



RESEARCH ARTICLE

Genetic diversity of traditional and improved rice (*Oryza sativa* L.) genotypes assessed using agro-morphological and physiological traits

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Abstract

Rice (*Oryza sativa* L.) is a major staple crop possesses extensive genetic variability, particularly among traditional landraces that serve as valuable resources for yield improvement, stress tolerance and nutritional enhancement. The present study evaluated 130 rice genotypes for 21 agro-morphological traits and physiological traits under field conditions using an augmented design during kharif 2024. Genetic divergence was estimated using Mahalanobis D² statistics and genotypes were grouped using Tocher's clustering method. The analysis classified genotypes into 33 clusters, with Cluster 1 comprising the highest number of entries (22), while Clusters 12–33 were represented by highly divergent singleton genotypes. Large clusters were characterised by early flowering, moderate maturity and optimal plant height, whereas medium and singleton clusters exhibited distinct trait combinations such as higher grain yield, longer flag leaf, increased tiller number, elevated chlorophyll content (SPAD) and greater 1000-seed weight. The presence of substantial inter-cluster divergence suggests wide genetic variability among the studied genotypes. Selection of genetically distant parents, particularly from singleton and medium clusters, may enhance heterosis and recombination for yield and adaptive traits. These findings provide insights into the genetic diversity of rice germplasm and support strategic parent selection for developing high-yielding, climate-resilient and nutritionally improved rice varieties.

Keywords: cluster analysis; genetic diversity; germplasm characterisation; mahala-nobis D² analysis; physiological traits; yield-related traits

Introduction

Rice (*Oryza sativa* L.) is one of the most important food crops globally, providing sustenance to more than half of the world's population. Asia represents the primary centre of rice cultivation and diversity, where centuries of domestication and farmer-led selection has resulted in the development of numerous traditional landraces adapted to diverse agro-ecological conditions. These landraces constitute an important component of rice genetic resources, as they harbour unique alleles for agronomic performance, physiological efficiency and environmental adaptation (1, 2). Despite their significance, many traditional rice accessions are being rapidly replaced by modern high-yielding cultivars, leading to genetic erosion and a narrowing of the cultivated rice gene pool.

Traditional rice landraces are increasingly recognised for their resilience to biotic and abiotic stresses, including drought, submergence, poor soil fertility and pest pressure. Several indigenous Indian rice varieties, such as Karuppu Kavuni, Mappillai Samba, Poongar, Kattuyanam and Seeraga Samba, possess valuable traits related to stress tolerance, nutritional quality and medicinal properties (3). These germplasm lines are well adapted to

local environments and often exhibit stable performance under low-input and stress-prone conditions. Their systematic characterisation is therefore essential not only for conservation but also for effective utilisation in crop improvement programs aimed at enhancing yield stability and climate resilience.

Genetic diversity assessment using agro-morphological traits remains a practical and widely adopted approach for characterising crop genetic resources under field conditions, particularly for identifying variation in traits related to phenology (days to 50 % flowering (DFF), days to maturity (DM)), plant architecture (plant height (PH), internode length (IL), number of productive tillers per plant (NPT)), yield components (number of grains per panicle (NGP), thousand grain weight (TGW), number of grains per panicle (NGP), panicle length (PL)), root and shoot biomass (root length (RL), fresh root weight (FRW), dry shoot weight (DSR), dry seed weight (DSW)) and physiological efficiency linked to abiotic and biotic stress tolerance and productivity (soil plant analysis development (SPAD), leaf area index (LAI), dimethyl sulfoxide (DMSO), pollen viability (PV), single plant yield (SPY), number of filled grains per panicle (NFL)).

The inclusion of physiological traits such as chlorophyll content, LAI and root-related attributes has further improved the resolution of diversity analysis by capturing functional variation associated with photosynthetic efficiency and stress adaptation (4, 5). Multivariate statistical techniques, particularly Mahalanobis D^2 analysis, have been extensively used to quantify genetic divergence and to group accessions into clusters based on multiple traits simultaneously (6). Such analyses facilitate the identification of genetically distant and complementary parental lines, which is critical for exploiting heterosis and generating superior recombinants in breeding programs (7–9).

In this context, the present study aimed to assess the genetic diversity of 130 traditional and improved rice accessions using a combination of agro-morphological, yield-related and physiological traits under field conditions. The specific objectives were to (i) estimate genetic divergence among rice accessions using Mahalanobis D^2 statistics, (ii) classify accessions into distinct clusters through multivariate analysis and (iii) identify genetically diverse and agronomically superior lines that can serve as potential donor parents for rice improvement and conservation programs. The findings of this study are expected to contribute to the effective utilisation of indigenous rice genetic resources for sustainable crop improvement.

Materials and Methods

A total of 130 rice (*O. sativa*) genotypes were evaluated for yield and related traits under field conditions during kharif 2024 at the SRM College of Agricultural Sciences, SRM Institute of Science and Technology, Baburayanpettai, Chengalpattu, Tamil Nadu, India (Table 1). The experiment was conducted using an augmented design, where each genotype was grown in 3 rows with a spacing of 60 × 30 cm. Recommended agronomic practices were uniformly followed throughout the crop growth period.

Observations were recorded at appropriate growth stages and yield as well as yield component data were collected at physiological maturity from five randomly selected plants per genotype. A total of 21 traits were evaluated, comprising 11 agro-morphological and yield-related traits and 12 physiological traits.

The agro-morphological and yield-related traits included DFF, DM, PH, flag leaf length (FLL), flag leaf width (FLW), PL, IL, NPT, NGP, thousand seed weight (TSW) and SPY.

The physiological traits recorded were RL, FRW, fresh shoot weight (FSW), dry root weight (DRW), DSW, chlorophyll content measured as SPAD values, total chlorophyll content (TCC), LAI, pollen fertility percentage (PF) and number of leaves per plant (NL). All observations were recorded on a per-plant basis and mean values were used for subsequent statistical analyses.

Statistical analysis

Mean values for all recorded traits were computed for each genotype based on observations from the sampled plants. Genetic divergence among the 130 rice genotypes was estimated using Mahalanobis D^2 statistics by considering the standardised mean values of all studied traits. Based on the D^2 values, genotypes were grouped into clusters following Tocher's method as described by Rao (1).

The relative contribution of individual traits to total genetic divergence was determined by ranking the characters according to

their frequency of appearance in the first rank across all pairwise comparisons. Inter- and intra-cluster distances were calculated to assess the magnitude of genetic diversity within and between clusters. These analyses facilitated the identification of genetically divergent genotypes that could serve as potential parents in rice breeding programs aimed at yield improvement and stress adaptation.

Results

Genetic divergence and cluster composition

Mahalanobis D^2 analysis grouped the 130 rice (*O. sativa*) genotypes into 33 distinct clusters, indicating the presence of substantial genetic variability within the experimental material. The clustering pattern revealed the coexistence of closely related genotypes and highly divergent genetic groups.

Cluster III was the largest, comprising 23 genotypes, followed by Cluster I with 22 genotypes, suggesting high intra-cluster similarity and relatively low genetic divergence among genotypes within these clusters (Fig. 1). Cluster II contained 13 genotypes and represented a medium-sized group with moderate divergence. Clusters IV to XX included 2–12 genotypes each, indicating intermediate genetic divergence. In contrast, 13 singleton clusters (Clusters XXI–XXXIII) were identified, each represented by a single genotype, highlighting the presence of genetically unique and highly divergent entries (Table 2).

The uneven distribution of genotypes across clusters indicates broad but unevenly structured genetic diversity, with singleton clusters contributing substantially to overall divergence.

Cluster mean performance for yield and associated traits

Considerable variation was observed among clusters for flowering duration, maturity period, plant stature, yield components and physiological traits (Table 3).

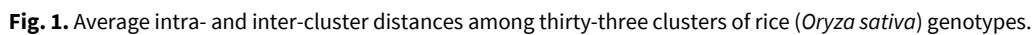
Cluster I was characterised by relatively early flowering and maturity, moderate plant height and balanced performance for yield and grains per panicle, indicating wide adaptability. Cluster II exhibited slightly delayed flowering and maturity but recorded higher values for PH, NPT, suggesting superior vegetative vigour. Cluster III consisted of late-flowering and late-maturing genotypes and recorded the highest grains per panicle and thousand-seed weight, highlighting its potential contribution to yield improvement through enhanced sink capacity.

Among the medium-sized clusters, Cluster IV was notable for high SPY combined with relatively early maturity, while Cluster VII combined high yield, tall plant stature and a greater number of grains per panicle, indicating strong yield potential. Cluster V included short-statured and low-yielding genotypes, suggesting possible adaptation to stress-prone or low-input environments. Cluster VI exhibited tall plants with a high NPT and moderate yield performance.

Several clusters (VIII–XI) showed early flowering, higher SPAD values and compact panicle architecture, reflecting improved photosynthetic efficiency and assimilate partitioning. Singleton clusters (XII–XXXIII) displayed extreme trait expressions, including ultra-early flowering, high chlorophyll content, long flag leaves, high tillering ability, enhanced root biomass and high grain yield. Notably, Cluster XV and Cluster XXXI recorded the highest single-plant yield, emphasising their potential as elite donor genotypes.

Table 1. List of 130 rice (*Oryza sativa*) genotypes used for Mahalanobis D² statistical analysis

Genotype code	Rice variety name	Genotype code	Rice variety name
G1	Kattu samba	G66	Sorna kuruvai
G2	Thanga samba	G67	Sempalai
G3	Sempalai	G68	Vellai milaku samba
G4	Ottu kitchili	G69	Puzhuthi kar
G5	Panakaatu kudai vazhai	G70	Kotha malli samba
G6	Sandikaar	G71	TKM13
G7	Pisini	G72	Karun kuruvai
G8	Burma kavuni	G73	Mathimuni
G9	Thavalai kanna matta	G74	Arcot kichili
G10	Ona matten	G75	Muttakkar
G11	Paal kudai vazhai	G76	Poli nel
G12	Poongar	G77	Pillai milagu samba
G13	Mappilai samba	G78	Iravai pandi
G14	Kadai kazuthaan	G79	Raja manna
G15	Cochin samba	G80	Norungan
G16	Samba mosanam	G81	Arikiravi
G17	Neelan samba	G82	Kannaki nel
G18	Varappu kudainchan	G83	Kattu yanam
G19	Jil jeera	G84	Chettinadkaruppu kavuni
G20	Pachai perumal	G85	Sempini panni
G21	Sona masoori	G86	Saagar
G22	Thirunelveli kichili	G87	Kaala satta
G23	Vaasansi seeraga samba	G88	Sempalai tkm
G24	Kullakkar	G89	Aathur kichili
G25	Sempalai	G90	Poda peru nel
G26	Karupu varma kavuni	G91	Thuya malli
G27	Sengini	G92	Kattu ponni
G28	Iluppaipoo samba	G93	Kanthasaari
G29	Jil jil vaigunda	G94	Poonvan samba
G30	Thenkai poo samba	G95	Kalamanaku
G31	Selam sanna	G96	Krishna ponni
G32	Kandasala	G97	Kollikar
G33	Swarna masoori	G98	Mysormalli
G34	ADT 39	G99	Chinnar
G35	Orissa vasanai seeraga samba	G100	Kalabhat
G36	Kichili samba	G101	Puzhuthi samba
G37	Kulla kar	G102	Semputhi samba
G38	Kandasali	G103	Aanai komban
G39	Kumsala	G104	Kuruvai
G40	Navara	G105	Kallundai samba
G41	Kumpalai	G106	Ottaiyan
G42	Chengalpattu sirumani	G107	Paiyur 1
G43	Chithirai kar	G108	Mani samba
G44	Ottadai	G109	Velan nel
G45	Vellai kuruvikar	G110	Karuni Nel
G46	Adukku nel	G111	MTU-1156
G47	Vellai poongkar	G112	GEB-24
G48	Arubatham kuruvai	G113	Karukaruvai samba
G49	Kuththarisi	G114	Seerga samba
G50	Raja mudi	G115	Vadan samba
G51	Kuruvai kalanjiyam	G116	Thengai poo samba
G52	Karunjeeraga samba	G117	Shivan samba
G53	Payan kundathan	G118	Kattu vaniban
G54	Vaikunda	G119	Mozhikarruppu samba
G55	Selam sanna	G120	Nattu basmati
G56	Sivappu kuruvikar	G121	Kudai vazhai
G57	Kottara samba	G122	BPT 5204
G58	Konakkuruvai	G123	Mutrina sannam
G59	Mullan kaima	G124	Kallu valai
G60	Sivappu sirumani	G125	NLR3354
G61	Rasakadam	G126	Guna parva
G62	Katta samba	G127	Sinigar
G63	Thulasi vasana seeraga samba	G128	Sabari
G64	Melaku seeraga samba	G129	Jaya
G65	Swarna masuri	G130	TPS-5



Cluster	No. of genotypes	Genotype IDs
Cluster I	22	G31, G55, G41, G20, G121, G69, G75, G78, G28, G10, G21, G33, G91, G59, G71, G39, G103, G35, G29, G64, G114, G92
Cluster II	13	G81, G82, G112, G101, G83, G84, G102, G50, G94, G73, G76, G65, G62
Cluster III	23	G126, G129, G100, G99, G89, G15, G93, G111, G90, G96, G95, G57, G122, G127, G63, G56, G43, G88, G24, G60, G49, G23, G8
Cluster IV	7	G3, G25, G105, G67, G51, G30, G107
Cluster V	7	G7, G128, G72, G85, G116, G37, G104
Cluster VI	6	G11, G117, G74, G4, G48, G32
Cluster VII	11	G53, G54, G42, G16, G106, G108, G110, G79, G68, G2, G17
Cluster VIII	4	G26, G27, G9, G19
Cluster IX	3	G130, check3, check1
Cluster X	3	G97, G125, G70
Cluster XI	2	G58, G123
Cluster XII	2	G14, G44
Cluster XIII	2	G13, G115
Cluster XIV	2	G34, G118
Cluster XV	2	G80, G119
Cluster XVI	2	G86, G113
Cluster XVII	2	G12, G47
Cluster XVIII	2	G77, G124
Cluster XIX	2	G6, G46
Cluster XX	2	G5, G36
Cluster XXI	1	G18
Cluster XXII	1	G22
Cluster XXIII	1	G38
Cluster XXIV	1	G40
Cluster XXV	1	G45
Cluster XXVI	1	G52
Cluster XXVII	1	G61
Cluster XXVIII	1	G66
Cluster XXIX	1	G87
Cluster XXX	1	G98
Cluster XXXI	1	G109
Cluster XXXII	1	G120
Cluster XXXIII	1	check2

Table 3. Mean performance of 33 clusters for agro-morphological, physiological and yield-related traits in rice (*Oryza sativa* L.)

Cluster	DFF	DM	PH	fil	LW	PL	IL	NPT	NGP	TGW	RL	FRW	FSW	DRW	DWS	SPAD	DMSO	LAI	PV	NFL	SPY
1	59.20	126.00	118.00	32.90	0.89	29.40	23.80	21.40	107.00	20.00	104.00	95.70	108.00	61.30	47.50	79.30	1.42	1.15	97.50	85.10	46.50
2	67.40	136.00	134.00	34.10	0.81	39.10	27.80	20.30	83.60	21.00	106.00	97.40	121.00	61.40	48.10	77.90	1.43	1.03	97.50	72.80	36.40
3	60.60	124.00	138.00	46.60	0.94	32.30	25.10	20.80	77.70	20.60	103.00	96.60	100.00	61.30	46.20	79.70	1.54	1.02	93.80	76.50	33.80
4	51.60	106.00	131.00	47.60	0.93	32.80	24.70	22.30	127.00	23.80	113.00	93.20	106.00	61.30	46.60	78.70	1.45	0.98	91.50	80.70	68.40
5	58.30	119.00	93.10	19.50	0.62	21.20	18.20	14.30	83.20	23.60	100.00	96.10	116.00	61.30	48.50	77.10	1.42	0.94	91.10	74.90	31.30
6	57.20	120.00	155.00	37.60	1.07	37.80	28.00	30.10	112.00	15.40	112.00	94.80	109.00	61.20	47.50	75.90	1.44	0.96	91.90	68.10	51.40
7	77.40	158.00	154.00	47.50	0.99	35.10	26.70	21.60	131.00	21.50	112.00	100.00	120.00	61.40	48.10	78.10	1.45	1.06	95.20	76.80	63.00
8	63.00	132.00	72.80	17.80	1.08	18.90	16.40	14.00	152.00	20.70	100.00	97.60	98.20	61.30	47.00	75.00	1.38	0.98	86.80	77.80	40.70
9	54.00	125.00	152.00	38.90	1.07	26.90	24.10	21.70	69.00	15.10	60.50	77.60	42.90	61.30	33.10	89.30	1.48	0.83	43.00	49.40	26.10
10	63.20	126.00	98.80	43.10	0.69	38.60	30.10	17.80	63.70	26.70	109.00	101.00	104.00	61.30	46.40	78.10	1.45	1.10	89.20	74.30	31.30
11	60.50	122.00	164.00	52.00	1.03	57.90	35.30	20.50	83.80	26.40	107.00	89.20	104.00	61.40	44.60	79.20	1.48	1.08	93.20	71.40	48.50
12	77.00	153.00	146.00	45.80	0.95	34.20	26.30	14.70	134.00	28.90	103.00	92.20	88.10	61.10	45.40	75.90	1.54	1.06	74.60	91.60	56.10
13	77.00	156.00	127.00	51.40	1.46	35.40	28.50	12.10	127.00	22.40	109.00	87.20	104.00	61.30	46.30	75.70	1.37	0.97	86.80	94.90	34.70
14	55.00	120.00	128.00	40.80	1.20	26.00	19.20	15.60	148.00	17.80	107.00	95.10	122.00	61.40	47.80	79.00	1.50	1.06	97.70	56.80	41.20
15	58.00	119.00	145.00	38.90	0.82	40.00	29.80	24.20	150.00	29.20	108.00	91.10	122.00	61.30	48.10	83.80	1.46	0.93	112.00	71.40	103.00
16	53.00	112.00	152.00	50.00	0.99	40.60	30.10	18.20	76.00	19.70	99.70	96.60	156.00	61.40	50.70	82.60	1.49	1.18	102.00	64.10	26.60
17	34.00	71.20	135.00	35.30	1.17	27.40	19.90	16.20	79.80	14.20	109.00	99.90	120.00	61.40	48.70	74.40	1.50	0.99	89.40	76.20	19.10
18	75.20	152.00	92.10	27.00	0.73	21.80	16.80	11.90	63.50	19.20	111.00	94.80	117.00	61.50	47.00	76.90	1.41	1.08	90.90	60.80	15.40
19	69.20	144.00	138.00	57.40	1.15	21.60	17.90	24.00	102.00	29.20	106.00	90.90	104.00	61.20	45.60	154.00	1.44	0.90	89.00	61.60	68.10
20	65.00	132.00	143.00	59.30	0.89	39.40	26.50	19.30	104.00	18.40	104.00	93.70	77.70	61.20	43.70	76.10	1.46	1.03	72.20	101.00	34.30
21	74.50	156.00	122.00	26.40	1.03	20.10	19.70	20.00	158.00	32.00	96.50	80.50	100.00	61.20	45.20	77.20	1.47	1.23	80.30	106.00	103.00
22	65.00	136.00	142.00	22.20	0.92	25.90	24.40	22.50	198.00	18.50	116.00	82.90	106.00	61.20	46.30	77.10	1.31	1.08	85.80	51.10	83.70
23	49.50	108.00	132.00	47.80	0.80	37.20	28.80	19.70	159.00	9.00	96.60	87.60	118.00	61.20	48.60	76.70	1.52	1.08	111.00	67.30	28.60
24	42.50	86.50	112.00	38.80	0.93	30.00	24.00	11.90	93.50	35.00	124.00	93.50	75.40	61.20	43.90	76.20	1.46	1.23	82.40	103.00	39.40
25	57.50	115.00	154.00	39.80	1.10	34.20	26.60	33.20	38.50	35.20	105.00	92.40	107.00	61.20	47.80	81.10	1.48	1.36	119.00	72.20	44.20
26	55.50	116.00	119.00	17.10	0.56	42.70	32.70	11.80	132.00	24.80	111.00	105.00	132.00	61.40	49.80	77.10	1.34	1.18	120.00	62.40	39.10
27	63.00	125.00	122.00	59.20	0.98	29.80	23.60	20.00	58.50	15.60	92.90	99.10	140.00	188.00	45.50	79.00	1.36	0.84	94.60	70.50	19.40
28	63.50	126.00	93.20	46.90	0.92	33.10	25.10	30.50	81.00	22.00	117.00	116.00	164.00	61.60	58.40	85.50	1.56	0.91	113.00	86.80	54.20
29	63.50	132.00	146.00	22.20	1.04	28.50	21.80	17.00	83.50	19.50	106.00	135.00	161.00	61.80	60.30	78.00	1.48	0.81	101.00	68.90	27.90
30	63.50	132.00	128.00	10.60	1.20	17.90	12.40	8.20	71.00	20.00	111.00	99.70	113.00	61.10	50.00	81.90	1.45	1.02	94.80	77.00	11.80
31	62.50	126.00	123.00	57.00	1.02	43.70	31.00	32.50	131.00	38.60	94.90	102.00	113.00	61.30	47.00	72.90	1.40	1.08	92.30	83.50	168.00
32	72.50	148.00	114.00	39.00	1.11	24.60	18.60	13.00	129.00	14.20	117.00	96.40	98.40	61.40	48.60	83.90	1.40	1.20	90.70	91.60	24.00
33	62.00	125.00	132.00	19.00	0.80	22.00	19.00	15.00	84.00	17.00	50.50	82.00	51.30	61.60	32.90	91.70	1.62	0.64	28.60	57.60	25.00
mean	61.54	126.81	128.97	38.47	0.97	31.70	24.33	19.28	105.80	22.28	103.68	95.54	109.67	65.17	47.01	81.36	1.45	1.03	90.87	75.28	46.79
max	77.40	158.00	164.00	59.30	1.46	57.90	35.30	33.20	198.00	38.60	124.00	135.00	164.00	188.00	60.30	154.00	1.62	1.36	120.00	106.00	168.00
min	34.00	71.20	72.80	10.60	0.56	17.90	12.40	8.20	38.50	9.00	50.50	77.60	42.90	61.10	32.90	72.90	1.31	0.64	28.60	49.40	11.80

DFF: days to 50 % flowering; DM: days to maturity; PH: plant height; fil: flag leaf length; LW: leaf width; PL: panicle length; IL: internode length; NPT: number of productive tillers per plant; NGP: number of grains per panicle; TGW: thousand grain weight; RL: root length; FRW: fresh root weight; FSW: fresh shoot weight; RW: dry root weight; DWS: dry weight of shoot; SPAD: soil plant analysis development; DMSO: dimethyl sulfoxide; LAI: leaf area index; PV: pollen viability; NFL: number of filled grains per panicle; SPY: single plant yield.

Discussion

The grouping of 130 rice genotypes into 33 clusters clearly demonstrates substantial genetic diversity within the studied germplasm, as commonly revealed through Mahalanobis D²-based divergence analysis (10–13). The formation of large clusters indicates genetic similarity among several genotypes, possibly due to shared ancestry or selection for similar agronomic traits, which aligns with earlier rice diversity studies (14–18). Such clusters often represent genetically uniform groups suitable for developing stable breeding materials. Large clusters indicate genetic similarity likely arising from repeated use of a narrow genetic base and selection for common agronomic traits, while medium-sized clusters represent an ideal balance of diversity and stability, making them valuable for recombination breeding. Medium-sized clusters exhibited moderate genetic divergence and are particularly valuable for breeding programs because they balance genetic diversity with agronomic stability. Similar observations, emphasising the usefulness of moderately divergent clusters for effective parent selection and recombination breeding, have been reported earlier (19–22).

A major outcome of the present study is the identification of a relatively large number of singleton clusters, representing genetically distinct genotypes with rare or extreme trait combinations. Previous studies have demonstrated that genotypes belonging to highly divergent clusters often produce superior heterotic combinations and transgressive segregants when used as parents (23). The singleton clusters identified in this study expressed desirable traits such as early maturity, high tillering ability, long flag leaves and exceptionally high grain yield, highlighting their potential as valuable donors for targeted trait improvement in rice breeding programs. The presence of numerous singleton clusters is particularly significant, as these genotypes are genetically distinct and may possess rare alleles or unique trait combinations shaped by isolation or specific selection pressures; their desirable traits such as early maturity and high yield make them important donors for breeding. The major contribution of traits like DFF, PH, grain yield and grain type to overall divergence suggests that both adaptive and selection-driven traits play a key role in differentiating genotypes.

The integration of physiological traits along with conventional yield components enhanced the resolution of the genetic divergence analysis. Similar enhancement of divergence through the inclusion of physiological traits has been emphasised earlier, reporting that traits related to flowering behaviour, yield and grain dimensions contribute substantially to total genetic divergence (24–25). Inclusion of physiological traits further enhanced the resolution of diversity, indicating the importance of functional variation alongside morphology.

Contribution analysis revealed that DFF, grain yield, grain length/breadth ratio and plant height were the major contributors to total divergence, closely conforming with earlier reports in rice. The presence of high inter-cluster distances between specific cluster combinations further indicates wide genetic diversity among genotypes, suggesting that crosses between these clusters could produce desirable recombinants and transgressive segregants (23, 26). High inter-cluster distances highlight opportunities for selecting diverse parents and strategic crosses between distant

clusters with complementary traits (e.g., high yield and early maturity) can enhance heterosis and generate superior recombinants. Overall, the study emphasises the need to move beyond identifying diversity to effectively utilising genetically distinct and complementary genotypes for targeted rice improvement.

Conclusion

The Mahalanobis D² cluster analysis revealed a high level of genetic diversity among the 130 rice genotypes, which were grouped into 33 clusters of varying sizes. Large clusters represented genetically similar genotypes with relatively comparable agronomic performance. While medium-sized clusters provided useful genetic variation for selection and recombination. The presence of numerous singleton clusters highlighted genetically unique genotypes possessing desirable traits such as high yield, early maturity, enhanced photosynthetic efficiency, high tillering ability and superior biomass accumulation.

These genetically divergent genotypes constitute valuable donor parents for broadening the genetic base and improving yield stability and stress tolerance in rice breeding programs. The study demonstrates that multivariate cluster analysis based on agromorphological and physiological traits is an effective approach for characterising rice genetic resources and for guiding strategic parent selection aimed at developing high-yielding, climate-resilient rice varieties. For future research, breeders should validate these findings through hybridisation programs to assess heterotic performance, incorporate molecular marker or genomic tools to better understand the genetic basis of divergence and integrate multi-environment testing to identify stable, climate-resilient genotypes. Additionally, combining physiological traits with genomic selection approaches could further accelerate the development of high-yielding, stress-tolerant rice varieties.

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Authors' contributions

H designed the study, performed data analysis, and drafted the manuscript. RM assisted in data interpretation and statistical analysis. KS contributed to laboratory work and data collection. RN supported physiological trait analysis and interpretation of results. JV supervised the study, coordinated the research work, and finalised the manuscript. All authors have read and approved the final manuscript.

Compliance with ethical standards

Conflict of interest: The authors do not have any conflict of interests to declare.

Ethical issues: None

References

1. Khush GS. What it will take to feed 5.0 billion rice consumers in 2030. *Plant Mol Biol.* 2005;59:1–6. <https://doi.org/10.1007/s11103-005-2159-5>
2. Kumar A, Dixit S, Ram T, Yadav RB, Mishra KK, Mandal NP. Breeding high-yielding drought-tolerant rice: Genetic variations and conventional breeding. *Field Crops Res.* 2014;162:7–15.
3. Shoba N, Singh R, Senthil A. Nutritional and medicinal importance of traditional rice landraces of India. *Genet Resour Crop Evol.* 2021;68:173–89.
4. Shin SY, Lee JH, Kim JH. Stay-green traits and photosynthetic efficiency in rice under stress environments. *Plant Prod Sci.* 2020;23(4):449–59.
5. Rao CR. *Advanced Statistical Methods in Biometrical Research.* New York: John Wiley & Sons; 1952.
6. Dutta P, Dutta PN, Borua PK. Morphological traits as selection indices in rice: A multivariate analysis. *Field Crops Res.* 2013;150:71–7.
7. Ramesh T, Latha S, Anandan A. Genetic diversity and trait association studies in rice for yield improvement. *J Crop Improv.* 2023;37(2):145–62.
8. Kuchanur P. Studies on genetic variability and divergence in 'new plant type' (NPT) rice genotypes. *Crop Improv.* 2009;36:20–4.
9. Singh PK, Mishra MN, Hore DK, Verma MR. Genetic divergence in lowland rice of north-eastern region of India. *Commun Biometry Crop Sci.* 2006;1(1):35–40.
10. Kandhola SS, Panwar DVS. Genetic divergence studies in rice (*Oryza sativa* L.) using Mahalanobis D^2 statistics. *Ann Agric Res.* 1999;20:43–8.
11. Behera PP, Singh SK, Singh DK, Reddy YS, Habde S, Khaire A, et al. Genetic diversity analysis of rice (*Oryza sativa* L.) genotypes with high grain yield and yield traits. *J Pharmacogn Phytochem.* 2018;7(4):1319–23.
12. Bhati PK, Singh SK, Dhurai SY, Sharma A. Genetic divergence for quantitative traits in rice germplasm. *Electron J Plant Breed.* 2015;6(2):528–34.
13. Gunasekaran M, Rajendran R, Kumar S. Genetic diversity analysis of rice landraces using quantitative traits. *J Crop Improv.* 2023;37:215–30.
14. Singh RK, Kumar S, Yadav S. Genetic divergence in rice using D^2 statistics. *J Plant Breed Crop Sci.* 2021;13:85–93.
15. Vennela PR, Singh SK, Singh R, Gayatonde V, Singh DK. Genetic divergence studies in rice (*Oryza sativa* L.) for yield and yield-related traits. *Vegetos.* 2017;30:191–5. <https://doi.org/10.5958/2229-4473.2017.00059.3>
16. Lakshmi L, Prasad B, Reddy DM. Multivariate analysis for genetic diversity in rice. *Indian J Genet Plant Breed.* 2022;82:56–63.
17. Muthuramu S, Sakthivel S. Genetic diversity analysis for yield traits in upland rice (*Oryza sativa* L.). *J Rice Res.* 2017;10(1):40–3.
18. Vadigeri VG, Hittalmani S, Gangaprasad S, Raghavendra P. Multivariate analysis for genetic divergence in rice under irrigated conditions. *Electron J Plant Breed.* 2021;12(2):456–62.
19. Rani PJ, Reddy KHP, Kumar SS, Ramesh T. Genetic diversity and clustering pattern in rice (*Oryza sativa* L.) genotypes for yield and yield traits. *J Cereal Res.* 2022;14(1):67–74.
20. Amegan E, Efisue A, Akoroda M, Shittu A, Tonegnikes F. Genetic diversity of Korean rice (*Oryza sativa* L.) germplasm for yield and yield-related traits for adoption in rice farming systems in Nigeria. *Genomics.* 2020;8(1):19–28. <https://doi.org/10.11648/j.ijgg.20200801.13>
21. Devi KR, Singh NB, Sharma PR. Genetic divergence studies in rice using multivariate analysis. *Genet Resour Crop Evol.* 2019;66:1087–98.
22. Khaire AR, Patil SS, Deshmukh PS. Genetic divergence and heterosis prediction in rice. *Cereal Res Commun.* 2022;50:345–56.
23. Ranjith P, Sahu S, Dash SK, Bastia DN, Pradhan BD. Genetic diversity studies in rice (*Oryza sativa* L.). *J Pharmacogn Phytochem.* 2018;7(2):2529–31.
24. Sudeepthi K, Srinivas T, Kumar BNVSRR, Jyothula DPB, Umar SN. Genetic divergence studies for anaerobic germination traits in rice (*Oryza sativa* L.). *Curr J Appl Sci Technol.* 2020;39(1):71–8. <https://doi.org/10.9734/cjast/2020/v39i130482>
25. Beevi HA, Venkatesan M. Contribution of physiological traits to genetic divergence in rice (*Oryza sativa* L.). *Indian J Agric Res.* 2015;49(3):231–6.
26. Raghavendra P, Kumar BD, Kumar HS, Madhuri R, Gangaprasad S, Murthy SK, et al. Exploration of genetic diversity in traditional landraces of rice for yield and its attributing traits under saline stress condition. *Int J Curr Microbiol Appl Sci.* 2018;7(6):3359–66. <https://doi.org/10.20546/ijcmas.2018.706.394>

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