(1), 226-232. https://doi.org/10.37992/2024.1501.026

Husnah, Y. A., Turhadi, T., Safitri, A., & Fatchiyah, F. (2024). Morphoagronomical Evaluation of Several Indonesian Pigmented Rice (*Oryza sativa* L.) Accessions from East Java and Central Java, Indonesia. Plant Breeding and Biotechnology, 12, 122-137. https://doi.org/10.9787/PBB.2024.12.122

Izhar, M., & Zakaria, S. (2025, April). Agronomic performance and productivity of improved landraces rice lines under upland cultivation system. *In IOP Conference Series: Earth and Environmental Science* (Vol. 1476, No. 1, p. 012042). IOP Publishing. https://iopscience.iop.org/article/10.1088/1755-1315/1476/1/012042/meta

Jagadeesh, K., Mahto, C. S., Kumar, N., & Lal, H. C. (2024). Genetic diversity and character association studies for agro-morphological and quality traits of advanced breeding lines in field pea (*Pisum sativum* L.). *Electronic Journal of Plant Breeding*, 15(4), 912-920. https://doi.org/10.37992/2024.1504.098

Jin, Y., Liu, T., Hu, J., Sun, K., Xue, L., Bettembourg, M., ... & Sun, C. (2025). Reducing methane emissions by developing low-fumarate high-ethanol eco-friendly rice. *Molecular Plant*, 18(2), 333-349. https://www.cell.com/molecular-plant/abstract/S1674-2052(25)00029-2

Jing, C. Y., Zhang, F. M., Wang, X. H., Wang, M. X., Zhou, L., Cai, Z., ... & Ge, S. (2023). Multiple domestications of Asian rice. *Nature Plants*, 9(8), 1221-1235. https://doi.org/10.1038/s41477-023-01476-z

Khoury, C. K., Brush, S., Costich, D. E., Curry, H. A., De Haan, S., Engels, J. M., ... & Thormann, I. (2022). Crop genetic erosion: understanding and responding to loss of crop diversity. *New Phytologist*, 233(1), 84-118. https://doi.org/10.1111/nph.17733

Kumar, R. H., Sharma, U., Kumar, B., & Verma, P. (2023). Comparative Analysis of Traditional Scented Rice (*Oryza sativa* L.) Varieties under Organic Cultivation Based on DUS Testing and Yield Assessment. *International Journal of Plant & Soil Science*, 35(18), 1474-1483. https://doi.org/10.9734/ijpss/2023/v35i183415

Laghari, A. A., Ahmad, A., Memon, S., Musavi, S. A. M., Ali, A., Kumar, A., & Guo, Q. (2025). Genetic diversity in F3 segregating populations of rice (*Oryza sativa* L.) genotypes under salt stress. *Frontiers in Plant Science*, 16, 1568859. https://doi.org/10.3389/fpls.2025.1568859

Li, Y., Zhang, W., Li, M., Ling, X., Guo, D., Yang, Y., ... & Wang, J. (2025). Discovery of OsODC as a key enhancer of aroma and development of highly fragrant rice. *Plant Communications*, 6(1). https://www.cell.com/plant-communications/fulltext/S2590-3462(24)00537-6

Mahajan, S., Gupta, S., & Sharma, M. (2023). India vs China: scenario of rice crop. International Journal of Agricultural & Statistical Sciences, 19(2). http://dx.doi.org/10.59467/IJASS.2023.19.629

Maiti, A., Hasan, M. K., Sannigrahi, S., Bar, S., Chakraborti, S., Mahto, S. S., ... & Zhang, Q. (2024). Optimal rainfall threshold for monsoon rice production in India varies across space and time. *Communications Earth & Environment*, 5(1), 302. https://doi.org/10.1038/s43247-024-01414-7

Minitab, LLC. (2025). *Minitab statistical software* (Version 22.1) [Computer software]. https://www.minitab.com/en-us/

Mohanty, S. P., Khan, A., Patra, S., Behera, S., Nayak, A. K., Upadhyaya, S., ... & Sah, R. P. (2025). Unraveling the genetic diversity in selected rice cultivars released in the last 60 years using gene-based yield-related markers. *Genetic Resources and Crop Evolution*, 72(3), 3733-3747. https://doi.org/10.1007/s10722-024-02175-0

Moulick, D., Ghosh, D., Skalicky, M., Gharde, Y., Mazumder, M. K., Choudhury, S., ... & Hossain, A. (2022). Interrelationship among rice grain arsenic, micronutrients content and grain quality attributes: An investigation from genotype× environment perspective. *Frontiers in Environmental Science*, 10, 857629. https://doi.org/10.3389/fenvs.2022.857629

Mulsanti, I. W., Risliawati, A., & Yunani, N. (2021, December). Agro-morphological characterization based genetic diversity of Indonesian local rice germplasm. In IOP Conference Series: Earth and Environmental *Science* (Vol. 948, No. 1, p. 012004). IOP Publishing. .https://iopscience.iop.org/article/10.1088/1755-1315/948/1/012004

Ozturk, O., Jarrett, R., & Kravchuk, O. (2024). Order Restricted Randomized Block Designs. *Journal of Agricultural, Biological and Environmental Statistics*, 29(4), 831-852. https://doi.org/10.1007/s13253-023-00590-x

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

Ribeiro-Filho, N., dos Santos Borges, S. R., de Menezes, P. H., de Oliveira, M. R. T., & da Silva, A. P. G. (2024). Red rice (*Oryza sativa* L.) composition and its water interaction. *Food and Humanity*, 2, 100299. https://doi.org/10.1016/j.foohum.2024.100299

Sarkar, N. S., Kalaimagal, T., Kavithamani, D., Chandirakala, R., Manonmani, S., Raveendran, M., & Senthil, A. (2024). Assessing genetic relationships, trait associations and diversity patterns in sorghum germplasm through correlation, cluster and principle component analysis. *Agricultural Science Digest*, 44(3), 445-452. https://doi.org/10.18805/ag.D-5896

Senthilvel, V., Pelhania, G., Moorthy, G., Sukumar, Y., Rajendran, P. A., Krishnaswamy, S. K., ... & Jegadeesan, R. (2025). Stacking of elite indica rice genotype with bacterial blight, blast, and Brown plant hopper resistance genes through marker assisted selection. *Physiological and Molecular Plant Pathology*, 138, 102730. https://doi.org/10.1016/j.pmpp.2025.102730

Singh, A. K., Lal, K., Singh, V., Tripathy, S., Kumar, A., Singh, N., & Singh, A. (2024). Studies on estimates of heritability and genetic advance for certain quantitative traits in fieldpea (*Pisum sativum* L. var. arvense). *International Journal of Plant & Soil Science*, 36(7), 393-398. https://doi.org/10.9734/ijpss/2024/v36i74744

SPSS Inc. (2009). *PASW Statistics for Windows* (Version 18.0) [Computer software]. https://www.ibm.com/spss

Thilavech, T., Suantawee, T., Chusak, C., Suklaew, P. O., & Adisakwattana, S. (2025). Black rice (*Oryza sativa* L.) and its anthocyanins: mechanisms, food applications, and clinical insights for postprandial glycemic and lipid regulation. Food Production, *Processing and Nutrition*, 7(1), 15. https://doi.org/10.1186/s43014-024-00288-8

Tran, X. H., Tran, T. S., Ho, T., Truong, T. H., Nguyen, D. T., & Nguyen, T. L. (2025). Agro-Morphological Characteristics and Genetic Diversity of Traditional Glutinous Rice Varieties in Quang Ngai Province, Vietnam. *International Journal of Environment, Agriculture and Biotechnology*, 10(1), 592922. https://dx.doi.org/10.22161/ijeab.101.11