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Genetic Diversity Analysis to Identify Superior and Physiologically Efficient Farmers Varieties of Rice Collected from Madhya Pradesh

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ABSTRACT: An experiment was conducted on 30 farmer's rice varieties collected from different districts of Madhya Pradesh to identify the genetic components contributing to phenophasic development, physiological, yield attributes and biochemical traits. Principal component analysis was performed to rank the farmer's varieties based on PC scores acquired as per the trait studied. Out of twenty one traits studied, only five principal components (PCs) exhibited more than 1.00 Eigen value and showed 84.24 % of total cumulative variability. The PC1 showed 42.46%, while PC 2, PC 3, PC 4 and PC 5, exhibited 20.97%, 9.60%, 6.18% and 5.02% variability, respectively. The PC1 which accounted for the highest variability (42.46%) was mostly associated with major physiological parameters and yield related traits. The PC 2 was dominated by biochemical traits, while PC3 was mostly dominated for some phenophases and yield related traits. The PC 4 was dominated by only one trait *i.e.* chlorophyll content index, and PC5 was dominated by test weight. Farmer's variety Pandu was superior for Chlorophyll content index (38.27), total dry matter production (38.15 g plant'), Leaf area index (4.09). Leaf area duration (17982 cm days) and crop growth rate (0.00282 g m^2 day), PCA revealed that the genotype Garudluchai (7.260) acquired highest positive value PCs followed by Navari (4.161), Vishnubhog (3.641) and Krishnabhog (3.063) respectively. Farmer's varieties Garudluchai, Uraiboota, Karhani contributed their presence in maximum PCs of this investigation. The identified lines will be utilized in the rice breeding programme to develop improved rice varieties for high yield and maximum physiological efficiency.

Keywords: Principal component analysis, farmer's varieties, rice, physiological parameter and morphological responses.

INTRODUCTION

Rice is the staple food of nearly half the world's population, which depends on this crop for survival. In many countries, rice accounts for more than 70% of human caloric intake and the main protein source for poor people in developing countries. It provides 21% of global human per capita energy and 15% of per capita protein. For rice cultivation program, farmers prefer those varieties which perform well in their agro-climatic condition and provide good yield and quality. In many places of India, farmers accept. Their varieties for cultivation due to good adaptability and more net return. Released and notified rice varieties are now in the seed production chain and most common in farmers' cultivation programmes, resulting in depletion of very important yields and quality genes. The plant varieties in the form of farmer's variety have been in existence in India for a long time. "Farmers varieties" are defined as varieties that have traditionally been cultivated and developed by farmers in their fields or varieties that are a wild relative or landrace of any variety about which farmers possess common knowledge (Cullet and Koluru 2002). Farmer's varieties have the high potential to withstand the heat, drought and biotic stress which enables them to survive global warming and climate change. However, the yield is not too much higher as compared to commercially cultivated varieties and hybrids. Yield and yield associated traits of different field crops are complex, controlled by various genes and are highly influenced by environmental conditions (Shi *et al.*, 2009). Accordingly, improving crop productivity by selecting yield-contributing characters has been an important factor for higher rice production (Wang and Li 2008). For instance, rice grain yield production depends on tiller number per plant, grain number per panicle, grain size, grain fertility, panicle length, and rachis branching of the panicle (Yan *et al*., 2013).

Besides this grain yield in rice was found to be positively associated with physiological attributes such as net assimilation rate (NAR), leaf area index (LAI), photosynthesis, specific leaf weight (SLW) and total dry matter (TDM), however, in path coefficient analysis TDM and photosynthesis were found most important (Sharma and Singh 2000; Islam, 2010). Further, the variety with higher dry matter production come from the roots and shoots which constitute the plant structure that helped in higher grain yield production. The optimum proportion of dry mass production between different parts should be properly partitioned for maximizing the grain yield (Gorney and Larson 1989). In addition, morphological and physiological traits also have the important role on the genetic improvements in rice yield potential, which ultimately improve the efficiency of resource capture. The high-yielding rice varieties showed higher leaf photosynthetic rates and chlorophyll content (Peng *et al.* 2000) and their metabolism regulates the plant development. Several researchers reported that the genotypes with higher TDM also produced higher yield due to large root system and leaf area (Flood *et al.*, 1995; Mondal *et al.*, 2012). The rice kernel (such as the content of protein, fat, crude fiber, and ash) are also important parameters for rice quality (Yadav and Jindal 2007). It ensures that the identification of high yielding material, the study of farmer varieties for morpho-physiological and seed quality level is required, leading to a multi-purpose problem of ensuring food and nutritional security. Identifying superior genotype with corresponding efficient economic traits is an important step for crop improvement and sustainable crop production (Elameen *et al.*, 2007). In addition, understanding the genetic variability and genetic interrelationship present among germplasm collections is valuable for plant breeders to select potential parents with desirable traits and effective utilization of plant genetic resources. .

The principal component analysis (PCA) is a powerful statistical method widely applied to classify phenotypic traits in crop germplasm into groups based on similarities. PCA assists in the decision-making of choice of parents for genetic improvement (Afuape *et al*., 2011). PCA reduces the original variables into a new kit of uncorrelated variables known as principal components (PCs). These Principal components define the connections between traits and distribute the total variance of the original traits into a small number of uncorrelated new variables (Wiley and Lieberman 2011). The PCA allows visual differentiation among entries and identifies possible associations. (Mohammadi and Prasanna, 2003) by producing a two dimensional scatter plot consisting of individual entries. The geometrical distances among individuals in this plot exhibit the genetic distances among them. The objectives of this study was to apply principal component analysis to identify superior and physiologically efficient farmer's varieties for breeding.

MATERIALS AND METHODS

The present investigation was carried out during kharif 2019 at Rice Research Farm, Department of Plant Breeding and Genetics, College of Agriculture, Jawaharlal Nehru Krishi Vishwa Vidyalaya, Jabalpur Madhya Pradesh (India). The rainfall during the crop season was 1739.1 mm, which was received on 56 rainy days. During crop season, average minimum and maximum temperatures were 19.7°C and 30.9°C. During this period, the average relative humidity was 62 and 87% morning and evening, respectively. Sunshine hours ranged from 0.0 to 7.0 hours per day. The experiment consisted of 30 farmers' rice varieties, and all were grown in randomized complete block design with three replications. Twenty-one-day old seedlings were transplanted in the experimental site. Each genotype was planted in three rows of five-meter length and spacing of 15 × 20 cm with one seedling per hill. All the agronomic practices were adopted for good crop growth and development. Five random plants were tagged from each plot to record the data for yield and its related traits. A detailed list of the 30 Farmer's varieties are given below (Table 1).

Observations recorded-

Physiological growth parameters

Physiological traits were performed as per standard evaluation system of rice Gardner *et al*. (1985); Watson (1952), as listed below:

(a) Leaf Area Index (LAI)

$$\mathrm{LAI} = \frac{\text{Total leaf area}}{\text{Land area}}$$

$$\mathrm{LAI} = \frac{\mathrm{LA_2 + LA_1}}{2/\mathrm{P}}$$

(b) Leaf Area Duration (LAD)

$$\mathrm{LAD} = \frac{(\mathrm{LA_2 + LA_1})}{2} \times (\mathrm{t_2 - t_1})\ (\mathrm{cm^2\ days})$$

(c) Crop Growth Rate (CGR)

$$\mathrm{CGR} = \frac{\mathrm{w_2 - w_1}}{\mathrm{p\ (t_2 - t_1)}} \times (\mathrm{g\ cm^{-2}\ day^{-2}})$$

(d) Relative Growth Rate (RGR)

$$\mathrm{RGR} = \frac{\mathrm{LnW_2 - LnW_1}}{\mathrm{t_2 - t_1}}\ (\mathrm{g\ g^{-1}\ day^{-1}})$$

Chlorophyll content is expressed as grams of chlorophyll per unit leaf area. It was determined at 30.

DAT, 60 DAT and at 90 DAT stage using a non destructive method that uses an optical instrument called chlorophyll meter (Model: CCM 200 Made in USA).

Morphophysiological yield attributing traits. Morpho-physiological yield and yield attributes *viz.*, days to panicle initiation, 50% panicle initiation, milking stage, dough stage, physiological maturity and harvestable maturity, plant height (cm), number of tillers plant, number of panicle plant, length of panicle (cm), number of grains panicle^{1}, test weight (g) (1000 seeds), biological yield (g plant and kg ha), grain yield (g plant and kg ha) and harvest index (%) were recorded at different stages of crop growth.

Biochemical parameters

The biochemical estimation in the seeds of farmers' rice varieties for fat (%), crude fiber (%), and ash (%) were determined by using the following methods given below.

(a) Fat (%). The fat content in the seed sample was estimated by Pelican Equipment Socs Plus based on principle of Soxhlet's extraction method as described in AOAC (1980). The percent of fat was calculated by using following formula.

Calculate-

$$\text{Fat (\%)in ground sample} = \frac{\text{Wt. of flask (B)} - \text{Wt. of flask } (A)}{\text{Weight of sample}} \times 100$$

(b) Total crude fiber estimation. The crude fibre content in the seed sample was estimated, according to AOAC (1980). The percent of crude fiber was calculated by using following formula.

Calculate: -

$$\text{Crude fibre \%} = \frac{\text{Loss in wt. of ignition } \times \{(\mathrm{W}_2 - \mathrm{W}_1) - (W_3 - W_1)\}}{\text{Weight of sample}} \times 100$$

(c) Total ash (%). The ash content in the seed sample was estimated, according to AOAC (1980). The percent of Total ashwas calculated by using the following formula.

Calculate –

$$\text{Ash (\%)} = \frac{\text{Weight of ash}}{\text{Weight of sample}} \times 100$$

Principal components analysis. The Principal component analysis (PCA) is an Eigen vector based multivariate statistical technique which analyze and simplify the inter-relationship among a large set of variables in a small set of variables or components without losing any essential information of original data set, hence it reduces a large series of data into smaller number of components. Each component describes percent variation to the total variability. The objective of principal component analysis is to identify the minimum number of components, which can explain maximum variability out of the total variability (Anderson, 1972), and also to rank the genotypes on the basis of PC scores. Principal components are generally estimated either from the correlation matrix or covariance matrix. In the present investigation, correlation matrix was used to extract the principal components. PCA is a well-known method of dimension. Reduction (Massy, 1965), which seeks linear combinations of X columns with maximal variance, or equivalently high information.

Table 1: Details of farmer's rice varieties included for investigation.

T. No.	Treatments	Physiological maturity	Harvesting maturity	Grain Yield	
				g plant $^{-1}$	kg ha^{-1}
V1	Uresa	128.19	134.90	16.73	5675.00
V2	Nanha luchai	126.69	133.50	15.29	5475.30
V3	Navari	130.14	136.11	23.78	7899.56
V4	Kakera	128.17	133.49	19.53	6558.66
V5	Pusa khurri	122.68	131.57	20.61	7051.25
V6	Garudluchai	132.29	140.80	23.56	7947.47
V7	Uraiboota	132.17	140.89	23.78	7945.57
V8	Galgaliya	125.65	136.04	15.21	5160.24
V9	Lohandi	125.08	131.65	15.85	5351.58
V10	Vishnubhog	128.01	133.26	21.67	7591.96
V11	Chhindi kappoor	127.13	135.67	14.30	5142.66
V12	Jamunsurkhi	130.35	138.69	21.03	7058.41
V13	Tulsiamrit	128.71	137.06	19.16	6355.53
V14	Krishnabhog	124.10	137.51	19.80	6836.83
V15	Assamkoti	127.11	136.36	20.37	7043.22
V16	Jhular	119.33	128.04	9.31	3243.46
V17	Lakhoadhan	127.22	135.24	21.27	7138.89
V18	Lal lohandi	127.15	133.31	13.47	4580.57

V19	Patharchatti	122.89	132.68	20.95	7043.62
V20	Gurmatiya	123.70	131.34	20.16	6989.65
V21	Ranikajal	122.06	130.11	12.81	4484.45
V22	Rabuta	123.77	129.09	10.69	3753.49
V23	Chapti gurmatiya	120.15	128.02	9.16	3275.13
V24	Sathiya	125.73	130.59	10.73	3559.57
V25	Dhaur	119.81	127.97	9.24	3184.22
V26	Bhataphool	126.06	135.58	20.91	7274.15
V27	Karanphool	129.70	134.38	16.85	5841.44
V28	Karhani	123.21	137.99	21.65	7459.94
V29	Bharridhan	128.04	130.74	16.68	5765.70
V30	Akloni	123.78	131.98	19.22	6595.86

RESULTS AND DISCUSSION

In present investigation, principal component analysis was performed using physiological growth parameters and yield attributing components on rice genotypes. Out of twenty one traits studied, only five principal components (PCs) exhibited more than 1.00 Eigen value and showed 84.24 % of total cumulative variability among the traits studied. The PC1 showed 42.46 while PC 2, PC 3, PC 4 and PC 5, exhibited 20.97, 9.60, 6.18 and 5.02 variability respectively among the genotypes under study.

Scree plot. Scree plot is a simple line segment that depicts the percentage of total variation in the data associated with each principal component obtained. It is interpreted by drawing a graph between eigen values and principal component numbers. PC1 showed 42.46% variability with 8.918 eigen values which then declined gradually (Fig. 1).

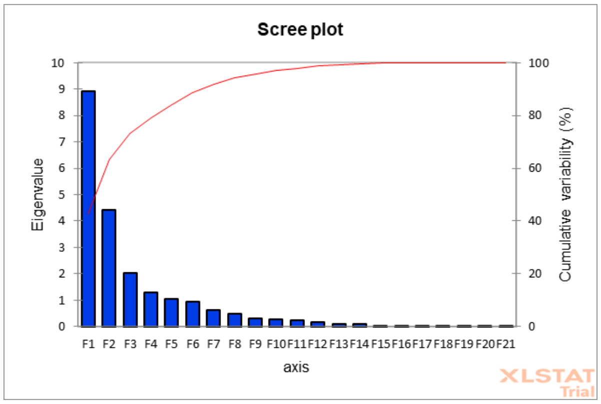

Fig. 1. Scree plot of principal component of farmer's varieties of rice between Eigen values and principal components.

Rotated component matrix. Rotated component matrix is depicted in Table 3 and 4. It represented that the PC 1 which reported highest variability (42.46%) was mostly associated with major physiological parameters and yield related traits such as leaf area index, leaf area duration, number of grain per panicle, number of panicle plant^{-1}, total dry matter, biological yield, harvest index and grain yield.

The PC 2 was dominated by phenophases and yield related traits such as total panicle initiation, 50% panicle initiation, milking stage, dough stage, length of panicle and number of tillers plant^{-1}.

The PC3 was dominated by some phenophases and yield related traits such as number of physiological maturity, harvesting maturity and plant height. The PC4 was dominated by chlorophyll content index. The PC5 was dominated by test weight.

Table 2: Eigen values, variance and cumulative percentage of different traits of rice genotypes under study.

Characters	**PC**	**Eigen value**	**Variability (%)**	**Cumulative (%)**
Days to panicle initiation	PC1	8.918	42.468	42.468
Days to 50% panicle initiation	PC2	4.404	20.970	63.438
Days to milking stage	PC3	2.017	9.603	73.040
Days to dough stage	PC4	1.298	6.182	79.222
Days to physiological maturity	PC5	1.054	5.020	84.242

Days to harvesting maturity	PC6	0.949	4.518	88.761
Total dry weight (g plant-1)	PC7	0.635	3.024	91.785
Leaf area index	PC8	0.493	2.348	94.133
Leaf area duration (cm2 days)	PC9	0.316	1.505	95.638
Chlorophyll content index	PC10	0.268	1.279	96.916
Plant height (cm)	PC11	0.220	1.049	97.966
Number of tillers plant-1	PC12	0.178	0.849	98.815
Number of panicle plant-1	PC13	0.102	0.486	99.301
Length of panicle (cm)	PC14	0.080	0.383	99.684
Number of grains panicle-1	PC15	0.024	0.112	99.796
Test weight (g)	PC16	0.017	0.079	99.875
Biological yield (gm/plant)	PC17	0.009	0.045	99.920
Biological yield (Kg/ha)	PC18	0.007	0.035	99.955
Harvest index (%)	PC19	0.006	0.027	99.982
Grain yield (gm/plant)	PC20	0.003	0.016	99.998
Grain yield (Kg/ha)	PC21	0.000	0.002	100.000

Table 3: Rotated component matrix for 28 yield attributing and quality related traits.

Traits	**Principal Components**				
	PC 1	**PC 2**	**PC 3**	**PC 4**	**PC 5**
PI	0.169	0.964	0.044	-0.016	-0.021
50 % PI	0.136	0.950	0.047	0.044	-0.051
MS	0.141	0.960	0.022	-0.014	-0.007
DS	0.165	0.968	0.050	0.007	-0.007
PM	-0.125	-0.882	0.036	0.030	-0.072
HM	-0.030	-0.877	0.080	0.030	-0.062
TDM	0.226	0.150	0.163	0.005	0.101
LAI	0.385	0.318	0.142	0.012	-0.038
LAD	0.244	0.113	0.209	0.122	0.115
CCI	0.543	-0.079	0.139	0.681	0.277
PH	0.067	0.032	0.902	0.065	0.057
NOT	-0.009	0.238	-0.226	0.053	-0.031
NOP	0.501	0.047	0.099	0.129	0.049
LOP	0.166	0.287	0.214	0.050	0.211
NOG	0.660	0.223	0.101	0.058	-0.350
TW	0.332	0.006	0.062	0.117	0.903
BI (gm/p)	0.946	0.211	0.041	0.014	0.145
BI (kg/ha)	0.930	0.132	0.048	-0.004	0.186
HI (%)	0.886	0.093	0.039	0.183	0.004
GY (gm/p)	0.966	0.138	0.020	0.062	0.077
GY (Kg/ha)	0.967	0.154	-0.002	0.060	0.102
Extraction Method: Principal Component Analysis Rotation Method: Varimax with Kaiser Normalization					

Extraction Method: Principal Component Analysis Rotation Method: Varimax with Kaiser Normalization

PL-Panicle initiation, 50% PI- 50% Panicle initiation, MS Milking stage, DS-Dough stage. PM-Physiological maturity. IIM Harvestable maturity, TDM- Total dry matter accumulation, LAl-Leaf area index, LAD- Leaf area duration. CGR-Crop growth rate. RGR- Relative growth rate, CCI Chlorophyll content index. PH- Plant height, NOT-Number of tillers plant, NOP-Number of panicle plant", LOP-Length of panicle plant', NOG- Number of grain panicle, TW- Test weight, HI- Harvest index, BY- Biological yield, GY- Grain yield. A- Ash %, CF- Crude Fibre%. F- Fat%

PC scores. On the basis of principal component scores (PC scores), the genotypes were classified in all the five PCs are presented in Table 5. In PC1, the genotype Garudluchai (7.260) acquired highest positive value PCs followed by Navari (4.161), Vishnubhog (3.641) and Krishnabhog (3.063) respectively (Table 5).

In PC2, the genotype Uraiboota (5.834) acquired highest positive value followed by Nanhaluchai (3.027), Navari (2.415) and Lohandi (2.230) respectively (Table 5). In PC3, the genotype Galgaliya (2.264) acquired highest positive value followed by Uraiboota (2.143), Nanhaluchai (1.978) and Lal lohandi (1.821) respectively (Table 5). In PC4, the genotype Ranikajal (2.841) acquired highest positive value followed by Bharridhan (2.816) respectively. In PC5, the genotype Vishnubhog (1.977) acquired highest positive value followed by Galgaliya (1.610) and Karhani (1.606) respectively (Table 5).

In the overall five PCs, genotype Garudluchai (7.260) contributing their presence in PC1 and has highest PC scores among all the genotypes followed by Navari (4.161), Vishnubhog (3.641) and Krishnabhog (3.063) respectively (Table 5).

Table 4: Principal Component Score of Farmer's varieties of rice.

T. No.	Genotypes	PC1	PC2	PC3	PC4	PC5
1	Urea	-0.689	-0.106	-0.471	-1.557	-1.006
2	Nanhaluchai	-2.060	3.027	1.978	1.345	1.581
3	Navari	4.161	2.415	1.292	0.082	0.411
4	Kakera	-0.948	2.214	-0.388	-0.163	-0.137
5	Pusakhurri	2.319	-1.934	-1.315	-1.167	0.272
6	Garudluchai	7.260	-0.572	1.592	1.237	-0.576
7	Uraiboota	2.690	5.834	2.143	-0.144	-0.101
8	Galgaliya	-1.501	-1.324	2.264	-0.381	1.610
9	Lohandi	-2.531	2.230	0.481	0.166	-2.375
10	Vishnubhog	3.641	-1.777	-0.883	0.119	1.977
11	Chhindikappoor	-1.893	-0.119	-0.132	0.650	0.172
12	Jamunsurkhi	-0.919	2.133	-3.364	-0.274	-1.138
13	Tulsiamrit	0.382	1.216	0.310	-0.964	-1.045
14	Krishnabhog	3.063	-2.553	-0.041	-1.221	-1.024
15	Assamkoti	1.603	0.049	0.249	-0.951	-0.215
16	Jhular	-6.628	-0.063	-0.093	-0.379	0.392
17	Lakhoadhan	0.009	1.889	-0.903	-1.302	0.961
18	Lal lohandi	-1.313	-0.564	1.821	-1.765	-0.898
19	Patharchatti	2.446	-0.574	-0.179	-0.137	0.693
20	Gurmatiya	1.171	-1.109	-2.718	-0.644	0.263
21	Ranikajal	0.282	-2.533	-0.675	2.841	-2.087
22	Rabuta	-1.452	-2.889	1.343	1.587	-0.616
23	Chaptigurmatiya	-7.537	0.162	-0.695	-0.183	0.380
24	Sathiya	-2.445	-2.988	1.075	0.131	-0.015
25	Dhaur	-2.609	-3.806	1.795	-0.432	0.680
26	Bhataphool	1.543	0.851	-1.481	-0.368	0.046
27	Karanphool	-1.622	1.707	-1.063	0.451	1.052
28	Karhani	2.027	-0.680	-2.250	1.547	1.606
29	Bharridhan	-0.918	1.329	-0.531	2.816	-0.333
30	Akloni	2.468	-1.464	0.839	-0.941	-0.530

In this study, the genotypes contributing their presence in more than one principal components and also have >1.0 PC score were selected here for further consideration.

From this study, it was reported that PC1 was constituted by most of the physiological parameters and yield attributing traits; hence genotypes belonging to these PCs like Garudluchai, Navari, Vishnubhog and Krishnabhog should be used for rice improvement programme to develop promising rice genotypes. Similarly, PC2 reported for the phenophasic development and some yield attributing traits, hence genotypes like Uraiboota, Nanhaluchai, Navari and Lohandi should be selected from these PCs can be utilized for rice variety improvement programme. Genotypes that were common in all the above mentioned five PCs are (Table 4) Garudluchai, Uraiboota, Karhani, Nanhaluchai, Vishnubhog, Gagaliya, Rabuta and Navari.

Table 5: Interpretation of rotated component matrix for the traits having highest value in each PCs.

PC1	PC2	PC3	PC4	PC5
GY (Kg/ha)	DS	PH	CCI	TW
GY (gm/p)	PI	HM		
BI (gm/p)	MS	PM		
BI (kg/ha)	50 % PI			
HI (%)	LOP			
NOG	NOT			
NOP				
LAI				
LAD				
TDM				

PI-Panicle initiation, 50% Pi- 50 % Panicle initiation, MS Milking stage, DS- Dough stage, PM-Physiological maturity. HM-Harvestable maturity, TDM- Total dry matter accumulation, LAI-Leaf area index, LAD-Leaf area duration. CGR-Crop growth rate, RGR- Relative growth rate, CCI Chlorophyll content index, PH- Plant height, NOT-Number of tillers plant, NOP-Number of panicle plant, LOP-Length of panicle plant. NOG - Number of grain panicle'. TW- Test weight, III- Harvest index, BY-Biological yield, GY- Grain yield, A-Ash%, CF-Crude Fibre%, F-Fat%

In this investigation twenty six traits were selected for PCA analysis. The first principal component (PC1), PC1 accounted maximum proportion of total variability in the set of all variables and remaining components accounted for progressively less amount of variation. Out of all principal components, only five principal components (PCs) exhibited more than 1.00 Eigen value and showed 84.24 % of total cumulative variability among the traits studied. The PC1 showed 42.46 while PC 2, PC 3, PC 4 and PC 5, exhibited 20.97, 9.60, 6.18 and 5.02 variability, respectively among the genotypes under study. This finding was in agreement with Gour *et al.* (2017).

Table 6: Line selected on the basis of high PC score (>1.0) in each component contributing positive values.

PC1	PC2	PC3	PC4	PC5
Garudluchai	Uraiboota	Galgaliya	Ranikajal	Vishnubhog
Navari	Nanhaluchai	Uraiboota	Bharridhan	Galgaliya
Vishnubhog	Navari	Nanhaluchai	Rabuta	Karhani
Krishnabhog	Lohandi	Lal lohandi	Karhani	Nanhaluchai
Uraiboota	Kakera	Dhaur	Nanhaluchai	Karanphool
Akloni	Jamunsurkhi	Garudluchai	Garudluchai	
Patharchatti	Lakhoadhan	Rabuta		
Pusakhurri	Karanphool	Navari		
Karhani	Bharridhan	Sathiya		
Assamkoti	Tulsiamrit			
Bhataphool				
Gurmatiya				

Rotated component matrix revealed that the PC1 which accounted for the highest variability (42.46) was mostly associated with major physiological parameters and yield related traits such as leaf area index, leaf area duration, number of grains panicle^{-1}, number of panicles plant^{-1}, total dry matter, biological yield, harvest index and grain yield. Hence PC1 contributed major physiological parameters and yield related traits. The genotypes showed presence under this PC will be potent for transfer of yield as well as physiological traits after hybridization for the transfer of dominated traits in the deficient lines/cultivars for the development of high yielding rice lines. These findings were in agreement with the findings of Gour *et al.* (2017); Pachauri *et al.* (2017).

The PC2 was dominated by phenophases and yield related traits such as total panicle initiation, 50% panicle initiation, milking stage, dough stage, length of panicle and number of tillers plant^{-1}. This PC would be helpful for the selection of desired rice lines for the improvement of phenophasic development and yield parameters.

The PC3 was dominated by some phenophases and yield related traits such as number of physiological maturity, harvesting maturity and plant height. Selection of genotypes from this PC will be advisable.

The PC4 was dominated by only one trait *i.e.* chlorophyll content index. The PC5 was dominated by test weight. Selection of genotypes from these PCs would be potent for the traits dominated in these clusters.

From this study, it is clear that most of the important physiological parameters and yield attributing traits were present in PC1. Hence, genotypes belonging to these PCs should be selected for development of high yielding genotypes. Similarly, for the improvement in phenophesic development components, genotypes should be selected from PC2. Therefore an effective breeding programme could be initiated by selecting lines from these principal components.

In overall PCs, PC1, the genotype Garudluchai (7.260) acquires highest positive value PCs followed by Navari (4.161), Vishnubhog (3.641) and Krishnabhog (3.063) respectively.

Genotype Garudluchai (7.260) contributed highest PC score among all the genotypes included in this study. According to PCA analysis, this genotype dominated in PC1. Similarly, genotype Navari (4.161) and Vishnubhog (3.641) from PC1 contributed highest positive value from all of the five PCs. Here, the genotypes contributing highest PC score (>5.0) are considered for the best genotypes selection. PC1 was dominated with physiological parameters and yield attributing traits and selection of genotypes from these PCs will be helpful for the identification of donor for the transfer of physiological parameters and yield attributing traits.

Genotypes contributing their presence in more than one PC with high PC score might be utilized in the rice improvement programme to contribute as parent donors, or directly released as variety exhibiting good physiological growth and high yielding attributes. On the basis of study, such type of genotypes were Garudluchai (PC1, PC3, and PC4), Uraiboota (PC1, PC2, and PC3), Nanhaluchai (PC2, PC3, PC4, and PC5), Karhani (PC1, PC4, and PC5), Navari (PC2, PC3), Karanphool (PC2, PC5) and Bharridhan (PC2, PC4). Satyanarayana *et al*. (2023) has also utilized principal component analysis as an important multi-variate analysis tool for identification of promising traits for yield improvement in rice crop,

On the basis of PCA findings, among all genotypes contributing their presence in more than one PC with high PC score were only three genotypes *viz*., Garudluchai, Uraiboota, Karhani and confined with desirable physiological, yield associated traits. These lines might be utilized in hybridization programme for the development of promising rice cultivars.

CONCLUSIONS

In the present investigation the genotype Garudluchai (7.260) contributed highest PC score among all the genotypes included in this study. Similarly, genotype Navari (4.161) and Vishnubhog (3.641) from PC1 contributed highest positive value from all of the five PCs. Here, the genotypes contributing highest PC score (>5.0) could be considered for the best genotypes selection. PC1 was dominated with physiological parameters and yield attributing traits and selection of genotypes from these PCs will be helpful for the identification of donor for the transfer of physiological parameters and yield attributing traits.

On the basis of PCA findings, among all genotypes contributing their presence in more than one PC with high PC score only three genotypes *viz*., Garudluchai, Uraiboota, Karhani confine with desirable physiological, yield associated traits. These lines might be utilized in hybridization programme the development of promising rice cultivars.

FUTURE SCOPE

The study identifies Garudluchai, Uraiboota, and Karhani as promising rice genotypes with high PC scores linked to desirable physiological and yield traits, making them valuable for rice improvement. Future research should focus on using these genotypes in hybridization programs, conducting genomic and QTL analyses, and evaluating their performance across environments. Integrating their traits through marker-assisted selection and developing elite lines can accelerate the creation of high-yielding, stress-resilient cultivars to support future food security.

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Conflict of Interest. None.

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