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Diversity analysis of rice (*Oryza sativa* L.) germplasm accessions using principal component analysis

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Abstract

In the present study, fifty seven rice genotypes were chosen for diversity analysis using principle component analysis. The whole experiment was executed at Research cum Instructional Farm, Department of Genetics and Plant Breeding, College of Agriculture, Indira Gandhi Krishi Vishwavidyalaya, Raipur, during *Kharif* 2020. Principal components with Eigen values greater than 1 and variance level greater than 6 level is perceived to be the main PC. In this study, six components were displayed eigen values of >1 and presented cumulative variation of 79.59%. The first PC (24.70%) and second PC (17.34%) showed for cumulative variation 42.04%. The PC1 recorded 24.70%, although PC2, PC3, PC4, PC5 and PC6 displayed 17.34%, 12.90%, 9.93%, 8.55% and 6.17% variance respectively between the accessions for the characters in analysis. Genotypes IC125755, IC463062, IC121886, IC518800, IC377829, MTU-1010, DRR-42, Dagad Desi, Annada, IC593995, IC378553, IC74800X, IC203364, IC458046X, IC514243 and IC115726 were found to be promising and genetically divergent. As a result, these genotypes might be used in the hybridization programme to develop transgressive segregants.

Keywords: Diversity analysis, principle component analysis, germplasm accessions

Introduction

Rice (*Oryza sativa* L., $2n=2x=24$) belongs to the genus *Oryza*, which includes two cultivated species, *Oryza sativa* and *Oryza glaberrima*, as well as 22 wild species. It is India's most popular food crop and plays a crucial role in the country's agriculture. In India rice has covered 43.78 million hectares area, with 177.64 million tons production and 4057.70 kg/ha productivity (Anonymous, 2019) [1]. Chhattisgarh is known as the "Rice Bowl of India." Rice's rich biodiversity in Chhattisgarh provides strong evidence that it is cultivated as the main crop. This biodiversity serves as a source and allows for a great deal of variation. In Chhattisgarh, rice has covered an area of 3848.78 hectares producing 7823.33 tons and 2044.27 kg/ha productivity (Anonymous, 2021) [2].

Genetic diversity is essential for determining genetic differences within a genotype. Diversity not only generates variability, but it also introduces new gene combinations or different gene combinations. In general, knowledge of the extent and degree of genetic divergence aids in the selection of appropriate parents for a breeding programme.

Principal Component Analysis (PCA) is a multivariate statistical tool that analyses a set of data in which the results are expressed by a number of interrelated quantitative dependent variables. Its objective is to extract useful information from the table, represent it as a set of new orthogonal variables known as major variables and visualize similarity patterns between observations and parameters as map points. 'Eigen values' measure the relevance and importance of each factor to the total variance, while each individual vector coefficient measures the degree to which each original variable is associated with each main component (Nachimuthu *et al.*, 2014) [4].

Material and Methods

The experimental materials consisted of fifty rice germplasm accessions along with seven checks, namely Dagad Desi, RRF-127, RRF-140, DRR Dhan-42, MTU-1010, Annada and Swarna were used as biological material. These fifty germplasm accessions were selected randomly from five hundred germplasm accession from DBT, New Delhi. The experiment was laid out in a Randomized Block Design with two replications during *Kharif* 2020. The plant materials raised bed nursery was sown on last week of June 2021.

In randomized block design twenty three days old seedlings were transplanted into the field. The experimental materials were transplanted in two replications and individual replication consisted of fifty seven genotypes. Each entry was transferred in two rows where row to row spacing was 20 cm and plant to plant spacing was 15 cm. Check varieties were randomized within block.

Table 1: List of fifty germplasm accessions used in the experiment

S. No.	Accession No.	S. No.	Accession No.
1	IC-386140	26	IC-463986
2	IC-216827	27	IC-283005
3	IC-121886	28	IC-126331
4	IC-461904	29	IC-518800
5	IC-217358	30	IC-458608
6	IC-206758	31	IC-125755
7	IC-516693	32	IC-386358
8	IC-458657X	33	IC-458005
9	IC-449598	34	IC-459489
10	IC-203364	35	IC-514384
11	IC-217772	36	IC-377829
12	IC-463062	37	IC-115641
13	IC-218829	38	IC-459795
14	IC-126210	39	IC-378183
15	IC-126468	40	IC-218729
16	IC-114501	41	IC-206352
17	IC-115726	42	IC-300416
18	IC-377660	43	IC-74800X
19	IC-378252	44	IC-133944
20	IC-378553	45	IC-114573
21	IC216830	46	IC205951
22	IC134905	47	IC514243
23	IC593995	48	IC517398
24	IC378408	49	IC378032
25	IC458406X	50	IC207460

Statistical analysis

Principal Component analysis was used to determine genetic variability for these traits. Genotypic means were used for the PCA with respect to each trait. Each data analysis was conducted by using XLSTAT version 2020.3.

Results and Discussion

The analysis of variance indicated the existence of highly significant differences among genotypes for all the characters studied. This indicated presence of high variability among the genotypes, which provides ample scope for selection for different yield and yield attributing characters for rice improvement programme. Significant variation in all the traits studied indicated the presence of high genetic diversity among all the genotypes of rice.

PCA was performed on rice genotypes for yield and yield

attributing traits to identify the important components and genotypes identified for better characters related to rice improvement programmes. In this study, six components were displayed Eigen values of >1 and presented cumulative variation of 79.59%. The first PC (24.70%) and second PC (17.34%) showed for cumulative variation 42.04%. The PC1 recorded 24.70%, although PC2, PC3, PC4, PC5 and PC6 displayed 17.34%, 12.90%, 9.93%, 8.55% and 6.17% variance respectively between the accessions for the characters in analysis. Those genotypes that had higher paddy length, paddy width, paddy length/width ratio, brown rice length, brown rice width, brown rice length width ratio and grain yield per plant were categorized by the first principal component which explained that PC2 discriminated those genotypes having higher grain dimensions and grain yield per plant. The second principal component was contributed mostly by days to 50 percent flowering, plant height, panicle length, number of effective tillers per plant, filled grains per panicle, number of unfilled grains per panicle, biological yield per plant, harvest index, 100 seed weight and paddy width. Panicle length, number of unfilled grains per panicle and spikelet fertility percentage were the main traits contributing to PC3, whereas biological yield per plant and grain yield per plant were the main contributing traits for PC4.

PC5 was discriminated by days to 50 percent flowering, plant height, effective tillers per plant, filled grains per panicle, spikelet fertility percentage, paddy length, paddy width, brown rice length and brown rice width whereas PC6 was discriminated by days to 50 percent flowering, plant height, panicle length, effective tillers per plant, harvest index and paddy length. The characters days to 50 percent flowering, Traits that have both positive and negative effects on the PCs can be considered the main source of diversity and have largely contributed to the differentiation of rice genotypes. To have a wide range of gene transfer during crop improvement programmes, high-variability traits are desired (Nachimuthu *et al.*, 2014)^[4]. As a consequence, these traits can be used to select diverse genotypes from a particular principal component. The results of the present study were in close accordance with findings of Ojha *et al.*, (2017)^[5], Gour *et al.*, (2017)^[3], Sao *et al.*, (2019)^[6] and Vageeshvari *et al.*, (2021)^[7].

From the diversity analysis it can be concluded that the genotypes IC125755, IC463062, IC121886, IC518800, IC377829, MTU-1010, DRR-42, Dagad Desi, Annada, IC593995, IC378553, IC74800X, IC203364, IC458046X, IC514243 and IC115726 were found to be promising and genetically divergent. As a result, these genotypes might be used in the hybridization programme to develop transgressive segregants.

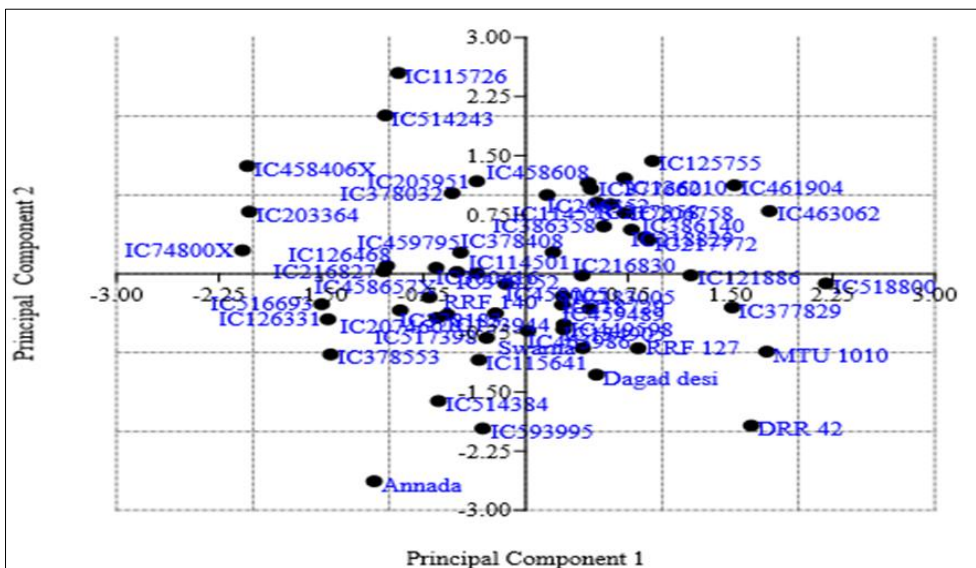


Fig 1: PCA scatter diagram showing the dispersion of rice genotypes across PC1 and PC2

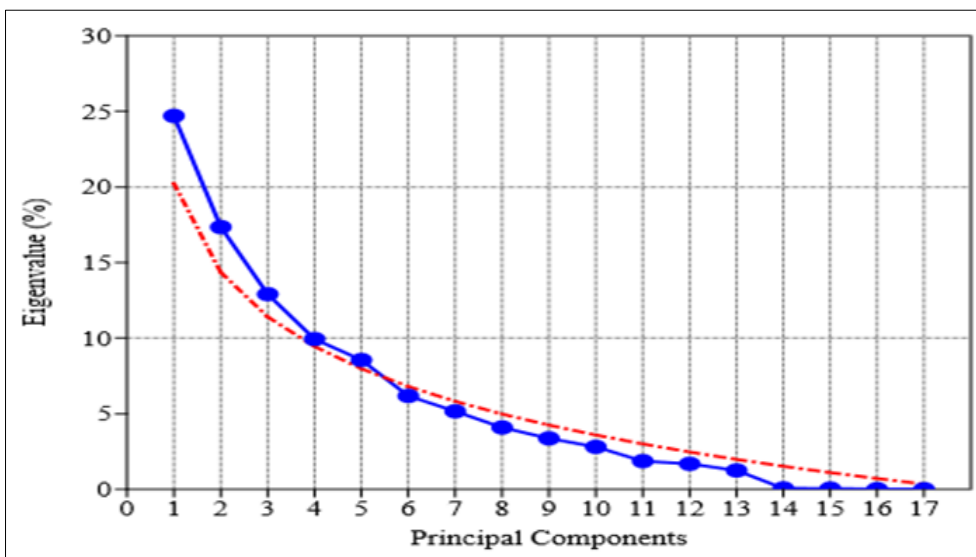


Fig 2: Scree test for component analysis

Table 2: Eigen value, percentage of variance and Eigen vector for fifty seven genotypes for yield and grain quality traits

Traits	Principal component					
	PC1	PC2	PC3	PC4	PC5	P6
Eigen values	4.19	2.94	2.19	1.68	1.45	1.05
% of Variance	24.70	17.34	12.90	9.93	8.55	6.17
Cumulative %	24.70	42.04	54.94	64.87	73.42	79.59
Component Matrix	Factor loading values					
Days to 50% flowering	0.08	0.26	-0.07	0.01	0.28	-0.51
Plant height(cm)	-0.11	0.31	0.18	-0.110	0.32	0.30
Panicle length(cm)	-0.02	0.26	0.29	-0.15	-0.01	0.23
Number of effective tillers/plant	-0.01	-0.24	-0.16	-0.07	-0.45	0.32
Number of filled grains/panicle	-0.02	0.42	-0.19	0.03	0.26	0.15
Number of unfilled grains/panicle	0.06	0.24	0.52	-0.15	-0.15	-0.10
Spikelet fertility percentage (%)	-0.05	-0.00	-0.58	0.15	0.28	0.16
Biological yield/plant(g)	0.11	0.21	0.10	0.65	-0.13	0.17
Harvest index (%)	0.19	-0.31	0.07	-0.00	0.16	-0.45
100 seed weight(g)	0.10	-0.37	0.20	0.08	0.07	0.18
Paddy length(mm)	0.36	-0.13	0.13	-0.02	0.26	0.23
Paddy width(mm)	-0.29	-0.27	0.22	0.13	0.31	0.03
Paddy L/W ratio	0.44	0.10	-0.06	-0.11	-0.05	0.13
Brown rice length(mm)	0.34	-0.18	0.06	-0.08	0.35	0.20
Brown rice width(mm)	-0.33	-0.18	0.19	0.08	0.28	0.13
Brown rice L/W ratio	0.45	0.00	-0.06	-0.13	0.03	0.03
Grain yield/plant(g)	0.22	0.03	0.15	0.63	-0.05	-0.08

Table 3: List of selected accessions in each principal component on the basis of top 10 PC score

S. No.	PC1	PC2	PC3	PC4	PC5	PC6
1	IC518800	Annada	IC126331	IC458005	Swarna	RRF-140
2	IC74800X	IC115726	IC114573	IC115726	IC516693	DRR-42
3	IC458406	IC514243	IC378553	Dagad desi	IC74800X	IC463062
4	IC203364	IC593995	IC458005	IC386140	Annada	IC114573
5	IC463062	DRR-42	IC378252	IC206758	IC458608	Swarna
6	MTU-1010	IC514384	IC459795	IC378408	IC283005	IC206352
7	DRR-42	IC125755	IC514243	IC377829	DRR-42	IC518800
8	IC461904	IC458406	IC378032	IC126468	IC300416	IC378032
9	IC377829	Dagad desi	IC463062	IC514243	IC378032	Dagad desi
10	IC516693	IC126210	IC126210	MTU-1010	IC217358	IC74800X

References

1. Anonymous. Food and Agriculture Organization of the United Nations 2019.
2. Anonymous. State level Agricultural Statistics, Directorate of Agriculture, Raipur, Chhattisgarh 2021.
3. Gour L, Maurya SB, Koutu GK, Singh SK, Shukla SS, Mishra DK. Characterization of rice (*Oryza sativa* L.) genotypes using principal component analysis including scree plot & rotated component matrix. International Journal of Chemical Studies 2017;5(4):975-83.
4. Nachimuthu VV, Robin S, Sudhakar D, Raveendran M, Rajeswari S, Manonmani S. Evaluation of rice genetic diversity and variability in a population pannel by principal component analysis. Indian J Sci. Technol 2014;7(10):1555-1562.
5. Ojha GC, Sarawgi AK, Sharma B, Parikh M. Principal component analysis of morpho-physiological traits in rice germplasm accessions (*Oryza sativa* L.) under rainfed condition. International Journal of Chemical Studies 2017;5(5):1875-1878.
6. Sao R, Saxena RR, Sahu PK. Assesment of genetic variation and diversity in rice genotypes based on principal component analysis. Journal of Plant Development Sciences 2019;11(12):725-730.
7. Vageeshvari, Chaudhari PR, Gauraha D. Genetic diversity analysis of grain yield and quality traits in rice germplasm accessions (*Oryza sativa* L.) by principal component analysis. International Journal of Chemical Studies 2021;8(6):108-111.