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MULTIVARIATE CHARACTERIZATION AND GENETIC DIVERSITY ANALYSIS OF RICE GENOTYPES UNDER TRANSPLANTED CONDITIONS USING PRINCIPAL COMPONENT, PRINCIPAL FACTOR AND HIERARCHICAL CLUSTER ANALYSES

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ABSTRACT

Multivariate characterization and genetic diversity analysis were carried out in rice (*Oryza sativa* L.) genotypes under transplanted conditions to assess the extent and structure of genetic variation and to identify promising genotypes and traits contributing to divergence. The investigation was conducted during *Kharif* 2025 at the Research Farm of Agriculture Research Station, Sakoli, Bhandara, using 51 genotypes derived from 12 crosses along with five checks, viz., Vandana, Samleshwari, MTU-1010, PDKV-Sadhana and Rajeshwari. The experimental material was evaluated in a Randomized Block Design with two replications for nine quantitative characters, namely days to 50% flowering, days to maturity, plant height, number of panicles plant⁻¹, panicle length, number of spikelets panicle⁻¹, spikelet fertility, 1000-grain weight and grain yield plant⁻¹. Analysis of variance revealed highly significant differences among genotypes for all the characters, indicating considerable genetic variability. Principal Component Analysis revealed that the first three components possessed eigenvalues greater than unity and accounted for 67.80% of the total variation, with PC1, PC2 and PC3 contributing 28.19, 20.66 and 18.95%, respectively. Principal Factor Analysis extracted four factors explaining 68.71% of the total variability; flowering and maturity traits predominated PF1, plant height and panicle-associated traits characterized PF2, grain yield plant⁻¹ and 1000-grain weight were prominent in PF3, while number of seeds panicle⁻¹ showed a strong loading on PF4. Hierarchical Cluster Analysis grouped the 56 entries into seven distinct clusters, with Cluster III recording the highest mean grain yield plant⁻¹ (38.35 g), whereas Cluster I showed the highest mean number of panicles plant⁻¹ (8.24). The maximum inter-cluster distance was observed between Clusters II and III (0.354), followed by Clusters V and VI (0.336), indicating substantial genetic divergence. Based on divergent cluster combinations and desirable performance for grain yield plant⁻¹ and number of panicles plant⁻¹, genotypes SKL-19-21-119-206-127-80, SKL-19-23-40-05-26-08, SKL-19-15-134-138-95-60, SKL-18-30-15-18-12 and SKL-19-21-108-105-80-54 were identified as promising and may serve as valuable genetic resources for rice improvement under transplanted cultivation.

Key words : Rice, Genetic diversity, Principal component analysis, Principal factor analysis, Hierarchical cluster analysis, Transplanted condition.

Introduction

Rice (*Oryza sativa* L.) is a major staple cereal and an important component of food security, particularly in Asia. Its productivity is influenced by the genetic

constitution of the cultivar and the production environment. Conventional transplanted cultivation remains an important rice establishment system and evaluation of diverse genotypes under this condition is

essential for identifying superior materials with desirable phenological, morphological and yield attributes. The availability of genetic variability within germplasm provides the foundation for effective selection and development of improved cultivars.

Assessment of genetic diversity based on several interrelated quantitative traits is more informative when multivariate approaches are employed. Principal Component Analysis (PCA) reduces correlated variables into a smaller number of independent components and identifies traits contributing substantially to total variation, whereas Principal Factor Analysis (PFA) helps elucidate groups of associated traits contributing to the underlying variation. Hierarchical Cluster Analysis (HCA) classifies genotypes according to their overall similarity and provides information on genetic divergence that can assist in selecting diverse parents for breeding programmes (Mohammadi and Prasanna, 2003).

Multivariate analysis has demonstrated considerable utility in rice germplasm characterization under contrasting establishment systems. Rudresh *et al.* (2021) evaluated 600 rice germplasm lines under dry-seeded, wet-seeded and transplanted conditions and reported that the first three principal components explained 76.54, 78.07 and 80.05% of the total divergence, respectively. Their study also demonstrated differential clustering of genotypes across establishment systems, emphasizing the importance of evaluating genetic diversity under the

intended production environment.

Therefore, the present study was undertaken to characterize the genetic diversity among rice genotypes under transplanted conditions through Principal Component Analysis, Principal Factor Analysis and Hierarchical Cluster Analysis, with emphasis on identifying the major traits contributing to genetic variation, understanding relationships among genotypes and recognizing promising and genetically divergent genotypes for their potential utilization in rice improvement programmes.

Materials and Methods

Research details

The present investigation was conducted during *Kharif* 2025 at the Research Farm of Agriculture Research Station, Sakoli, District Bhandara, Maharashtra, India, to assess genetic diversity among rice (*Oryza sativa* L.) genotypes under transplanted conditions. The experimental material comprised 51 genotypes derived from 12 crosses along with five checks, viz., Vandana, Samleshwari, MTU-1010, PDKV-Sadhana and Rajeshwari, obtained from Agriculture Research Station, Sakoli. The experiment was laid out in a Randomized Block Design (RBD) with two replications. Each entry was accommodated in a plot of 3.0 m × 1.5 m with a spacing of 20 cm × 15 cm. Transplanting was carried out on 30 June 2025 and recommended agronomic practices

Table 1 : Experimental material comprising rice genotypes and checks evaluated under transplanted conditions.

S. no.	Genotypes	S. no.	Genotypes	S. no.	Genotypes
1	SKL-19-16-22-12-18-06	20	SKL-19-14-45-74-134-70	39	SKL-19-21-108-105-80-54
2	SKL-19-16-49-46-88-50	21	SKL-19-06-35-101-84-108	40	SKL-19-21-108-105-80-60
3	SKL-19-16-22-18-34-18	22	SKL-19-04-64-17-28-24	41	SKL-19-21-108-127-88-68
4	SKL-19-16-120-100-102-97S	23	SKL-19-04-103-225-108-90	42	SKL-19-21-108-186-108-75
5	KL-19-19-118-51-30-43	24	SKL-19-02-68-112-69-50	43	SKL-19-21-119-206-127-80
6	SKL-19-19-118-51-30-50	25	SKL-19-02-77-221-98-78	44	SKL-19-21-119-206-127-88
7	SKL-19-19-124-154-30-58	26	SKL-19-02-80-238-72-99	45	SKL-19-23-40-05-26-08
8	SKL-19-18-30-15-18-12	27	SKL-19-12-35-48-48-50	46	SKL-19-23-40-05-26-15
9	SKL-19-18-30-42-34-48	28	SKL-19-12-35-48-60-64	47	SKL-19-23-142-40-34-30
10	SKL-19-18-45-60-44-60	29	SKL-19-12-40-112-126-110	48	SKL-19-23-142-40-34-37
11	SKL-19-18-45-60-44-78	30	SKL-19-11-65-01-05-14	49	SKL-19-23-100-82-50-80
12	SKL-19-15-40-32-12-15	31	SKL-19-11-65-01-18-33	50	SKL-19-23-100-82-50-84
13	SKL-19-15-40-32-12-28	32	SKL-19-11-65-42-35-49	51	SKL-19-23-100-98-74-90
14	SKL-19-15-40-32-34-35	33	SKL-19-11-180-56-50-68	52	Vandana
15	SKL-19-15-107-100-58-48	34	SKL-19-11-180-111-67-84	53	Samleshwari
16	SKL-19-15-134-138-95-60	35	SKL-19-11-194-116-89-99	54	MTU-1010
17	SKL-19-14-30-15-18-12	36	SKL-19-21-21-08-35-28	55	PDKV Sadhana
18	SKL-19-14-30-42-90-48	37	SKL-19-21-21-08-35-38	56	Rajeshwari
19	SKL-19-14-45-60-120-60	38	SKL-19-21-32-42-45-48		

Source: Agriculture Research Station, Sakoli, District Bhandara, Maharashtra, India.

and plant-protection measures were followed throughout the crop period.

Study of traits

Ten plants per genotype and five plants per check were considered for recording observations. Observations were recorded on nine quantitative characters, namely days to 50% flowering, days to maturity, plant height (cm), number of panicles plant⁻¹, panicle length (cm), number of spikelets panicle⁻¹, spikelet fertility (%), 1000-grain weight (g) and grain yield plant⁻¹ (g).

Statistical analysis

Analysis of variance was performed according to the procedure described by Panse and Sukhatme (1985). Principal Component Analysis (PCA) and Hierarchical Cluster Analysis (HCA) were carried out using R software version 4.4.1 (R Core Team, Vienna, Austria) with the packages FactoMineR, factoextra, cluster and dendextend. Principal Factor Analysis (PFA) with varimax rotation was performed using XLSTAT 2024.1 (Addinsoft, Paris, France). Principal components with eigenvalues greater than one were retained according to the Kaiser criterion. Genetic divergence among the genotypes was estimated using Euclidean distances and clustering was performed by Ward's minimum variance method.

Results and Discussion

Analysis of variance (ANOVA)

The analysis of variance demonstrated highly significant genotypic differences for all nine quantitative characters among the 56 entries evaluated under

transplanted conditions (Table 2). The recorded genotype mean squares were 324.197 for days to 50% flowering, 316.240 for days to maturity, 95.547 for plant height, 0.824 for number of panicles plant⁻¹, 6.883 for panicle length, 651.127 for number of spikelets panicle⁻¹, 3.811 for spikelet fertility, 28.037 for 1000-grain weight and 77.051 for grain yield plant⁻¹. The significant variation across all characters indicates that the experimental material possessed sufficient diversity for subsequent multivariate characterization and identification of useful genotypes. Comparable genotypic variation for important agronomic traits in rice germplasm has been reported by Rudresh *et al.* (2021), Thakur and Sarma (2023) and Gayathridevi *et al.* (2023).

Principal Component analysis

Principal Component Analysis (PCA) provides a useful way of interpreting multivariate data by transforming several interrelated variables into a smaller set of independent components. Each component represents a particular proportion of the variation present in the original dataset, thereby helping to identify the traits that contribute most strongly to differences among genotypes. In crop genetic-diversity studies, PCA can consequently assist in summarizing complex trait relationships and recognizing genetically contrasting material for breeding purposes (Mohammadi and Prasanna, 2003).

The PCA results showed that three components had eigenvalues exceeding one and collectively percent variability represented 67.80% of the total variation present

Table 2 : Analysis of variance for different quantitative characters in rice.

Source of variation	df	DF	DM	PH	NPP	PL	NSP	SF	TW	GYP
Replication	1	7.00	5.14	2.17	0.28	0.58	191.57	7.40	0.0008	1.52
Treatment	55	324.19**	316.24**	95.54**	0.82**	6.88**	651.12**	3.81**	28.03**	77.05**
Error	55	2.61	1.59	35.36	0.42	0.55	108.61	1.98	0.043	12.04

*, ** Significant at 5 and 1 per cent level of significance, respectively; DF: Days to flowering; DM: Days to maturity; PH: Plant height; NPP: Number of Panicles per plant; PL: Panicle Length; NSP: Number of Spiklets per panicle; SF: Spiklet fertility; 100TW: 1000 test weight; GYP: Grain yield per plant.

Table 3 : Total variance of different principal components for transplanted condition.

Principal Component	Eigen Value	Percent Variability	Cumulative % Variability
PC1	2.537	28.193	28.193
PC2	1.859	20.657	48.85
PC3	1.705	18.945	67.795
PC4	0.96	10.67	78.465
PC5	0.919	10.214	88.679

in the experimental material (Table 2). The contribution of PC1 was highest, with an eigenvalue of 2.537 and percent variability 28.19% contribution, followed by PC2 with an eigenvalue of 1.859 and variability 20.66%, and PC3 with an eigenvalue of 1.705 and variability 18.95% (Fig. 1). Since the remaining components possessed eigenvalues below unity, the first three components were retained under the Kaiser criterion. Thus, a substantial part of the variability among the genotypes could be represented through three principal dimensions. Similar

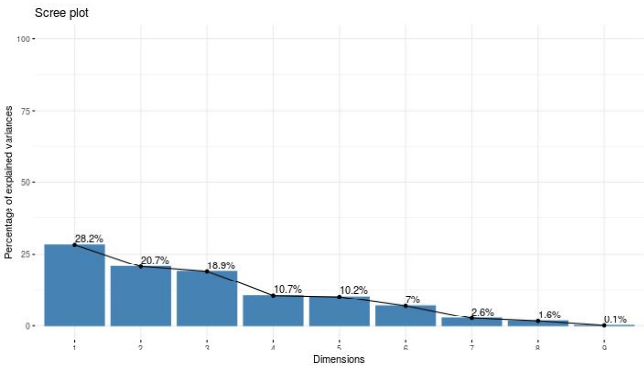


Fig. 1 : Screen plot showing Principal Components and percentage of variation.

effectiveness of PCA in summarizing complex variation in rice germplasm has been reported by Rudresh *et al.* (2021), Sar and Kole (2023) and Meena *et al.* (2023).

The distribution of the genotypes in the PCA biplot based on PC1 and PC2 demonstrated considerable dispersion, with the 56 entries occupying all four quadrants. Together, PC1 and PC2 accounted for 48.85% of the total variation (Fig. 2). Although, several entries were positioned near the centroid, entries 12, 35, 36, 44, 48, 49, 51, 53 and 56 were located comparatively farther away, indicating distinctive multivariate profiles. The separation observed in the PCA space suggests differences in the combined expression of the quantitative characters and provides a visual basis for recognizing relatively distinct genotypes. Comparable applications of PCA for discriminating rice germplasm based on multiple morphological attributes have been reported by Panika *et al.* (2023) and Thakur and Sarma (2023).

Principal Factor analysis

Principal Factor Analysis (PFA) is a multivariate approach that summarizes relationships among several interrelated characters into a smaller number of latent factors. These factors represent common patterns of variation among the original traits and help in identifying groups of characters that contribute to differences among genotypes. In crop diversity studies, factor analysis can therefore provide additional information on the structure of variation that may not be evident from individual-character analysis alone (Murty and Arunachalam, 1967).

The factor analysis resulted in four factors with eigenvalues greater than one, together accounting for 68.71% of the total variation (Table 4). PF1 contributed the largest proportion (24.62%) with an eigenvalue of 2.216, followed by PF2 (17.01%; 1.531), PF3 (14.10%; 1.269) and PF4 (12.98%; 1.168). The loading pattern indicated that PF1 was mainly represented by days to 50% flowering (1.031) and days to maturity (1.017). Plant

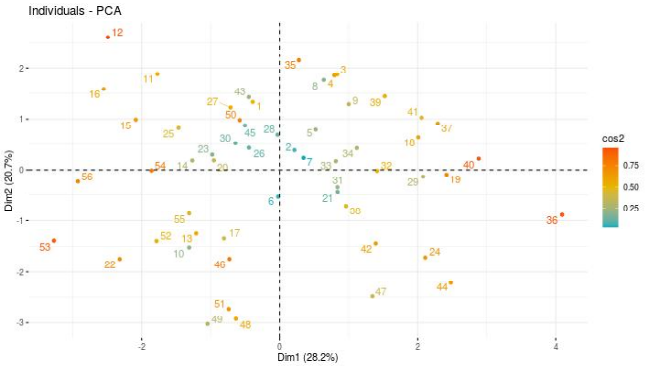


Fig. 2 : Distribution of rice genotypes on the first two principal component (PC1 and PC2) under transplanted condition.

height (1.000) and panicle length (0.697) were prominent in PF2, while grain yield plant⁻¹ (0.891) and 1000-grain weight (0.611) contributed strongly to PF3. PF4 was primarily associated with number of seeds panicle⁻¹ (0.970) and spikelet fertility (0.241). The prominence of phenological, architectural and productivity-related traits in the extracted factors is comparable with observations

Table 4 : Factor loadings of characters with respect to different principal factors (varimax rotation).

Trait	Factor 1	Factor 2	Factor 3	Factor 4
Days to 50% flowering	1.031	0.012	0.046	-0.061
Days to maturity	1.017	0.024	0.030	-0.044
Plant height (cm)	0.090	1.000	-0.062	0.060
Panicle length (cm)	-0.191	0.697	0.112	-0.135
Number of panicles plant ⁻¹	0.173	0.176	0.053	0.085
Grain Yield plant ⁻¹ (g)	0.131	0.010	0.891	0.362
Test Seed weight (g)	-0.103	-0.093	0.611	-0.068
Number of seeds panicle ⁻¹	-0.123	0.017	0.165	0.970
Seed fertility (%)	0.059	0.066	-0.228	0.241

Parameter	Factor 1	Factor 2	Factor 3	Factor 4
SS Loadings (eigenvalue)	2.216	1.531	1.269	1.168
Proportion of variance	0.246	0.17	0.141	0.13
Variance explained (%)	24.62	17.01	14.1	12.98
Cumulative variance (%)	24.62	41.63	55.73	68.71

Hypothesis Tested	Chi-square (χ ²)	df	P-value	Hypothesis Tested
H ₀ : Four factors are sufficient	9.362	6	0.154	H ₀ :Four factors are sufficient

Table 5 : Grouping of rice genotypes into different clusters in transplanted condition.

Cluster	No. of rice genotypes	Name of rice genotypes
I	16	SKL-19-21-32-42-45-48, SKL-19-21-108-186-108-75, SKL- 19-11-65-01-18-33, SKL- 19-11-180-56-50-68, SKL- 19-11-180-111-67-84, SKL- 19-11-65-42-35-49, SKL-19-16-49-46-88-50, SKL-19-21-108-105-80-54, SKL-19-16-22-18-34-18, SKL- 19-12-35-48-60-64, SKL-19-12-35-48-48-50, SKL-19-02-80-238-72-99, SKL-19-21-119-206-127-80, SKL- 19-11-194-116-89-99, SKL-19-23-100-82-50-84, SKL-19-16-22-12-18-06
II	10	SKL-19-21-119-206-127-88, SKL- 19-12-40-112-126-110, SKL-19-21-21-08-35-28, SKL-19-21-108-127-88-68, SKL-19-21-108-105-80-60, SKL-19-14-45-60-120-60, SKL-19-02-68-112-69-50, SKL-19-06-35-101-84-108, SKL-19-21-21-08-35-38, SKL-19-14-30-42-90-48
III	7	SKL-19-23-40-05-26-08, SKL-19-11-65-01-05-14, SKL-19-15-134-138-95-60, SKL-19-15-107-100-58-48, SKL-19-02-77-221-98-78, SKL-19-15-40-32-12-15, SKL-19-18-45-60-44-78
IV	9	MTU-1010, Rajeshwari, Samleshwari, PDKV – Sadhana, Vandana, SKL-19-04-103-225-108-90, SKL-19-04-64-17-28-24, SKL-19-15- 40-32-34-35, SKL-19-15- 40-32-12-28
V	5	SKL-19-18-30-15-18-12, SKL-19-18-30-42-34-48, SKL-19-19-124-154-30-58, SKL-19-19-118-51-30-43, SKL-19-16-120-100-102-97
VI	5	SKL-19-23-142-40-34-30, SKL-19-23-100-98-74-90, SKL-19-23-100-82-50-80, SKL-19-23-142-40-34-37, SKL-19-23-40-05-26-15
VII	4	SKL-19-14-30-15-18-12, SKL-19-18-45-60-44-60, SKL-19-14-45-74-134-70, SKL-19-19-118-51-30-50

Table 6 : Cluster-wise Mean performance of Rice genotypes for Nine quantitative traits.

Cluster	Days to 50 % flowering	Days to maturity	Plant height (cm)	No. of panicles plant ⁻¹	Panicle length (cm)	No. of spikelet Panicle ⁻¹	Spikelet fertility (%)	1000 Grain weight (g)	Grain yield plant ⁻¹ (g)
I	101.37	131.65	119.99	8.24	23.56	166.93	87.16	20.29	31.35
II	114.55	144.75	120.83	7.86	21.72	145.70	87.15	19.35	25.54
III	87.78	118.50	119.25	7.97	23.62	180.26	86.38	23.31	38.35
IV	79.61	110.27	117.34	7.86	23.42	149.08	86.84	24.93	29.98
V	98.70	129.60	105.63	8.13	19.62	169.75	87.52	22.63	32.20
VI	84.80	115.20	116.23	8.05	23.77	134.59	85.09	17.01	22.03
VII	89.50	119.25	113.33	6.87	23.25	155.92	86.93	21.27	28.39
S.D.	11.894	11.824	4.867	0.454	1.527	15.783	0.800	2.653	5.193
Variance	141.488	139.812	23.688	0.206	2.333	249.08	0.640	7.041	26.97

from earlier multivariate investigations in rice reported by Naik *et al.* (2022), Thakur and Sarma (2023) and Gayathridevi *et al.* (2023).

The adequacy of the extracted factor structure was indicated by the non-significant chi-square statistic ($\chi^2 = 9.362$; $P = 0.154$). The four factors consequently provided a simplified representation of the relationships among the nine characters, broadly reflecting phenological behaviour, plant and panicle attributes, productivity and grain-weight characteristics, and seed-development traits. Such reduction of correlated characters into a limited number of interpretable factors demonstrates the usefulness of factor analysis for understanding the underlying structure of variation in complex germplasm collections. Similar

applications of multivariate approaches for interpreting correlated characters in rice have been reported by Meena *et al.* (2023) and Gayathridevi *et al.* (2023).

Hierarchical Cluster Analysis and genetic divergence

Hierarchical Cluster Analysis (HCA) is a multivariate classification technique that organizes genotypes into groups according to their overall similarity across several characters. It progressively forms clusters based on a measure of distance or similarity, allowing genetically similar entries to be grouped together, while divergent groups can be identified. In plant genetic-diversity studies, HCA is useful for understanding relationships among

Table 7 : Average Intra- and Inter-Cluster Distances among Rice Genotypes.

Cluster	I	II	III	IV	V	VI	VII
I	(0.146)	0.227	0.226	0.245	0.205	0.280	0.204
II		(0.186)	0.354	0.321	0.262	0.310	0.276
III			(0.185)	0.219	0.260	0.309	0.224
IV				(0.152)	0.259	0.244	0.186
V					(0.128)	0.336	0.218
VI						(0.203)	0.221
VII							(0.155)

(Note: $\bar{D} = 0.256$)

genotypes and for selecting contrasting material for breeding programmes (Sneath and Sokal, 1973).

The hierarchical clustering procedure separated the 56 entries into seven clusters, confirming the presence of substantial multivariate differentiation within the material (Fig. 3). Cluster I comprised sixteen genotypes, followed by Cluster II with ten, Cluster III with seven, Cluster IV with nine, Clusters V and VI with five each, and Cluster VII with four entries. The five checks-MTU-1010, Rajeshwari, Samleshwari, PDKV-Sadhana and

Vandana-were placed together in Cluster IV along with four genotypes, reflecting comparatively similar overall performance across the characters considered (Table 5). Distinct grouping of rice germplasm based on multiple agro-morphological attributes has also been documented by Panika *et al.* (2023), Sar and Kole (2023) and Akhtar *et al.* (2022).

The cluster-wise mean performance revealed distinct differences among the seven clusters for all the nine quantitative characters under transplanted conditions (Table 6). Cluster II exhibited the highest mean values for days to 50% flowering (114.55 days), days to maturity (144.75 days) and plant height (120.83 cm), whereas Cluster I recorded the highest mean number of panicles plant⁻¹ (8.24). The longest mean panicle was observed in Cluster VI (23.77 cm), while Cluster III showed the highest mean number of spikelets panicle⁻¹ (180.26) and grain yield plant⁻¹ (38.35 g). Cluster V possessed the highest mean spikelet fertility (87.52%), whereas the maximum mean 1000-

Table 8 : Selected rice genotypes on the basis of average inter cluster distance for grain yield plant⁻¹ and number of panicles plant⁻¹ under transplanted condition.

S. no.	Clusters	Distance between clusters	Genotypes (Selection based on)	
			Genotypes selected for grain yield plant ⁻¹	Genotypes selected for number of panicles plant ⁻¹
1	II-III	0.354	SKL-19-21-108-105-80-54, SKL-19-23-40-05-26-08	SKL-19-21-108-105-80-54, SKL-19-15-134-138-95-60
2	V-VI	0.336	SKL-19-16-120-100-102-97, SKL-19-23-100-82-50-84	SKL-19-18-30-15-18-12, SKL-19-23-142-40-34-30
3	II-IV	0.321	SKL-19-21-108-105-80-54, SKL-19-04-103-225-108-90	SKL-19-21-108-105-80-54, SKL-19-15-40-32-34-35
4	II-VI	0.310	SKL-19-21-108-105-80-54, SKL-19-23-100-82-50-84	SKL-19-21-108-105-80-54, SKL-19-23-142-40-34-30
5	III-VI	0.309	SKL-19-23-40-05-26-08, SKL-19-23-100-82-50-84	SKL-19-15-134-138-95-60, SKL-19-23-142-40-34-30
6	I-VI	0.280	SKL-19-21-119-206-127-80, SKL-19-23-100-82-50-84	SKL-19-21-108-186-108-75, SKL-19-23-142-40-34-30
7	II-VII	0.276	SKL-19-21-108-105-80-54, SKL-19-14-45-74-134-70	SKL-19-21-108-105-80-54, SKL-19-19-118-51-30-50
8	II-V	0.262	SKL-19-21-108-105-80-54, SKL-19-16-120-100-102-97	SKL-19-21-108-105-80-54, SKL-19-18-30-15-18-12
9	III-V	0.260	SKL-19-23-40-05-26-08, SKL-19-16-120-100-102-97	SKL-19-15-134-138-95-60, SKL-19-18-30-15-18-12
10	IV-V	0.259	SKL-19-04-103-225-108-90, SKL-19-16-120-100-102-97	SKL-19-15-40-32-34-35, SKL-19-18-30-15-18-12

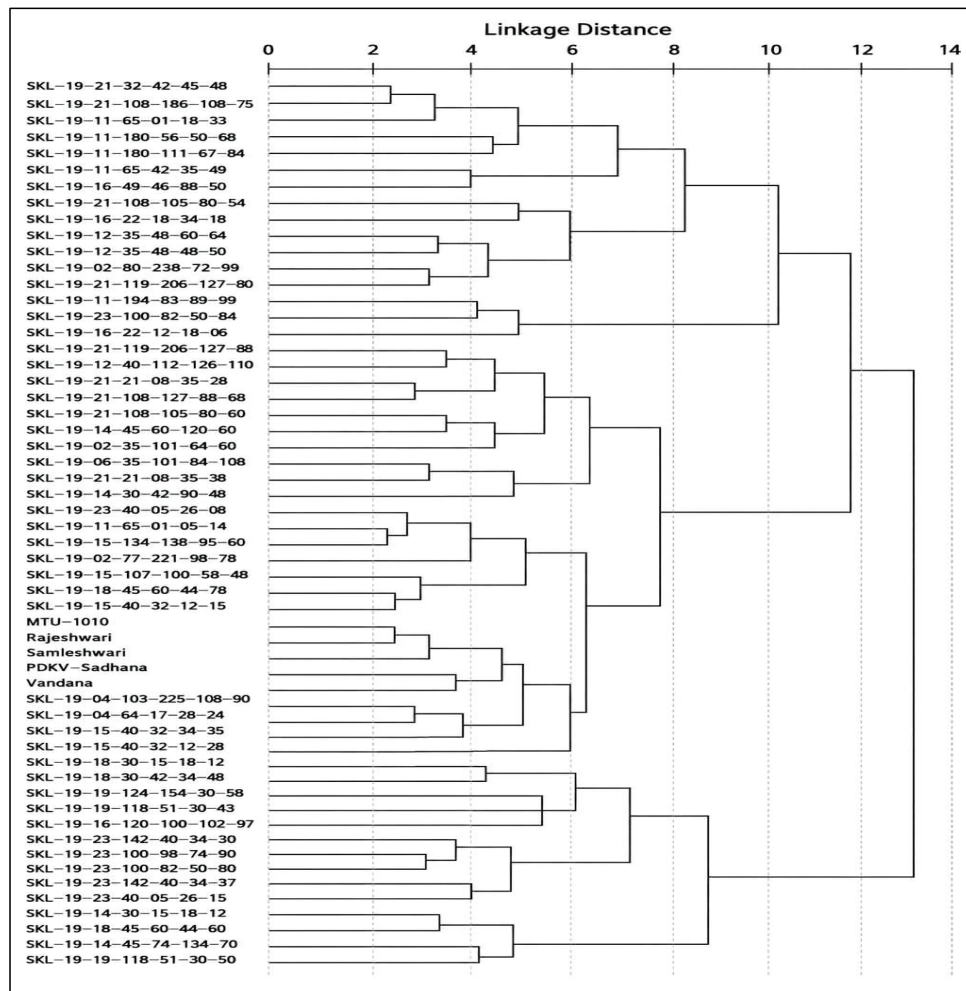


Fig. 3 : Dendrogram showing the clustering pattern of rice genotypes in transplanted condition.

grain weight was recorded in Cluster IV (24.93 g). In contrast, Cluster IV exhibited the lowest mean values for days to 50% flowering (79.61 days) and days to maturity (110.27 days), while Cluster VII recorded the lowest mean number of panicles plant⁻¹ (6.87). The lowest mean plant height was observed in Cluster V (105.63 cm), whereas Cluster VI showed the lowest mean 1000-grain weight (17.01 g) and Cluster VI also recorded the lowest mean grain yield plant⁻¹ (22.03 g). Among the characters, the highest variance among cluster means was observed for number of spikelets panicle⁻¹ (249.08), followed by days to 50% flowering (141.488), days to maturity (139.812) and grain yield plant⁻¹ (26.97), indicating their greater contribution to differentiation among clusters. Conversely, number of panicles plant⁻¹ exhibited the lowest variance (0.206), suggesting comparatively narrow differences among clusters for this trait. Overall, the contrasting cluster profiles demonstrated considerable diversity for phenological, morphological, reproductive and yield-associated traits among the rice genotypes evaluated under transplanted conditions.

Marked differences were observed among the clusters in terms of inter-cluster distance (Table 7). The greatest distance occurred between Clusters II and III (0.354), followed by Clusters V and VI (0.336), II and IV (0.321), II and VI (0.310) and III and VI (0.309). In contrast, Clusters IV and VII showed the smallest distance (0.186). The greater separation between Clusters II and III indicates a stronger contrast in their multivariate character composition, whereas the smaller distance between Clusters IV and VII suggests comparatively closer relationships. Such information is useful when choosing genetically contrasting parents, particularly when divergence is considered together with desirable agronomic attributes. Similar use of inter-cluster divergence for parental selection in rice has been reported by Panika *et al.* (2023), Thakur and Sarma (2023) and Mohanty *et al.* (2023).

The comparison of divergent cluster combinations provided a basis for identifying genotypes with desirable grain yield plant⁻¹ and number of panicles plant⁻¹ under transplanted conditions (Table 8). The II–III cluster

combination showed the highest inter-cluster distance (0.354), from which SKL-19-21-108-105-80-54 and SKL-19-23-40-05-26-08 were selected for grain yield plant⁻¹, while SKL-19-21-108-105-80-54 and SKL-19-15-134-138-95-60 were selected for number of panicles plant⁻¹. The V–VI combination (0.336) ranked second and contributed SKL-19-16-120-100-102-97 and SKL-19-23-100-82-50-84 for grain yield, together with SKL-19-18-30-15-18-12 and SKL-19-23-142-40-34-30 for panicle number. Other relatively divergent combinations included II–IV (0.321), II–VI (0.310) and III–VI (0.309). Notably, SKL-19-21-108-105-80-54 occurred repeatedly among the divergent combinations for both selection criteria, whereas SKL-19-23-40-05-26-08 and SKL-19-23-100-82-50-84 were repeatedly identified for grain yield plant⁻¹. The occurrence of desirable genotypes within widely separated clusters indicates their potential value for breeding programmes in which genetic divergence is considered together with agronomic merit. Similar approaches have been reported in rice, where genotypes belonging to highly divergent clusters were suggested for use as parents to generate wider and potentially useful segregating variation (Panika *et al.*, 2023; Hema Sai *et al.*, 2022; Bhoite *et al.*, 2023).

Conclusion

Considering the divergence among clusters together with the selection criteria of grain yield plant⁻¹ and number of panicles plant⁻¹, five genotypes were identified as particularly promising: genotypes SKL-19-21-119-206-127-80, SKL-19-23-40-05-26-08, SKL-19-15-134-138-95-60, SKL-18-30-15-18-12 and SKL-19-21-108-105-80-54. These entries represented desirable material within the divergent cluster combinations considered for selection. The maximum separation between Clusters II and III (0.354) and the next highest distance between Clusters V and VI (0.336) provide useful evidence for considering genotypes from these groups in future breeding programmes. The identification of superior genotypes in combination with genetic divergence is consistent with the approach adopted in rice diversity studies by Rudresh *et al.* (2021), Panika *et al.* (2023), Meena *et al.* (2023), Sar and Kole (2023) and Mohanty *et al.* (2023).

Taken together, PCA, PFA and HCA provided complementary descriptions of genetic diversity in the transplanted rice material. PCA condensed the total variation into a few major dimensions, PFA clarified the groups of characters associated with the principal sources of variation and HCA separated the entries according to their overall multivariate resemblance. The identification

of five promising genotypes from the divergent groups demonstrates the usefulness of integrating these analytical approaches for rice germplasm characterization and parental selection. Similar complementary application of multivariate techniques for rice diversity assessment has been reported by Rudresh *et al.* (2021), Panika *et al.* (2023), Gayathridevi *et al.* (2023) and Meena *et al.* (2023).

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