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Principal component analysis for yield and its attributing traits in indigenous germplasm accessions of rice (*Oryza sativa* L.)

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Abstract

The present investigation was carried out in *Kharif* 2017 to estimate the relative contribution of various traits for total genetic variability present in indigenous germplasm accessions by Principal Component Analysis. 50 rice germplasm accessions along with five check varieties were evaluated for 10 yield and yield attributing traits by Principal Component Analysis. Out of ten only three principal components (PCs) exhibited more than 1 Eigen value and explained at least 5% of variation along with 70.086% cumulative variability among the traits studied and PC1 showed 33.603% while PC2, PC3 exhibited 19.891% and 16.592% variability. In the first principal component analysis PC1 which accounted for the highest variability (37.836) and positively correlated with traits such as days to 50% flowering, number of effective tillers per plant and days to maturity. The second principal component PC2 accounted for 19.891% of total variability and is highly positively correlated with 100 seed weight, seed yield per plant and plant height. PC2 is highly loaded with genotype having increased 100 seed weight, seed yield and its attributing traits and in PC3 highly positively loaded traits like paddy length breadth ratio and 100 seed weight showed 16.592% of the total variability. All the principal components were showing positive contribution for yield and its attributing traits. These variations can be exploited in crop improvement programme for developing high yielding varieties.

Keywords: Principal component analysis, indigenous germplasm, rice

Introduction

'Rice is Life' for most of the World population and cultivation of rice has shaped culture, diet and economic status of millions of people. Rice is grown in more than 100 countries across the globe. It is an important staple food for more than half of the world's population and hence, is referred to as "Global Grain" (Prasad *et al.*, 2018) ^[11]. In view of the growing population, the basic objective of the plant breeders would always be towards yield improvement in staple food crops. It has been estimated that the world will have to produce 60% more rice by 2030 than what it produced in 1995. Therefore, to increase production of rice plays a very important role in food security and poverty alleviation. It is estimated that the demand for rice will be 121.2 million tonnes by the year 2030, 129.6 million tonnes by the year 2040 and 137.3 million tonnes by the year 2050 (Kumar *et al.*, 2014) ^[7]. The major resource of plant breeders is the genetic variability in gene pool accessible to the crop of interest (Thottappily *et al.*, 1996) ^[9]. The successes of crop improvement programs are highly reliant on the efficient manipulation of that genetic variability (Mignouna *et al.*, 1996) ^[9].

Multivariate analysis helps the plant breeders to formulate their selection approaches for improving the desired traits (Ravindra *et al.*, 2012)^[12]. Principal components analysis (PCA) is a multivariate statistical technique which is used to explore the variation among genotypes and remove redundancy in data sets when the variables are measured in different units (Maji and Shaibu, 2012)^[8]. Therefore, it becomes appropriate to standardize the variables for relating the variation of a data set. It explores the resemblance among the variable and classify the genotypes on basis of inter-correlated dependent quantity variables (Idris and Khalid, 2013)^[6]. By using a few components, each sample can be represented by relatively few numbers instead of by values for thousands of variables (Ringer, 2008)^[13]. The core objective of the PCA is to drive the significant information from the variable data and describe it as new orthogonal variable sets to show the similarity behavior of observations and variables as points in graph. The Eigen value describes and measures the contribution of each component to the total variance while each coefficient of proper vector shows the percentage of participation of each original variable with that each principle component is related (Nachimuthu *et al.*, 2014)^[10].

The higher the coefficients value, either positive or negative, the more effective it will be in discriminating between entries (Bhakta and Das, 2008) ^[2]. Considering the importance of PCA an investigation was carried out to study the principal component analysis for yield and its attributing traits in indigenous germplasm accessions of rice (*Oryza sativa* L.).

Materials and Methods

This experiment was carried out at Research cum Instructional Farm, Department of Genetics and Plant Breeding, College of Agriculture, Indira Gandhi Agricultural University, Raipur, Chhattisgarh during *kharif* 2017. The experimental material consists of 50 rice germplasm accessions along with five check varieties namely, Indira Barani Dhan 1, Indira Aerobic 1, Danteshwari, Chhattishgarh Zinc Rice 1 and Samleshwari were used in the present study. Nursery sowing was done in well prepared raised seed bed in first week of July 2017 and the crop was ready to harvest by mid of November 2017. Here twenty one days old seedlings were transplanted in well puddle field in Augmented Block Design as suggested by Federer, 1956. Each rice accession was transplanted in two rows of 2 m row length. The randomization of check varieties was done within each block. Five random but robust plants from inner rows were tagged from each plot for data collection. A total of ten yield and its attributing traits viz., days to 50 % flowering, plant height (cm), panicle length (cm), number of effective tillers per plant, days to maturity, 100 seed weight (g), seed yield per plant (g), paddy length (mm), paddy breadth (mm) and paddy length breadth ratio were recorded at particular stages of rice plant following the minimal descriptor of rice. The observations recorded were statistically analyzed using **OPSTAT** software.

Table 1: List of the rice germplasm accession used in the research study

S. No.	Accession No.	Accession Name	S.No.	Accession No.	Accession Name
1.	CGR: 56	Chhatri	29.	CGR: 131	Harad gundi
2.	CGR: 58	Chhota kabari (i)	30.	CGR: 136	Hardi chudi
3.	CGR: 59	Chhoti dhan	31.	CGR: 5423	Badweli
4.	CGR: 60	Chilhar	32.	CGR: 5424	Baga bija
5.	CGR: 62	Chinger	33.	CGR: 5425	Bagad
6.	CGR: 67	Chiraigodi	34.	CGR: 5426	Baggar
7.	CGR: 69	Chirounji fokla	35.	CGR: 5427	Bagi
8.	CGR: 71	Chirputi	36.	CGR: 5428	Bag much
9.	CGR: 72	Churhale dhan	37.	CGR: 5429	Bag muda
10.	CGR: 74	Dagad deshi	38.	CGR: 5430	Bagti nagkesar
11.	CGR: 75	Dahi chitari	39.	CGR: 5431	Bahala dugji
12.	CGR: 85	Deshi local	40.	CGR: 5433	Bahali bijo
13.	CGR: 86	Deshi safed	41.	CGR: 5434	Bahangi
14.	CGR: 90	Dihula	42.	CGR: 5435	Bahawar kanak
15.	CGR: 97	Dihula deshi	43.	CGR: 5436	Bahela
16.	CGR: 98	Dokra mechha	44.	CGR: 5437	Bahidra
17.	CGR: 100	Dubraj	45.	CGR: 5438	Bahra sinki
18.	CGR: 101	Dudh bhursi	46.	CGR: 5440	Baidlo
19.	CGR: 103	Dudhiya danwar	47.	CGR: 5441	Baigan
20.	CGR: 104	Dutari	48.	CGR: 5442	Baigani
21.	CGR: 106	Ek beej	49.	CGR: 5445	Baiha gunda
22.	CGR: 107	Fara	50.	CGR: 5446	Baikana
23.	CGR: 114	Gadur sela		Checks	
24.	CGR: 115	Gajaru	1.	Indira Barani Dhan 1	
25.	CGR: 117	Ganga baru	2.	Indira Aerobic 1	
26.	CGR: 122	Gidhan pankhi	3.	Danteshwari	
27.	CGR: 125	Gudma	4.	Chhattishgarh Zinc Rice 1	
28.	CGR: 130	Haldi gathi	5.	Samleshwari	

Results and Discussion

In the present investigation, PCA was performed for ten yield related traits in promising rice accessions. As per the criteria set by Brejda *et al.* $(2000)^{[3]}$, the PC with Eigen values >1 and which explained at least 5% of variation in the data were considered in present study. The PC with higher Eigen values and variables which had high factor loading were considered as best representative of system attributes. Out of 10, only three principal components (PCs) exhibited more than 1 Eigen value, and explained at least 5% of variation along with 70.086% cumulative variability among the traits studied. So, these three PCs were given due importance for further explanation.

PC1 showed 33.603% while PC2, PC3 exhibited 19.891% and 16.592% variability, respectively among the accessions

for the traits under (table 2). The first PC accounts for as much of the variability in the data possible, and each succeeding component accounts for as much of the remain variability as possible.

Rotated component matrix revealed that the PC1 which accounted for the highest variability and positively correlated with traits such as days to 50% flowering (0.913), number of effective tillers per plant (0.871), days to maturity (0.911). The first principal component PC1 exhibited more than 37% of total variance. Here number of days to 50% flowering, number of effective tillers per plant and days to maturity were the variables that contributed most positively and highly loaded. As a result, the first component PC1 differentiated those accessions having high loading factor for days to 50% flowering, number of effective tillers per plant and days to 50% flowering.

maturity. These findings are in agreement with Caldo *et al.* (1996) ^[4], who also report that maturity is the major factors contributing to the variation of parental lines of modern Philippine rice cultivars.

The second principal component PC2 accounted for 19.891% of total variability, and is highly positively correlated with 100 seed weight (0.568), seed yield (0.560) and plant height (0.462). PC2 is highly loaded with genotype having increased 100 seed weight, seed yield per plant and its attributing traits. As a result PC2 differentiated those accessions having high loading factor for 100 seed weight, seed yield per plant and plant height.

As a result of linear combination of highly positively loaded traits like paddy L/B ratio (0.745) the principle component showed 16.592% of the total variability. The principal component PC3 explained more than 16.00% of the variability. As a result, the PC3 differentiated those accessions having high loading factor for paddy L/B ratio and 100 seed weight.

 Table 2: Eigen value, contribution of variability and factor loadings for the principal component axes

Componenta	Principal component (PC)			
Components	1	2	3	
Eigen value	3.360	1.989	1.659	
Variability %	33.603	19.891	16.592	
Cumulative variability%	33.603	53.494	70.086	
Troita	factor loading after varimax			
Traits	rotation			
Day to 50 % flowering	0.913	0.129	-0.231	
No. of effective tillers per plant	0.871	0.309	-0.130	
Plant height (cm)	0.489	0.462	0.259	
Panicle length (cm)	-0.542	0.213	0.151	
Days to maturity	0.911	0.136	-0.244	
Paddy length breadth ratio	0.163	0.335	0.745	
100 seed weight (g)	-0.022	0.568	0.683	
seed yield per plant	-0.308	0.560	-0.242	

Note: Figure in bold letter showed highly loaded traits/character in respective PC

Extraction method: principal component analysis **Rotation method:** varimax with keiser normalization

The use of cumulative proportion to determine the amount of variance that the principal component explains. First three principal components explain 30 to 70 percent variance of the variable. PC1 showed 33.603 % while PC2, PC3 exhibited 53.494% and 70.086% cumulative variability percentage, respectively among the accessions for the traits. The cumulative variance of 70.086% by the first three axes with eigen value of >1.0 indicates that the identified traits with in the axes exhibited great influence on the phenotype of the accessions, and could effectively be used for selection among them. These results are corroborated by Ashfaq *et al.* (2012) ^[1], Chakravorty *et al.* (2013) ^[5], Sinha and Mishra (2013) ^[14] reported five principal components (PCs) exhibited more than 1.8 eigen value and showed about 68.34% variability.

Principal component score for all the accessions were estimated. The high score of accessions can be utilized for precise selection of parent, whose intensity is determined by variability explained by each PCs. Bahala dugji, Bahali bijo, Bahangi, Baidlo and Bagad had high PCs socre which is prsent in PC1. It means these accessions are high PC score for number of effective tillers per plant, days to 50% flowering and days to maturity. Baigan, Chiraigodi, Bahra sinki, Danteshwari and Bahawar kanak had high PC score for PC2 and highly loaded for plant height, 100 seed weight and seed yield per plant. Chiraigodi, Badweli, Baggar, Baigan and Bagi had high PC score for PC3 and highly loaded for 100 seed weight and paddy length breadth ratio. On the basis of top 5 PC score, accessions are selected and depicted in table: 3

Table 3: List of selected rice accessions in each PCs on the basis oftop 5 PC scores

S. No.	PC1	PC2	PC3
1.	Bahala dugji (2.163)	Baigan (1.981)	Chiraigodi (1.928)
2.	Bahali bijo (1.75)	Chiraigodi (1.773)	Badweli (1.703)
3.	Bahangi (1.671)	Bahra sinki (1.725)	Baggar (1.558)
4.	Baidlo (1.666)	Danteshwari (1.692)	Baigan (1.484)
5.	Bagad (1.615)	Bahawar kanak (1.673)	Bagi (1.369)

Conclusion

The first component PC1 differentiated those accessions having high loading factor for days to 50% flowering, number of effective tillers per plant and days to maturity and second component PC2 differentiated those accessions having high loading factor for plant height, seed yield per plant, 100 seed weight and third component PC3 differentiated those accessions having high loading factor for paddy length breadth ratio and 100 seed weight. On the basis of principal component score as depicted in table 3, rice germplasm accession Bahala dugji, Baigan and Chiraigodi have high PC score and showing maximum contribution for yield attributing traits.

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