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Uniqueness of Traditional Rice Cultivars of Kerala Revealed by Diversity Analysis

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ABSTRACT

Background: Farmer-maintained traditional rice landraces represent vital germplasm reservoirs for genetic enhancement programs. These genotypes often harbor adaptive traits conferring tolerance to diverse abiotic and biotic stressors. Comprehensive characterization and evaluation of such genetic resources are imperative for their effective utilization in rice improvement strategies aimed at developing resilient and high-yielding cultivars.

Methods: In this present study, seventy traditional rice landraces were assessed and classified using cluster analysis, which enabled the grouping of genotypes into distinct clusters based on their phenotypic and genetic similarities. The evaluated rice genotypes exhibited substantial variability across several agronomic traits, indicating significant potential for utilization in crop improvement programs. Genetic divergence analysis using Mahalanobis' D^2 statistics facilitated the categorization of genotypes into distinct clusters. The insights derived from this clustering approach can streamline the breeder's efforts by reducing the time needed to screen extensive germplasm collections for promising breeding material. Moreover, the identified clusters serve as a valuable resource for selecting suitable donor parents in the development of drought-tolerant rice genotypes.

Result: The seventy rice genotypes were classified into ten distinct clusters, with Cluster I comprising the majority, encompassing 61 genotypes. In contrast, each of the remaining clusters (Clusters II to X) was monogenic, containing a single genotype each. The study revealed nine cultivars namely Kokkan, Njavara Manja, Thekkan, Kadamkudy Kuruka, Karinellu, Nooranvella, Gandhakashala, Oorkayama and Thekkan chitteni formed individual clusters indicating their uniqueness.

Key words: Cluster analysis, Crop improvement, Genetic diversity, Traditional rice landraces.

INTRODUCTION

Rice genetic resources form a fundamental component of breeding programs, with farmers playing a crucial role in enhancing rice diversity through the selection, cultivation, and preservation of numerous traditional varieties over generations (Bellon *et al.,* 1997). This extensive reservoir of rice germplasm, comprising landraces and indigenous varieties, provides a rich source of beneficial alleles for the development of improved cultivars. These genetic materials serve as the cornerstone for rice improvement initiatives, offering traits essential for the advancement of high-performing and resilient varieties (Caldo *et al.,* 1996). The contribution of landraces to modern rice breeding is well documented. For instance, IR8, known as the "miracle rice" was derived from a cross between two traditional varieties: the semi-dwarf Dee-geo-woo-gen and the tall, vigorous Peta (Hargrove and Coffman, 2006; Ronald, 2012). The SUB1 QTL, conferring submergence tolerance, was discovered in the landrace FR13A and successfully introgressed into popular high-yielding varieties (Bailey *et al.,* 2010). More recently, the *NAL1* allele identified in the tropical *Japonica* landrace Daringan has been shown to significantly enhance yield potential when introduced into elite cultivars (Fujita *et al.,* 2013).

The evaluation and characterization of rice germplasm significantly enhance its potential application in breeding programs. Among various methods, the analysis of agro-morphological traits remains the most widely adopted strategy for determining genetic relationships among genotypes (Bajracharya *et al.,* 2006). This phenotypic approach has been effectively employed to assess genetic diversity in ancestral lines of improved rice cultivars in the Philippines (Caldo *et al.,* 1996), traditional rice varieties in Yunnan, China (Yawen *et al.,* 2003) and landraces in Nepal (Bajracharya *et al.,* 2006). The conservation and detailed characterization of these genetic resources are imperative not only to safeguard them for future use but also to facilitate their effective deployment in crop improvement programs targeting enhanced yield and resilience to biotic and abiotic

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Table 1: List of rice landraces used for the phytochemical profiling.

Sl. no.	Name of landraces
1.	Chenthadi
2.	Chettadi
3.	Cheruvellari
4.	Chuvanna Vellikannan
5.	Karutha Chitteni
6.	Kokkan
7.	Kuttadan
8.	Mullanchanna
9.	Mundakakutty
10.	Punchakayama
11.	Athikkirai
12.	Kariyadukkan
13.	Kavugin Poothoola
14.	Kalyanikutty
15.	Karutha Njavara
16.	Kothambarikayama
17.	Mattachembavu
18.	Neicheera
19.	Njavara Manja
20.	Nooranvella
21.	PTB-7
22.	PTB-16
23.	PTB-31
24.	PTB-33
25.	PTB-34
26.	Vellathondi
27.	Anakodan
28.	Chellaam Chettivirippu
29.	Chettivirippu
30.	Cheruvirippu
31.	Ezhupunna Pokkali
32.	Kadamkudy Kuruka
33.	Kadamkudy Pokkali
34.	Krishnakaomodha
35.	Kuthiru
36.	Nayarambalam Pokkali
37.	Oorkayama
38.	Ponkuruka
39.	Pokkali
40.	Rakthashali
41.	Traditional Virippu
42.	Varapuzha Pokkali
43.	Vyttila Kuruka
44.	Kunju Kunju
45.	Valichoori
46.	Kannan Kulamban
47.	Paalthondi
48.	Vellari
49.	Oorpandi
50.	Kodukanni
51.	Ittikandan
52.	Thavalakannan
53.	Thekkan Cheera
54.	Kanali
55.	Vadakkan Vellarikayama
56.	Marathoni
57.	Chuvanna Chitteni
58.	Thekkan Chitteni
59.	Kochuvittu
60.	Mullanchayama
61.	Karinellu
62.	Karutha Kuruka
63.	Eravapandy
64.	Thekkan
65.	Gandhakashala
66.	Jeerakashala
67.	Orthadian
68.	Karuthacheera
69.	Vellamundakan
70.	Veluthakattamodan

Table 1: Continue....

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stresses. Assessing the genetic diversity within these germplasm materials is crucial for elucidating their variability and informing their strategic use in breeding efforts.

This study evaluated the phenotypic variation among farmers' rice varieties conserved in research stations. The phenotypic data generated can serve as a foundation for future germplasm collection missions aimed at enriching gene bank diversity and provide essential baseline information to support their effective utilization in rice breeding initiatives.

Cluster analysis serves as an effective tool for examining genetic diversity, facilitating the formation of core subsets by categorizing accessions with similar traits into homogeneous groups. This method enhances the understanding of genetic relationships by summarizing kinship information through the grouping of phenotypically or genetically similar genotypes (Ulaganathan *et al.,* 2015). The current investigation aimed to perform a classification of traditional rice landraces using cluster analysis to group the available germplasm based on their genetic diversity. The insights gained from this analysis are expected to support the formulation of efficient rice breeding strategies. Furthermore, quantifying the extent of genetic divergence among genotypes will aid in the identification of promising genotypes and key traits for incorporation into ongoing crop improvement programs.

MATERIALS AND METHODS

A total of seventy traditional rice cultivars native to Kerala were assembled from diverse sources and cultivated during the period from September 2022 to January 2023 under

upland conditions at the Onattukara Regional Agricultural Research Station, Kayamkulam. Genetic divergence was studied using Mahalanobis D^2 statistic as described by Rao (1952). The genotypes were clustered by Tochers method. The specific information pertaining to the cultivars evaluated in the study is presented in Table 1.

Table 2: Clustering pattern of the genotypes.

Cluster no.	Number of genotypes	Genotypes
I	61	Chenthadi, Chettadi, Cheruvellari, Chuvanna Vellikannan, Karutha Chitteni, Kuttadan, Mullanchanna, Mundakakutty, Punchakayama, Athikkirai, Kavugin Poothoola, Kalyanikutty, Karutha Njavara, Kothambarikayama, Mattachembavu, Neicheera, Nooranvella, Parambuvattan, Kavunginpoothala, Elappapoochampan, Arikkirai, Valiya Champan, Vellathondi, Anakodan, Chellaam Chettivirippu, Chettivirippu, Cheruvirippu, Ezhupunna Pokkali, Kadamkudy Kuruka, Kadamkudy Pokkali, Krishnakaomodha, Kuthiru, Nayarambalam Pokkali, Ponkuruka, Pokkali, Rakthashali, Traditional Virippu, Varapuzha Pokkali, Vyttila Kuruka, Kunju Kunju, Valichoori, Kannan Kulamban, Paalthondi, Vellari, Oorpandi, Kodukanni, Ittikandan, Thavalakannan, Thekkan Cheera, Kanali, Vadakkan Vellarikayama, Marathoni, Chuvanna Chitteni, Kochuvittu, Mullanchayama, Karutha Kuruka, Eravapandy, Jeerakashala, Orthadian, Karuthacheera, Vellamundakan, Veluthakattamodan
II	1	Kokkan
III	1	Njavara Manja
IV	1	Thekkan
V	1	Kadamkudy kuruka
VI	1	Karinellu
VII	1	Nooranvella
VIII	1	Gandhakashala
IX	1	Oorkayama
X	1	Thekkan Chitteni

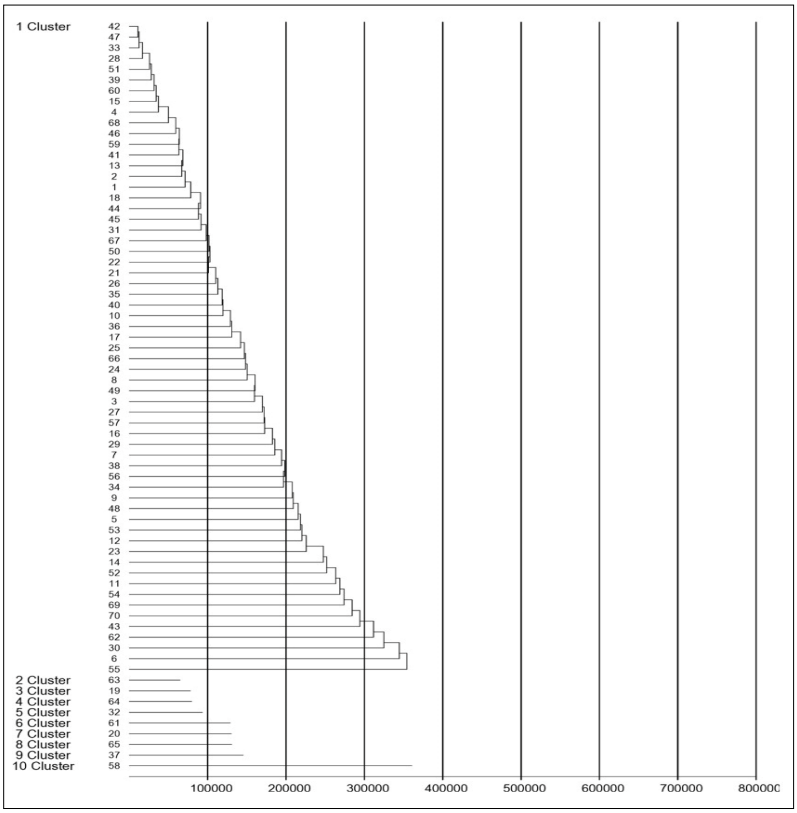


Fig 1: Clustering by tocher met.

RESULTS AND DISCUSSION

Clustering pattern of the genotypes

Study was conducted using 70 rice genotypes to assess the extent and pattern of genetic divergence through Mahalanobis D^2 analysis. Based on Euclidean cluster analysis, these genotypes were categorized into 10 distinct clusters in the Table 2 and Fig 1. The cluster I contained a maximum of 61 genotypes. All clusters except cluster I has one genotype each. Existence of considerable level of morphological and molecular diversity among rice genotypes were earlier reported by Shamim and Sharma (2025); Singh *et al.* (2025); Sheeba and Mohan (2025) and Waghmare *et al.* (2025).

Average intercluster and intracluster distances

The mean inter-and intra-cluster distances were calculated using the overall Mahalanobis D^2 values (Table 3). Cluster I exhibited the highest intra-cluster distance (453.36), comprising 61 genotypes, which suggests a high degree of genetic variability among the genotypes within this cluster. Clusters II to X each contained only a single genotype, resulting in an intra-cluster distance of zero for these clusters. Conversely, clusters exhibiting minimal intra-cluster distances despite containing multiple genotypes suggest the influence of past unidirectional selection, which may have contributed to genetic uniformity and reduced variability among the genotypes within those clusters.

The highest inter-cluster distance was recorded between clusters V and IX (1181.91), followed by clusters IX and X (1156.30), VI and X (1095.28), VIII and X (1052.23), V and VI (1044.03) and again between V and X (1011.57). In contrast, the lowest inter-cluster distances were observed between clusters II and III (279.31) and clusters VI and IX (381.45).

Cluster mean of the various characters in traditional rice germplasm

The cluster means for the 19 characters under divergence study is presented in the Table 4. The genotype in cluster III flowered earliest while those in cluster II was the last to initiate flowering. Cluster IX exhibited highest cluster means for the characters flag leaf length (42.40), panicles per plant (8.55), crop duration (149.25), 100 grain weight (3.15) and RBO content (16.45) Highest cluster means for flag leaf width (2.00), panicle length (40.20), carotene content (0.57) and anthocyanin content (1.03) was shown by cluster III. Highest cluster means for crop duration (149.25), grain width (2.39), Fe content (288.85) was shown by cluster X. Plant height (198.46), crop duration (149.25), K content (4.29) had the highest cluster means in VIII. Highest cluster means for Flag leaf width (2.00) and Na content (0.72) was shown by cluster VII. Number of tillers (15.65) and Oryzanol content (33.70) had the highest cluster means in IV. Highest cluster means for days to flower initiation (77.35) and crop duration (149.25) was shown by cluster II. Grain length (9.15) had the highest cluster means in V. Highest cluster means for Zn content (46.07) was shown by cluster VI. Highest cluster means are not there for cluster I.

Table 3: Average intercluster and intracluster distances.

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII	Cluster IX	Cluster X
Cluster I	453.36									
Cluster II	616.02	0								
Cluster III	610.77	279.31	0							
Cluster IV	700.12	833.17	872.34	0						
Cluster V	652.67	738.95	666.57	919.17	0					
Cluster VI	724.72	828.28	826.66	855.63	1044.03	0				
Cluster VII	641.29	946.82	913.89	500.47	694.52	828.10	0			
Cluster VIII	636.81	923.54	902.33	767.59	847.96	1005.47	680.41	0		
Cluster IX	744.43	893.90	905.14	912.33	1181.91	381.45	933.16	929.65	0	
Cluster X	885.39	600.60	686.42	632.53	1011.57	1095.28	981.94	1052.23	1156.3	0

Lowest cluster means for flag leaf width (1.50), panicles length (16.55), grain length (5.70), Na content (0.35) shows lowest values in cluster II. Flag leaf width (1.50), Panicles per plant (2.20), plant height (18.75) and Carotene content (0.17) had the lowest values in cluster IV. Lowest cluster mean for days to flower initiation (61.70) and crop duration (93.55) was shown by cluster III. Lowest cluster means for Flag leaf width (1.50), 100 grain weight (1.18), Fe content (31.05) was shown by cluster VIII. Flag leaf width (1.50) had the lowest values in cluster VI, while RBO content (0.83) had the lowest values in cluster VII. Flag leaf width (1.50), panicles per plant (2.20), grain width (1.70), K content (0.75), Zn content (4.68) had the lowest values in cluster V. Lowest cluster means for anthocyanin content (4.68) was shown by cluster I. Number of tillers (3.00) and Oryzanol content (0.06) had the lowest values in cluster IX, while Flag leaf length (31.05), panicles per plant (2.2) had the lowest values in cluster X.

The clusters with extreme characters for various characters have been identified and is presented in Table 5. The cluster I did not exhibit highest values for any of the characters indicating its inclusiveness of majority of the genotypes. The genotypes in cluster II were the last to flower but with highest crop duration. Flag leaf width, panicle length, carotene and anthocyanin content were recorded to be highest in the genotypes in cluster III. Cluster IV included genotypes with highest number of tillers and oryzanol content but with lowest flag leaf width, panicle per plant, plant height and carotene content. The cluster VI had the genotypes which flowered early with maximum carotene content.

Table 4: Cluster mean of the various characters in traditional rice germplasm.

Characters	I	II	III	IV	V	VI	VII	VIII	IX	X
Days to flower initiation (in days)	65.59	77.35	61.70	74.30	64.70	64.10	64.70	70.20	64.70	69.65
Flag leaf length (cm)	39.35	39.97	40.00	31.36	32.35	29.99	31.40	40.97	42.40	31.05
Flag leaf width (cm)	1.66	1.50	2.00	1.50	1.50	1.50	2.00	1.50	1.80	1.6
Number of tillers	7.73	10.75	7.50	15.65	11.75	7.20	5.00	7.41	3.00	8.95
Panicles per plant	5.06	2.40	2.30	2.20	2.20	2.40	6.75	8.15	8.55	2.2
Panicle length (cm)	22.54	16.55	40.20	16.35	26.80	18.35	18.47	23.70	20.50	16.66
Plant height (cm)	125.19	153.10	120.30	18.75	113.55	94.60	144.85	198.46	128.85	82.4
Crop duration (in days)	130.15	149.25	93.55	142.30	127.35	123.40	127.35	149.25	149.25	149.25
Grain length (mm)	7.88	5.70	7.84	7.85	9.15	7.75	7.79	5.84	8.77	7.82
Grain width (mm)	1.97	1.80	1.72	2.12	1.70	1.72	2.24	1.74	2.13	2.39
100 grain weight (g)	2.64	2.96	2.37	2.49	2.45	2.93	2.41	1.18	3.15	3.07
RBO content (%)	5.22	5.31	13.27	1.00	4.45	4.89	0.83	2.32	16.45	1
Oryzanol content (%)	6.80	3.20	1.67	33.70	7.58	3.18	25.61	14.16	0.06	28.34
Na content (%)	0.54	0.35	0.55	0.44	0.51	0.44	0.72	0.54	0.71	0.51
K content (%)	2.68	2.57	2.16	2.53	0.75	1.28	1.07	4.29	3.04	3.05
Fe content (kg/g)	74.67	203.70	166.65	149.15	55.10	75.0	34.85	31.05	66.65	288.85
Zn content (kg/g)	21.16	24.77	21.59	23.78	4.68	46.07	16.82	13.34	44.38	23.39
Carotene content (%)	0.29	0.34	0.57	0.17	0.28	0.34	0.43	0.34	0.28	0.25
Anthocyanin (%)	0.57	0.86	1.03	0.59	0.62	0.89	0.61	0.97	0.72	0.97

Table 5: Distribution of characters in clusters.

Cluster	Lowest value	Highest value
I	Anthocyanin content	-
II	Flag leaf width, panicles length, grain length, Na content	Days to flower initiation, Crop duration
III	Days to flower initiation, Crop duration	Flag leaf width, Panicle length, Carotene content, Anthocyanin content
IV	Flag leaf width, Panicles per plant, Plant height, Carotene content	Number of tillers, Oryzanol content
V	Flag leaf width, panicles per plant, grain width, K content, Zn content	Grain length
VI	Flag leaf width	Zn content
VII	RBO content	Flag leaf width, Na content
VIII	Flag leaf width, 100 grain weight, Fe content	Plant height, crop duration, K content
IX	Number of tillers, Oryzanol content	Flag leaf length, Panicles per plant, crop duration, 100 grain weight, RBO content
X	Flag leaf length, Panicles per plant	Crop duration, grain width, Fe content

The clustering pattern of genotypes and the identification of extreme characters in specific clusters provide valuable insights for breeders in designing effective crop improvement strategies. The fact that Cluster I did not exhibit the highest value for any character indicates its role as a representative group encompassing the majority of genotypes, reflecting average performance across traits. Such clusters may serve as a source for stabilizing traits or as baseline material for hybridization programs where extreme values are not the primary target.

The genotypes in cluster II, which flowered late and had the longest crop duration, could be strategically utilized in breeding programs aimed at developing long-duration varieties. These genotypes can be particularly useful in regions where extended growing seasons are advantag-eous or in breeding for ratooning ability and biomass accumulation.

Cluster III, characterized by maximum flag leaf width, panicle length, carotene, and anthocyanin content, represents an important genetic pool for both yield and nutritional improvement. The presence of wider flag leaves and longer panicles suggests higher photosynthetic efficiency and sink strength, while elevated carotene and anthocyanin content points to its biofortification potential. Genotypes from this cluster could be crossed with others to simultaneously enhance both yield and nutritional quality.

Conversely, cluster IV, though having the highest number of tillers and oryzanol content, showed the lowest values for flag leaf width, panicles per plant, plant height, and carotene. Such contrasting trait expression indicates the presence of unique genetic combinations, which can be exploited for breaking undesirable linkages and recombining tiller number with favorable plant stature and nutritional quality through strategic crossing.

The early flowering genotypes of cluster VI with maximum carotene content are especially valuable for breeding early-maturing biofortified varieties. These genotypes can cater to regions with short cropping seasons or terminal drought stress, while also meeting nutritional security goals through enhanced carotene levels.

Overall, the differential trait expression across clusters underscores the importance of cluster analysis in germplasm characterization, as it facilitates the identification of divergent parents for hybridization. By exploiting the genetic diversity present in clusters with extreme values, breeders can generate transgressive segregants combining earliness, high yield components, and nutritional traits. Thus, the results have direct implications for developing high-yielding, nutritionally enriched and climate-resilient crop varieties.

Table 6: Contribution of various characters towards divergence.

Character	Contribution in descending order
Anthocyanin content	26.54%
Zn content	22.73%
K content	19.54%
Oryzanol content	13.91%
Fe content	13.83%
Plant height	3.02%
Flag leaf width	0.17%
Rice bran oil content	0.08%
Na content	0.08%
Crop duration	0.04%
Panicle length	0.04%

Contribution of various characters towards divergence

The contribution of various characters towards divergence is presented in Table 6. Among the 19 characters considered, only 11 characters contributed towards divergence. The maximum contribution was for anthocyanin content (26.54%) indicating the wide range observed among the genotypes. The character Zn content also had a covetable contribution towards divergence (22.73%). Shrivastav *et al.* (2025) reported that the character spikelets per panicle followed by grains per panicle contributed maximum towards divergence, while grain yield per plant had the least influence on divergence. While Toshimenla *et al.* (2016) gave contradictory results where, seed yield per plant was the major contributor towards the total genetic divergence. Days to 50% flowering and 1000 grain weight manifested highest contribution towards total divergence as recorded by Chandramohan *et al.* (2016). High degree of divergence among the genotypes within a cluster produces more segregating breeding materials. Selection within such clusters might be executed based on maximum mean value for the desirable characters.

CONCLUSION

The rice genotypes evaluated in this study exhibited substantial variability across multiple traits, indicating their potential utility in crop improvement programs. Genetic divergence analysis using Mahalanobis D^2 statistics facilitated the classification of genotypes into distinct clusters. The resulting information can significantly reduce the time and effort required by plant breeders to identify promising candidates from large germplasm collections. Furthermore, the clustering pattern provides a valuable framework for selecting suitable donor genotypes for use as parents in breeding programs aimed at developing drought-tolerant rice varieties.

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Disclaimers

The views and conclusions expressed in this article are solely those of the authors and do not necessarily represent the views of their affiliated institutions. The authors are responsible for the accuracy and completeness of the information provided, but do not accept any liability for any direct or indirect losses resulting from the use of this content.

Conflict of interest

The authors declare that there are no conflicts of interest regarding the publication of this article. No funding or sponsorship influenced the design of the study, data collection, analysis, decision to publish or preparation of the manuscript.

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