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RESEARCH ARTICLE

Unravelling genetic diversity in rice germplasm for yield and related traits under organic conditions in South India

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Abstract

It is challenging to obtain high yield and productivity while growing rice in organic conditions. This study aimed to identify diverse parental lines, bring desirable genes for yield and related traits and select a superior line derived from genetic segregation and recombination, particularly for organic conditions. During kharif 2023, a diverse panel of 72 rice germplasm accessions was evaluated using an alpha lattice (6 ×12) design and replicated thrice at the agriculture farm of Vellore Institute of Technology, Vellore. For all fourteen quantitative traits included in the study, the results demonstrated significant differences ($p < 0.001$) among genotypes. High phenotypic and genotypic coefficient of variation (PCV, GCV) were noted for hundred seed weight, number of grain per panicle, number of filled grains per panicle, number of tillers per plant and number of productive tillers per plant. The study also found high heritability (h^2) coupled with high genetic advance per mean (GAM) for all traits, indicating additive gene action. Single plant yield showed a highly significant correlation with number of tillers per plant and number of productive tillers per plant, suggesting they could serve as direct selection criteria for yield improvement. Diversity analysis (D^2) classified the 72 genotypes into seven distinct clusters, with cluster IV and VI identified as the most genetically diverse. Principal component analysis found that the first five PCs contributed to 78.26 % cumulative variation with eigen value greater than one. The traits that contribute maximum to divergence are panicle length, hundred seed weight, flag leaf length, plant height, number of grains per panicle and days to 50 % flowering. The selection of genotypes in cluster IV and VI based on specific traits could be utilized in future crop improvement initiatives, with a focus on cultivar development for organic conditions.

Keywords: genetic divergence; landraces; organic condition; PCA; rice; variability

Introduction

The development of chemical-free and environmentally safe food has led to a discernible global movement towards organic agriculture (1, 2). It has been found that conventional (inorganic or high-input) conditions are easier to produce rice than organic (low-input) conditions. Additionally, due to the low soil fertility, organic conditions only use natural inputs for crop production and protection, which makes it challenging for farmers to achieve the best yield (3, 4). India is expected to cultivate only a few rice cultivars, Ezhome 1, Ezhome 2, Jaiva, KAU Mithila, Sikkim Dhan-1 and Sikkim Dhan-3 exclusively for organic conditions. Organic farming employs over 95 % of cultivars bred under conventional high-input conditions, making them unstable at organic conditions. It requires important traits like strong root systems, early vigour, tillering ability and nutrient use efficiency for better crop performance (5-7). To develop novel cultivars that can thrive in organic, low-input environments, organic plant breeding processes must be used (8).

In India, northeastern state of Sikkim has been in the forefront of organic agriculture (9). However, organic rice breeding programmes are still in their nascent stages in other states. Early attempts were made to evaluate the performance of rice germplasm in organic conditions for yield improvement (10-11). Interestingly, they found both increasing (12, 13) and decreasing trends in yield performance (14, 15) under organic conditions.

In fact, rice landraces can tolerate environmental extremes as well as pest and disease outbreaks better than modern cultivars because they have untapped gene(s) that contribute to increased resilience (16, 17). There were 8000 different types of rice landraces worldwide, with India accounting for almost half (4000) (18, 19). Therefore, the best and most sustainable way to develop new rice cultivars suitable for organic conditions would be to exploit these novel rice landraces found in India, while representing the rich agricultural heritage of early humans and realizing its full potential for our current and future generations.

By including rice landraces, this study provides a comparative perspective on genetic potential, aiming to identify the best-performing genotypes under organic conditions. Against this background, the current research was carried out to assess the genetic variability and diversity among rice germplasm, with the objective of identifying superior parents for yield and yield-related traits under organic conditions.

Materials and methods

A field experiment was conducted at the agriculture farm of Centre for Bio-Medical Research (CBMR) (12°58'7"N and 79° 9'40"E) within the VIT School of Agricultural Innovation and Advanced Learning (VAIAL), Vellore Institute of Technology, Vellore, during kharif 2023 cropping season under organic conditions. The soil at the experiment site is clay loam and mildly alkaline (pH 8.1) with an organic matter content of 1.21 %. The study involved 72 diverse rice germplasm accessions, comprising 61 landraces and 11 modern cultivars collected from various districts of Tamil Nadu (Supplementary table 1). The 72 rice genotypes were arranged in an alpha lattice (6 ×12) design with three replications. Each replication was subdivided into six blocks, each containing twelve plots. 25 days old rice seedlings were transplanted in three rows, each 3 meters long, at a spacing of 20 × 20 cm. To maintain soil fertility and enhance crop growth, organic amendments such as farmyard manure, vermicompost, neem cake and gypsum were applied. All recommended organic farming practices for rice as outlined in the TNAU Agritech Portal were followed to ensure optimum crop establishment and growth. Measurements were taken from five randomly selected plants per genotype across replications for the following quantitative traits: days to 50 % flowering (DFF), plant height (PH), flag leaf length (FLL), flag leaf breadth (FLB), number of tillers per plant (NTPP), number of productive tillers per plant (NPTP), panicle length (PL), number of grains per panicle (NGPP), number of filled grains per panicle (NFGPP), hundred seed weight (HSW), single plant yield (SPY), kernel length (KL), kernel breadth (KB) and length to breadth ratio (LBR).

Statistical analyses were carried out using the R Studio packages: 'agricolae' for variance analysis (20), 'corrplot' for correlation (21) and 'FactoMineR' (22) along with 'factoextra' (23) for principal component analysis. The 'TNAU STAT' program was used to perform D^2 statistics (24).

Results and Discussions

Analysis of variance

Generally, ANOVA is used to partition the total variation into different components of variation. The alpha lattice design is preferred over the randomized block design, as it minimizes environmental influence by maintaining homogeneity within small, incomplete blocks. In the present study estimates of ANOVA (Supplementary table 2) showed highly significant ($p < 0.001$) variation among 72 germplasm for all traits examined. This suggests the presence of substantial genetic variability, indicating a higher potential for developing desirable cultivars suited to organic farming conditions.

Descriptive statistics and population characteristics

In Table 1, the descriptive statistics of fourteen traits under organic conditions are provided. The presence of both short and long-duration rice germplasm was indicated by the mean values of DFF, which ranged from 82.07 (ASD 16) to 125.40 (Kattuyanam). The PH varies between 76.87 cm (IR 50) to 166.40 cm (Arcot kitchadi). FLL and FLB vary from 20.03 cm (Ottu kitchadi I) to 43.61 cm (Garudan samba) and 0.69 (ADT 46) to 1.96 (Basmati) respectively. The PL varies from 16.20 cm (Ottu kitchadi I) to 29.42 cm (Pisini). While the NTPP values varies from 12 (Mappillai samba) to 41 (Rathasali II), the NPTP varies from 11 (Karuppu kavuni) to 39 (Nei kitchadi). Similarly, a widespread of variation was identified for vegetative traits among different rice landraces (4, 17).

Since HSW and NGPP were key determinants for increased single plant yield (SPY), the present study displayed wider variation for those traits as well. The two varieties with the highest and lowest HSW were Kuzhiyadichan (3.40 g) and Thulasi vasanai seeraga samba (0.94 g). Conversely, ADT 53 recorded the highest NGPP and NFGPP, with 253.05 and 237.93 respectively. Rathasali II scored the lowest NGPP of 82.49 and NFGPP of 71.50. Nei kitchadi had the highest SPY (36.76 g), while Annam Alagi had the lowest (19.17 g). The KL ranged from 4.79 mm (Milagu samba) to 11.59 mm (Basmati), the KB ranged

Table 1. Descriptive statistics and population characteristics of quantitative traits studied

Traits	Mean	SE	Maximum	Minimum	Skewness	kurtosis
DFF	96.14	1.21	125.40	82.07	1.03	0.54
PH (cm)	120.25	2.60	166.40	76.87	-0.05	-0.54
FL (cm)	31.96	0.64	43.61	20.03	0.10	-0.62
FB (cm)	1.19	0.02	1.96	0.69	0.71	2.31
PL (cm)	23.54	0.34	29.42	16.20	-0.42	-0.46
NTPP	21.53	0.52	40.68	12.40	1.57	5.10
NPTP	19.59	0.48	39.00	11.81	1.63	6.10
HSW (g)	2.18	0.06	3.40	0.94	-0.11	-0.32
NGPP	151.93	3.79	253.05	82.49	0.38	0.75
NFGPP	137.89	3.67	237.93	71.50	0.52	0.96
KL (mm)	7.54	0.14	11.59	4.79	0.47	1.67
KB (mm)	2.60	0.05	3.35	1.64	0.10	-0.92
LBR	2.96	0.07	4.91	1.96	0.86	0.43
SPY (g)	27.15	0.52	36.76	19.17	0.44	-0.69

SE - Standard error, **DFF** - Days to fifty percent flowering, **PH** - Plant height, **FL** - Flag leaf length, **FB** - Flag leaf breadth, **PL**- Panicle length, **NTPP**- Number of tillers per plant, **NPTP**- Number of productive tillers per plant, **HSW** - Hundred seed weight, **NGPP** - Number of grains per panicle, **NFGPP** - Number of filled grains per panicle, **KL** - Kernel length, **KB** - Kernel breadth, **LBR** - Length to breadth ratio, **SPY** - Single Plant Yield.

from 1.64 mm (Sivan samba) to 3.35 mm (Kalluputhan) and the LBR varied from 1.96 (Milagu samba) to 4.91 (Basmati). These significant changes were observed in rice grain characteristics. Rice germplasm exhibited differential responses under organic conditions, as indicated by significant reductions in PH, NTPP, PL and HSW, resulting in lower grain yield (4).

The term 'skewness' refers to the asymmetry of a frequency distribution curve, while 'kurtosis' indicates the peakedness or flatness of the curve's top relative to a normal distribution with the same variance. In this study, all traits except for PH, PL and HSW showed positive skewness towards the right end of the frequency curve. The traits PH, FLL, PL, HSW, KB and SPY showed relatively flat peakedness (platy) in their curves. The measured frequency curve was extremely peaked (lepto) for all other traits.

Measures of variation

To identify superior genotypes, breeders must assess the genetic differences within a population. This process is facilitated by variability parameters such as phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability (h^2), genetic advance (GA) and genetic advance as a percentage of the mean (GAM). Among these, PCV and GCV are particularly useful for estimating the extent of diversity present in the available germplasm.

In this study PCV values was somewhat higher than GCV values for all the traits studied (Table 2). This highlights the low level of environmental influence (25). The PCV and GCV estimates for the traits ranged from moderate (10-20 %) to high (>20 %). Traits such as NFGPP (22.78 %, 22.57%) and HSW (24.28 %, 24.22 %) were recorded highest PCV and GCV. Notably moderate PCV (10.8 %) and GCV (10.72 %) were observed for DFF, signifying a greater impact of the environment on DFF than the other traits. Comparable results were consistent in previous experiments as well (25–28). The findings showed significant variation in yield and associated traits, indicating that it may be beneficial to select for those traits under organic conditions.

Genes and the environment are the main factors that influence h^2, which aids breeders in identifying traits for breeding. Similarly, breeding techniques are guided by GAM, which indicates the extent of genetic improvement possible in the future generation. In this study, all examined traits exhibited high h^2 (> 60 %) and high GAM (> 20 %). Among the observed traits, h^2 values ranged from 86.18 % for SPY to 99.7 % for KL, while GAM ranged from 21.92 for DFF to 49.76 for HSW. High h^2, in combination with high GAM indicates the existence of additive gene action, which plays a critical role in trait transmission and expression in subsequent generations (17, 28, 29). Consequently, simple selection strategies can be effectively employed by breeders to enhance rice yields in future generations.

Character association

Correlation is a valuable tool in plant breeding; correlation coefficients (r) determine both the strength and direction of relationships among traits. It is an essential indicator for breeders to select desired traits that must be introduced into the selection cycle to achieve increased productivity. In this study, a significant positive and intermediate association was observed between NTPP and NPTP (r = 0.46) with SPY, indicating that high-tillering plants tend to yield more grains (Fig. 1). Thus, selecting these traits directly could contribute to enhancing grain yield (30). Furthermore, a highly significant positive correlation was observed for NTPP with NPTP, as well as NGPP with NFGPP. A similar association was previously observed in rice by several researchers (31, 32).

Table 2. Estimates of genetic variances, heritability, genetic advance and genetic advance as percent of mean for studied quantitative traits

Traits	PCV (%)	GCV (%)	h^2 (%)	GA	GAM (%)
DFF	10.8	10.72	98.57	21.08	21.92
PH (cm)	18.31	18.22	99.09	44.94	37.37
FL (cm)	17.44	17.01	95.01	10.91	34.13
FB (cm)	18.35	17.47	90.59	0.41	34.25
PL (cm)	12.34	12.08	95.88	5.74	24.37
NTPP	21.41	20.31	89.99	8.54	39.69
NPTP	22.16	20.75	87.66	7.84	40.02
HSW (g)	24.28	24.22	99.49	1.09	49.76
NGPP	21.31	21.14	98.37	65.61	43.19
NFGPP	22.78	22.57	98.18	63.53	46.07
KL (mm)	15.21	15.19	99.7	2.36	31.25
KB (mm)	16.32	16.26	99.22	0.87	33.35
LBR	20.68	20.59	99.15	1.25	42.24
SPY (g)	17.05	15.83	86.18	8.13	30.27

PCV - Phenotypic coefficient of variation, **GCV** -Genotypic coefficient of variation, **h^2** - Broad sense heritability, **GA** - Genetic advance, **GAM** - Genetic advance as percent of mean, **DFF** - Days to fifty percent flowering, **PH** - Plant height, **FL** - Flag leaf length, **FB** - Flag leaf breadth, **PL**- Panicle length, **NTPP** - Number of tillers per plant, **NPTP** - Number of productive tillers per plant, **HSW** - Hundred seed weight, **NGPP** - Number of grains per panicle, **NFGPP** - Number of filled grains per panicle, **KL**- Kernel length, **KB** - Kernel breadth, **LBR** - Length to breadth ratio, **SPY** - Single Plant Yield.

PH (r = 0.47), FLL (r = 0.42), PL (r = 0.34), NGPP (r = 0.33) and NFGPP (r = 0.36) were significantly and positively correlated with DFF. This indicates that taller plants tended to flower later and were associated with longer flag leaves and panicles. The results further suggest that a longer vegetative period due to delayed flowering enhances the source-sink relationship, enabling the production of more grains per panicle, which ultimately increases single plant yield (33–36).

A significant intermediate positive correlation was found between HSW with KL (r = 0.55), KB (r = 0.50), FLL (r = 0.25) and PL (r = 0.29). There was a significant negative correlation between NTPP (r = –0.24) and NPTPP (r = –0.27). These results indicate that grain yield was directly associated with PL and FLB, whereas yield was indirectly correlated with the NTPP. Similar results have been reported in previous studies using different sets of rice germplasm (29, 37, 38).

Genetic divergence analysis (D^2)

By determining the degree of genetic variability between the genotypes, genetic divergence (D^2) analysis assists in selecting heterogeneous parents for a hybridisation procedure that maximises heterosis and genetic gain. By D^2 analysis 72 rice germplasm were categorized into seven clusters. According to the clustering pattern shown in Table 3, cluster I contained the highest number of genotypes (37), while clusters IV and VII were

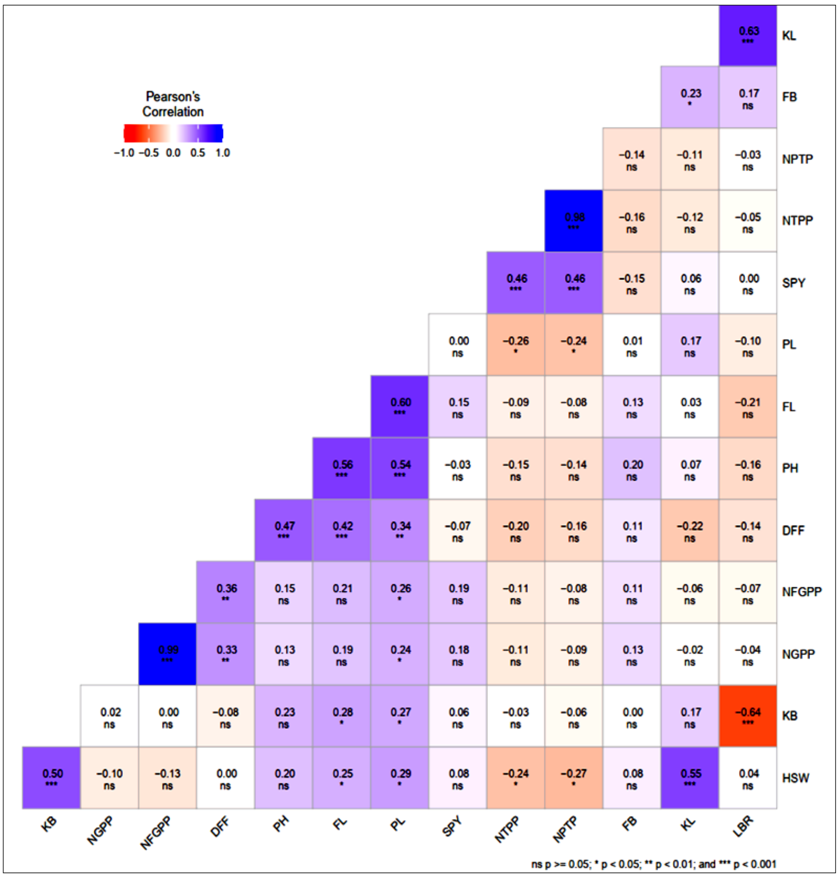

Fig. 1. Association analysis of fourteen quantitative traits studied. **DFF** - Days to fifty percent flowering, **PH** - Plant height, **FL** - Flag leaf length, **FB** - Flag leaf breadth, **PL** - Panicle length, **NTPP** - Number of tillers per plant, **NPTP** - Number of productive tillers per plant, **HSW** - Hundred seed weight, **NGPP** - Number of grains per panicle, **NFGPP** - Number of filled grains per panicle, **KL** - Kernel length, **KB** - Kernel breadth, **LBR** - Length to breadth ratio, **SPY** - Single plant yield.

Table 3. Toucher's clustering pattern in rice genotypes

Cluster number	Number of genotypes	Constituent genotypes
I	37	Navara, Swarna malli, Karuthukkar, Mani samba, Kochin samba, Varakkal , Kalluputhan, Karun kuruvai, Annam alagi, Ottu kitchadi I, Edakkal, Vadakathi samba, Ottu kitchadi II, Pal kudai valzhai, Sempuli samba, Kuzhiyadichan, Illupai poo samba, Kamban samba, Poongar, Pisini, Sivappu kavuni, Chinna adukku nel, Vaigunda red, Kitchadi samba, Sengal pattu sirumani, Ramakali, Thanga samba, Thooyamalli, ASD 37, TRY 5, ADT 46, ADT 51, Anna (R) 4, CO 51, IR 50, ADT 16
II	8	Annai komban, Jasmine, Buthakaima, Chinnar, Bavani, Nattu basmati, Indhurani, Valan samba
III	12	Arcot kitchadu, Kadai kalluthan, Ponmani samba, Samba mosanam, Garudan samba, Nei kitchadi, Vaigunda white, Mappillai samba, Kuthiraivali samba, Kattuyanam, Karuppu kavuni, ADT 54
IV	1	Basmati
V	2	Kaluyundaiyan, Sivan samba
VI	11	Kitchali samba, Sempalai, Seeraga samba, Rathasali I, Polinel, Rathasali II, Thulasi vasanai seeraga samba, Vasanai seeraga samba, Milagu samba, ADT 53, TKM 13
VII	1	Vellai kudai valzhai

solitary, each consisting of a single genotype.

The estimated intra and inter cluster D^2 values for seven clusters were presented in Table 4. Among the clusters, Cluster IV and VI had the highest inter-cluster D^2values (6385.48), followed by IV and V Cluster (3527.79). Cluster III and VII showed the lowest divergence (729.84). This demonstrated the divergence between the genotypes dealt within each cluster. The highest intra cluster D^2value was observed in cluster I (560.32), indicating a high degree of genetic diversity among the genotypes within this cluster. In contrast, Clusters IV and VII exhibited the lowest intra-cluster values, as they were solitary clusters containing only a single genotype each.

In Table 5, the seven cluster means of fourteen quantitative features were shown. At 28.64 g, Cluster II had the maximum SPY. Cluster III, however, achieved the highest mean values for NGPP (177.13), NFGPP (165.38), PL (25.32 cm) and DFF (108.92). The solitary genotype Basmati in Cluster IV recorded the highest FLB (2.0 cm), HSW (2.45 g) and KL (11.53 cm), while solitary Vellai kudai valzhai genotype in Cluster VII showed the highest mean values for PH (164.27 cm), FLL (37.60 cm) and LBR (2.60).

Principal component analysis (PCA)

To find important contributing traits for breeding and selection, PCA streamlines complicated trait datasets. Based on divergence among the lines, 72 rice germplasm were grouped into seven clusters, using D^2 analysis. To determine which characteristics significantly contributed to the divergence, PCA was used (41). The first five PCs had eigen vector values of more than one and accounted for 78.26 % of cumulative variation, according to the PCA results (Fig. 2). It

Table 4. Inter and intra (Bold) cluster D^2 values between each cluster.

Cluster	I	II	III	IV	V	VI	VII
I	**560.32**	1086.41	736.04	3315.25	1116.12	1380.70	903.43
II		**471.34**	1046.64	1275.28	1570.01	2908.44	1020.28
III			**496.38**	3094.13	1443.26	1512.34	729.84
IV				**0.00**	3527.79	6385.48	2360.83
V					**435.43**	1454.45	1905.55
VI						**525.46**	2210.93
VII							**0.00**

Table 5. Cluster mean values for quantitative traits studied.

Cluster	DFF	PH	FL	FB	PL	NTPP	NPTP	SPY	HSW	NGPP	NFGPP	KL	KB	LBR
I	93.66	114.47	31.05	1.30	23.16	21.78	19.83	26.96	2.26	145.99	131.41	7.52	2.79	2.74
II	92.00	121.36	33.79	1.23	24.78	20.42	18.62	28.64	2.57	142.16	126.45	9.19	2.40	3.83
III	108.92	143.20	35.75	1.20	25.32	19.91	18.03	26.89	2.33	177.13	165.38	7.74	2.60	2.99
IV	88.67	124.25	26.78	2.00	23.40	20.66	19.33	25.20	2.45	160.33	137.33	11.53	2.36	4.87
V	88.61	85.92	24.98	1.67	19.58	22.33	20.83	25.92	1.85	143.83	129.00	7.47	1.74	4.29
VI	96.82	116.28	31.12	1.22	22.71	23.27	21.27	25.69	1.47	152.06	140.33	5.78	2.17	2.69
VII	87.00	164.27	37.60	1.50	24.95	19.30	17.00	20.00	2.10	174.66	152.33	8.56	3.30	2.60

DFF - Days to fifty percent flowering, **PH** - Plant height, **FL** - Flag leaf length, **FB** - Flag leaf breadth, **PL** - Panicle length, **NTPP** - Number of tillers per plant, **NPTP** - Number of productive tillers per plant, **HSW** - Hundred seed weight, **NGPP** - Number of grains per panicle, **NFGPP** - Number of filled grains per panicle, **KL** - Kernel length, **KB** - Kernel breadth, **LBR** - Length to breadth ratio, **SPY** - Single plant yield.

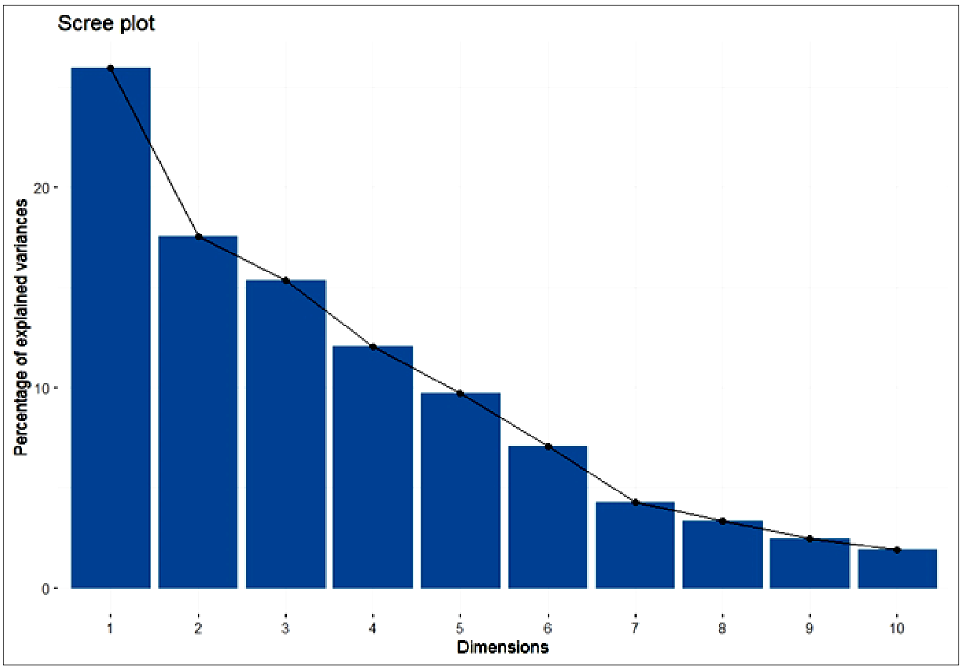

Fig. 2. Scree plot representing principal components and their variations.

suggested that the first five PCs effectively captured the essential features of the traits. The factor loading values obtained from PCA for the fourteen traits are presented in Table 6. Traits such as PL, FLL, PH, DFF, NGPP, NFGPP, FLB and KB showed high significance to the PC 1, while HSW, KL and LBR for PC 2. However, PC 3 displayed high significance for NTPP, NPTP and SPY. These results were consistent with the findings of previous studies (17, 42, 43).

In the present study, the biplot of PC 1 and PC 2 explained 43.8 % of the total variation, with PC 1 accounting for the highest proportion at 26.05 %. The length of the arrows in PCA biplot represents the contribution of those traits to variability and direction of arrows suggests correlations between traits. Fig. 3, 4 showed the variables and genotypes tapped under the biplot. It was observed that except SPY, KB, FB and LBR all other traits contribute more to the variation. Also, biplot (Fig. 3) revealed that all the eleven traits except LBR, NTPP, NPTP had a positive association with PC 1 and PC 2 respectively. Genotypes located near specific trait vectors indicate their superiority for those traits (Fig. 4). Traits grouped within different PCs should be prioritized in breeding programs, as they tend to be inherited together. According to previous research, variation in PC 1 and PC 2 was positively correlated with yield and yield-related characteristics (44).

Table 6. Eigen vector of quantitative traits, eigen values, standard deviation and proportion of five principal components.

Components	PC 1	PC 2	PC 3	PC 4	PC 5
EV	3.358	2.285	1.995	1.566	1.264
SD	1.853	0.164	0.147	0.128	0.092
PV	26.052	17.659	15.522	10.834	8.196
CPV	26.052	43.711	59.234	70.068	78.264
DFF	0.587	-0.362	-0.121	0.059	0.427
PH	0.689	-0.031	0.214	-0.172	0.413
FL	0.701	-0.101	0.282	-0.227	0.284
FB	0.254	0.185	-0.293	-0.222	0.095
PL	0.745	0.052	0.153	-0.153	0.154
NTPP	-0.519	-0.420	0.355	-0.642	0.030
NPTP	-0.504	-0.439	0.318	-0.656	0.053
HSW	0.405	0.648	0.286	-0.182	-0.240
NGPP	0.512	-0.512	-0.471	-0.188	-0.458
NFGPP	0.525	-0.548	-0.457	-0.166	-0.423
KL	0.148	0.726	-0.200	-0.547	-0.182
KB	0.391	0.152	0.698	-0.010	-0.510
LBR	-0.221	0.450	-0.692	-0.415	0.231
SPY	0.278	-0.193	0.376	0.528	-0.163

EV- Eigen values, **SD** - Standard deviation, **PV** - Proportion of variation, **CPV** - Cumulative proportion of variation, **DFF** - Days to fifty percent flowering, **PH** - Plant height, **FL** - Flag leaf length, **FB** - Flag leaf breadth, **PL** - Panicle length, **NTPP** - Number of tillers per plant, **NPTP** - Number of productive tillers per plant, **HSW** - Hundred seed weight, **NGPP** - Number of grains per panicle, **NFGPP** - Number of filled grains per panicle, **KL** - Kernel length, **KB** - Kernel breadth, **LBR** - Length to breadth ratio, **SPY** - Single plant yield.

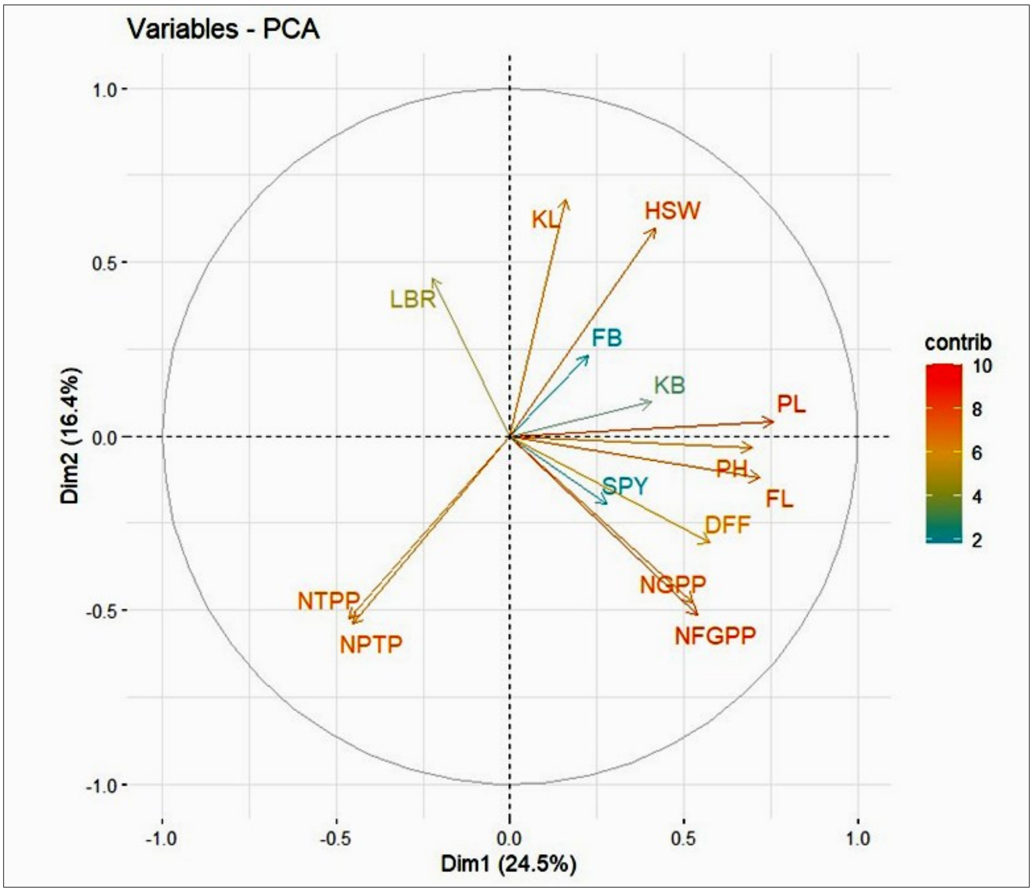

Fig. 3. Clustering of variables towards principal components. **DFF** - Days to fifty percent flowering, **PH** - Plant height, **FL** - Flag leaf length, **FB** - Flag leaf breadth, **PL** - Panicle length, **NTPP** - Number of tillers per plant, **NPTP** - Number of productive tillers per plant, **HSW** - Hundred seed weight, **NGPP** - Number of grains per panicle, **NFGPP** - Number of filled grains per panicle, **KL** - Kernel length, **KB** - Kernel breadth, **LBR** - Length to breadth ratio, **SPY** - Single plant yield.

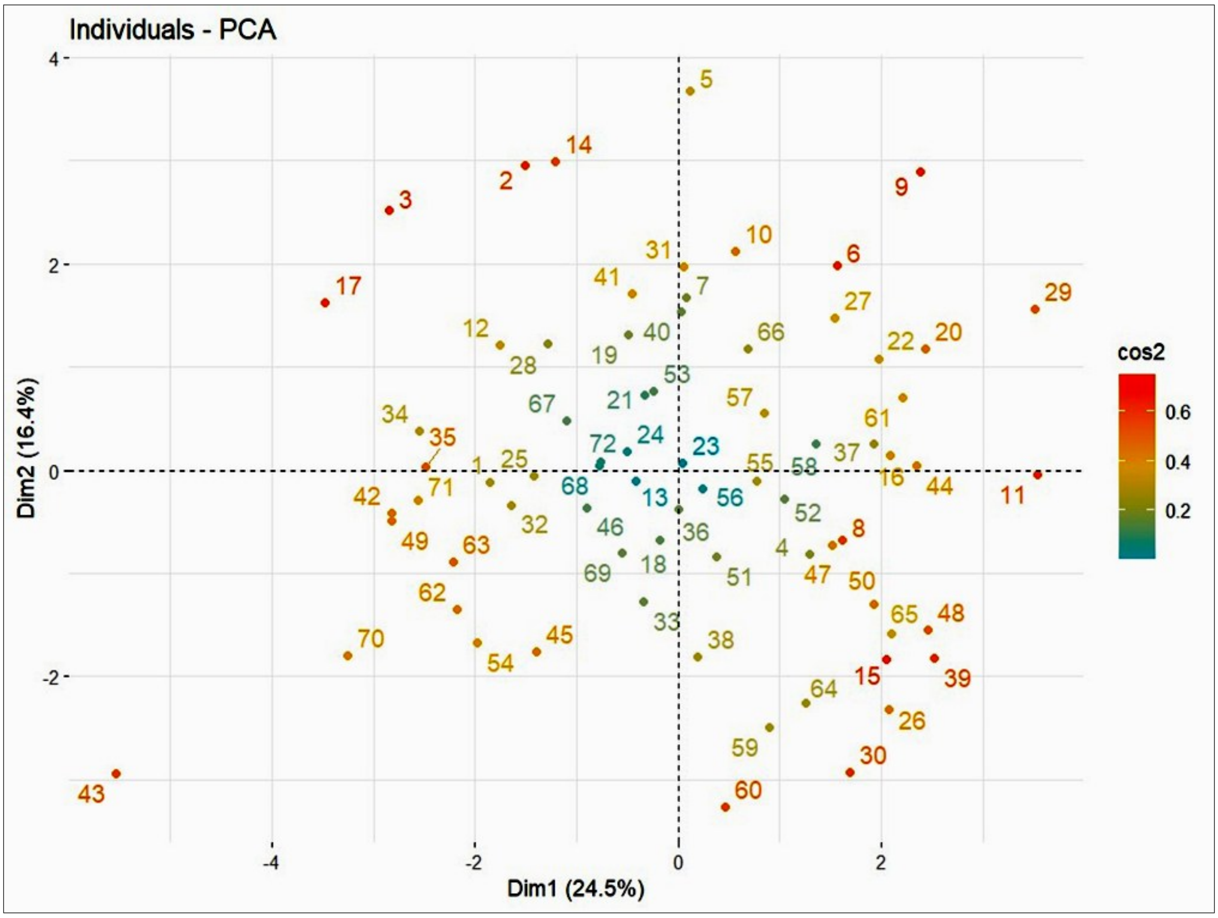

Fig. 4. Clustering of genotypes based on principal components. (Numbers indicating the corresponding genotypes listed in Supplementary Table 1).

Conclusion

Rice landraces possess a large number of potential untapped genes, making them a valuable source for varietal improvement programs. This study revealed significant variation among rice germplasm under organic conditions across all evaluated traits. Using D^2 analysis, the genotypes were divided into seven clusters. PCA identified PL, FLL, PH, NGPP, DFF and HSW as key contributors to divergence. Selection based on these traits in genotypes belonging to Cluster IV and VI could be used in future breeding programs to increase yield under organic conditions.

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Authors' contributions

KR conceptualized and supervised the work. SDV performed the experiments, conducted the statistical analysis and wrote the manuscript. KR edited and finalized the manuscript. All authors have read and approved the final version of the manuscript for publication.

Compliance with ethical standards

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