

Principal component analysis for yield and related attributes in rice genotypes

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ABSTRACT: More than one-third of the world's population relies on rice as a main food source, and it is a model cereal species used as a genetic study platform for gene functions. 25 genotypes were examined for the ten different traits in the present study. To evaluate the relative contribution of several qualities to overall variability, Principal Component Analysis was used. It was discovered that three components have Eigen values greater than 1. A total of 49.20, 24.50, and 10.30 percent of the variability was supplied by PCs 1, 2, and 3. They indicated the traits causing the variation and collectively accounted for 84% of the variability of the genotypes employed in the study.

Keywords: Eigen value, genotypes, PCA, rice, variability.

INTRODUCTION

For the majority of the world's population, "Rice is Life," and the production of rice has influenced millions of people's diet, culture and economic standing. More than 100 nations around the world grow rice. It is considered to as "Global Grain" since it is a significant staple meal for more than half of the world's population (Prasad *et al.*, 2018). At least fifteen nations in Asia and the Pacific, ten in Latin America and the Caribbean, one in North Africa, and seven in sub-Saharan Africa all have rice as their main staple food (FAOSTAT, 2005). Nearly two billion people in Asia rely on rice for 60–70% of their daily caloric intake (Diouf 2003; Khush 2005). Rice with a productivity of 2713 kg/ha, India ranks first in area (45.06 million hectares) and second in production output (122.27 million tonnes) (Anonymous, 2021-22). Studies on genetic diversity are necessary before beginning any crop development endeavor. Two essential phases in plant breeding are hybridization and selection. Therefore, research on morphological traits in a variety found in germplasm is crucial for evaluating population variations and breeding potential. In order to evaluate, characterize, and manage germplasm, plant breeders frequently evaluate a large number of traits, some of which may not have enough discriminating power (Maji and Shaibu, 2012). Because of morphological and physiological changes in crop species are common, principal component analysis (PCA) may be utilized to

identify patterns and remove duplication in data sets in this situation (Mahalingam *et al.*, 2020). By seeking out groups with very strong inter-correlation and percent variation explained for each component towards the overall variability, PCA condenses a big data series into a smaller collection of variables without losing any significant information from the original data set (Das *et al.*, 2017). A two-dimensional chart representing a multidimensional dataset is used in statistics as part of the exploratory graph technique known as biplot analysis. The purpose of the study was to categorize genotypes using principal component analysis (PCA) and estimate genotype diversity. It is necessary to have sufficient understanding of the genetic variety in the gene pool in order to adapt a successful and worthwhile breeding strategy. Characterizing this current variety and realigning their features through selective breeding may go a long way toward addressing the current and upcoming issues that endanger global food security (Vanaja and Babu, 2006). One of the important techniques for locating the plant traits that distinguish the promising genotypes from one another is principal component analysis. Due to the regular variation that occurs in crop species, PCA aids in the elimination of redundancy in data sets (Maji and Saibu, 2012; Ramakrishnan *et al.*, 2016). As a result, the significance of PCA is taken into account, and the investigation was conducted on the rice germplasm.

MATERIALS AND METHODS

Twenty five genotypes of rice were used to reveal the genetic relationship between the different accessions. The experiment was conducted at the experimental field of Agricultural Research Station Ummedganj Kota in irrigated condition during *Kharif* 2019. On 20 June 2019, all 25 genotypes were sowed in the nursery, and on 14 July 2019, healthy seedlings were transplanted in a randomized block design with three replications. Each genotype was transplanted into a 10 m² plot with ten five meter long rows. The distances between plants and rows were kept at 10 and 20 cm, respectively. For the purpose of cultivating a productive crop, the suggested agronomic procedures and plant protection techniques were used during which appropriate. Data were collected on 10 agronomic characters *viz.* days to 50% flowering, days to maturity, plant height (cm), number of productive tillers per plant, panicle length (cm), number of grains per panicle, 1000-grain weight (g), amylose content (%), protein content (%) and grain yield per plant (g). Data were taken from 10 randomly selected plants of each genotype and the list of twenty five genotypes represented in Table 1. The Principal Component Analysis was carried out to identify plant traits that contribute most of the observed variations among the genotypes. Mean values of 25 genotypes for 10 traits were used. Principal Components are generally estimated from correlation matrix or covariance matrix. The analysis was conducted using R-studio software.

RESULTS AND DISCUSSION

The PCA results provided explanation for the genetic diversity of the rice collection. The primary objective of the PCA is to identify a small set of factors that account for the majority of the variability. Table 2 presents the standard deviation, eigenvalues, variance %, and cumulative percentage. Three of the components in this case had Eigen values that were higher than 1.0. Eigen values for PCA 1, 2, and 3 were 4.919, 2.448, and 1.030, respectively. The three factors respective percentages of variance were 49.20, 24.50, and 10.30. Together, they were responsible for 84% of the genotype variability employed in the diversity analysis. Table 3 illustrates the quality character contributions to the primary component. Only the amylose content displayed positive loadings in PC1, while the other parameters did not. In PC2 days to 50% flowering and number of grains per panicle both showed the same value of positive loadings (0.220). Subsequent days to maturity (0.192) and plant height (0.152) both showed positive loadings in PC2, whereas the remaining factors showed negative loadings. The PC3 exhibited positive

loadings for the parameters *viz.*, grain yield per plant (0.463), productive tillers per plant (0.451), and plant height (0.003), while the PC3 showed negative loadings for protein content (-0.627), grains per panicle (-0.260), and amylose content (-0.236). These characteristics contribute the most to the divergence and carry the majority of its variability. Nachimuthu *et al.* (2014) Gour *et al.* (2017) and Upadhyay *et al.* (2022) conducted related studies.

The distribution and the type of diversity for both the variables and the genotypes were explained by the biplot diagram (Fig. 2) between PCs 1 and 2. Nearly all of the genotypes and variables exhibited substantial levels of variation, as seen by the loading plot. Both Kumar *et al.* (2015) and Ravi *et al.* (2018) noted similar reports. In Fig. 1, the distribution of germplasm lines based on the first and second principle components reveals the population's phenotypic diversity and indicates how broadly they were scattered along both axes. All of the genotypes were dispersed broadly among various quarters (Fig. 2).

Table 1: Genotype used in the study.

Sr. No.	Name of the genotypes
1	R.S.K. 1155-2-4-1
2	R.S.K. 1155-3-3-1
3	R.S.K. 1157-4-5-1
4	R.S.K. 1157-6-3-1
5	R.S.K. 1157-9-2-2
6	R.S.K. 1161-1-1
7	R.S.K. 1163-8-1
8	R.S.K. 1165-4-2
9	R.S.K. 1165-4-3
10	R.N.S.K. 1167-11-1
11	R.N.S.K. 1168-2-1
12	R.S.K. 1164-1-1
13	R.S.K. 1172-1-1
14	R.S.K. 1221-1-1
15	R.S.K. 1162-8-1
16	R.S.K. 1164-6-1
17	R.S.K. 1164-6-2
18	R.S.K. 1165-3-1
19	R.S.K. 1165-3-2
20	R.N.S.K. 1167-5-1
21	R.S.K. 1155-6-1-2
22	R.S.K. 1155-6-3-1
23	P 1121
24	P 2511
25	P 1460

Table 2. Standard deviation, Eigen values, proportion of variance and cumulative proportion of rice genotypes.

Principle components	Standard deviation	Eigen value	Proportion of variance	Cumulative proportion
PC1	2.218	4.919	0.492	0.492
PC2	1.565	2.448	0.245	0.737
PC3	1.015	1.030	0.103	0.840
PC4	0.852	0.726	0.073	0.912
PC5	0.568	0.323	0.032	0.945
PC6	0.489	0.239	0.024	0.968
PC7	0.408	0.166	0.017	0.985
PC8	0.338	0.115	0.011	0.996
PC9	0.175	0.031	0.003	1.000
PC10	0.070	0.005	0.000	1.000

Table 3. Contribution of first four principal components to variation in rice varieties.

Parameters	PC1	PC2	PC3
Days to 50% flowering	-0.410	0.220	-0.067
Days to maturity	-0.419	0.192	-0.106
Plant height	-0.401	0.152	0.003
Number of productive tillers per plant	-0.269	-0.377	0.451
Panicle length	-0.350	-0.118	-0.087
Number of grains per panicle	-0.355	0.220	-0.260
1000-grain weight	-0.296	-0.377	-0.206
Amylose content	0.125	-0.493	-0.236
Protein content	-0.032	-0.382	-0.627
Grain yield per plant	-0.266	-0.394	0.463

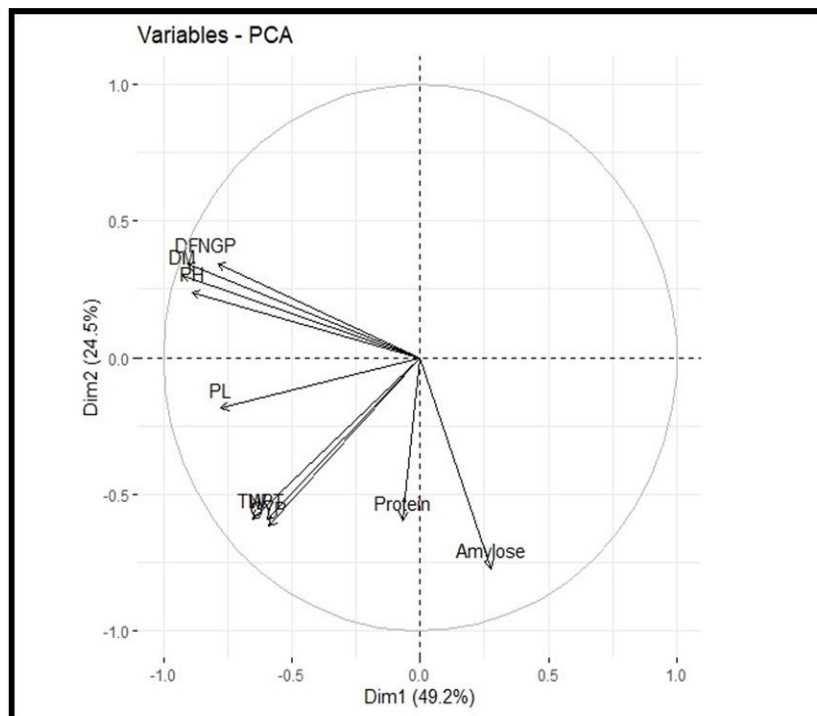


Fig. 1. Loading plot for rice genotypes.

the total variation. These components play a crucial role in understanding the variability and can be crucial in designing successful breeding programs.

FUTURE SCOPE

By distinguishing the essential components and their contributions to variance, Principal Component Analysis (PCA) facilitates crop improvement. Choosing a genotype it demonstrates the potential for high yield contribution which could be used as parents in further breeding programmes.

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Conflicts of Interest. None.

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