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Principal component analysis in screening of submergence tolerance in rice (*Oryza sativa* L.) genotypes of Manipur

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Abstract
The present experiment was carried out to estimate genetic diversity among 76 rice genotypes of Manipur and 4 checks using principal component analysis for submergence tolerance in the experimental field of College of Agriculture, Central Agricultural University, Imphal, Manipur. Principal component analysis was used to evaluate the variation and for estimation of relative contribution of various characters towards total variability. The results revealed that in submerged condition first four components were with Eigen values greater than one and it accounted for 73.09% of total explained variability. The first principal component (PC1) contributed maximum of 27.73% followed by PC2 with 17.27%, PC3 contributed 15.60% and PC4 had contributed 12.50% towards total variability. The characters *viz*., filled grains per panicle, spikelet per panicle, grain yield per plant and spikelet fertility percentage explained maximum variance in PC1. Thus, principal component analysis revealed wide genetic variability in the rice genotypes under study.

Keywords: Principal component analysis, submergence, variability, rice

1. Introduction
Rice (*Oryza sativa* L.) is the major staple food and source of energy for more than half of the world's population. In India, it is the staple food for almost two-thirds of the population which plays a major role in Indian economy. Rice is habitually the only cereal that can be grown in flood prone rainfed lowland ecosystem. Globally, rain-fed lowland and deep-water rice account for about one-third of the total rice-growing area, which is about 50 Mha (Bailey-Serres and Voesenek, 2010 and Singh *et al*., 2016) [1, 2]. These areas are particularly prone to recurrent flooding due to poor drainage of the excess rainwater during the monsoon season. About 75% of the world lowland rice is in the belt across Eastern India, Bangladesh, Myanmar and Thailand (Mohanty *et al*., 2000) [3]. Recently, due to extreme weather condition and climate change the extent of submergence stress has increased due to unexpected heavy rainfall that has inundated wider areas across many regions of Asia.
Traditional rice varieties are lower in yield however, it possesses some adaptive traits that are required for survival in the flooded or submergence condition. Principal component analysis is one of the important tools used for identifying the plant characters that categorize the distinctiveness among the promising genotypes (Sathya Sheela *et al*., 2020) [4]. PCA helps to eradicate redundancy in data sets due to regular variation occurring regularly in the crop species (Maji and Shaibu, 2016) [5]. It also helps in identifying the most relevant characters and present them in interpretable and more visualized dimensions through linear combinations of variables that accounts for most of the variation present in original set of variables. The present investigation was carried out to identify plant traits among the studied genotypes which contribute most of the observed variations.

2. Materials and Method
The experiment was conducted during kharif 2018 at College of Agriculture, Central University, Imphal, Manipur. The experimental materials comprised of 76 rice genotypes of Manipur and four checks which were two susceptible (Swarna and Samba) and two tolerant varieties (Swarna Sub-1 and Bahadur Sub-1) and were grown in Augmented Randomized

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Block Design with replications of the checks. The experimental plot was divided into 5 blocks with 16 plots in first block and each 15 plots in the remaining four blocks. Fourteen days old seedlings were transplanted in a spacing of 20 cm between row to row and 20 cm between plant to plant. After seven days of transplanting, plants were kept in completely submerged condition for 14 days and after which excess water was drained out and kept just like in normal condition. The recommended package of practices was carried out to ensure healthy plant growth. The data collected were subjected to standard statistical procedures and principal component analysis was done using the software R-studio.

3. Results and Discussions

The purpose of PCA is to obtain a small number of factors which account for maximum variability out of the total variability (Sathya Sheela *et al*., 2020) [4]. The principal component with the Eigen values less than one were considered to be non-significant and hence were ignored as they are unlikely to have any practical significance (Tejaswini *et al*., 2018) [6]. The Eigen values, percentage of variance, cumulative percentage of variance and factor loading of different variables are presented in Table No. 1.

In the present study, it was found out that the first five principal components contributed 81.68 per cent of the total variability however the first four components show Eigen values greater than 1.0 and they accounted for 73.09 per cent of explained variability. Similar results were reported by Yadav *et al*., 2013 [7] where four principal components described the maximum variance of the data set.

The percentage of variation is explained by the Scree plot in a graph which is plotted between percentage of explained variances and Principal Components (i.e., dimensions in graph) and it is shown in figure no. 1. It is clearly seen from the graph that maximum variation was observed in PC1, PC2, PC3 and PC4 which confirms the findings of Gour *et al*., 2017. To identify the characters which influenced most in PCA value, individual loadings (Eigen values) for different variables are observed. On the basis of factor loadings, an exact picture of the component traits that contributes maximum variability can be obtained.

The first principal component (PC 1) accounted for 27.73% which was maximum towards the total variability. The characters filled grains per panicle (0.93) followed by spikelet per panicle (0.79), grain yield per plant (0.73), spikelet fertility percentage (0.60), panicle length (0.53), days to maturity (0.45), days to 50% flowering (0.39), effective tillers per plant (0.15) and plant height (0.06) were positively loaded whereas only total tillers per plant (-0.01) was negatively loaded.

The second principal component (PC 2) was characterized by 17.27% contribution of the total variation. PC 2 was highly positively influenced by the characters effective tillers per plant (0.71) followed by total tillers per plant (0.66), grain yield per plant (0.44) and spikelet per panicle (0.12) whereas it was highly negatively influenced by days to maturity (-0.47) followed by plant height (-0.47) and days to flowering (-0.47).

The third principal component (PC 3) described 15.60% of the total variation. Characters *viz*., days to flowering (0.74) followed by days to maturity (0.70), effective tillers per plant (0.43), total tillers per plant (0.42) and spikelet fertility percentage (0.04) contributed positively to the total variation while PC 3 was highly negatively influenced by spikelet per panicle (-0.35) followed by filled grains per panicle (-0.23) and plant height (-0.30).

The fourth principal component (PC 4) accounted for 12.50% of the total variability. The character contributing most positively were test weight (0.77) followed by plant height (0.47), spikelet fertility percentage (0.42) and effective tillers per plant (0.30) whereas it was highly negatively influenced by spikelet per panicle (-0.37) followed by panicle length (-0.31) and days to maturity (-0.07).

The prominent traits that were coming together in different principal components and which contributed towards explaining the total variability have the tendency to remain together (Mahendran *et al*., 2015) [9]. In breeding program, it can be kept into consideration during utilization of these traits. Those characters that have high variability are expected to provide high level of gene transfer during breeding programs (Gana, 2013 and Varthini, 2014) [10, 11].

The biplot is presented in figure no. 4 and it can be seen from the biplot that the characters were in two groups in the first quarter and second quarter whereas the genotypes are scattered over all the four quarters. In the first quarter (+ve PC1, +ve PC2), total tillers, effective tillers, yield per plant, spikelet per panicle and filled grains were the influential characters. Therefore, those genotypes that were in first quarter are assumed to have higher values of all the characters falling in this quarter. In the second quarter (+ve PC 1, -ve PC 2), plant height days to flowering, days to physiological maturity, panicle length, fertility percentage are the most influential characters and the genotypes falling in this quarter have higher values of all these characters. The loading plot depicted that almost all the genotypes and variables have shown high degree of variation and similar results were observed by Ravi *et al*., 2018 [12].
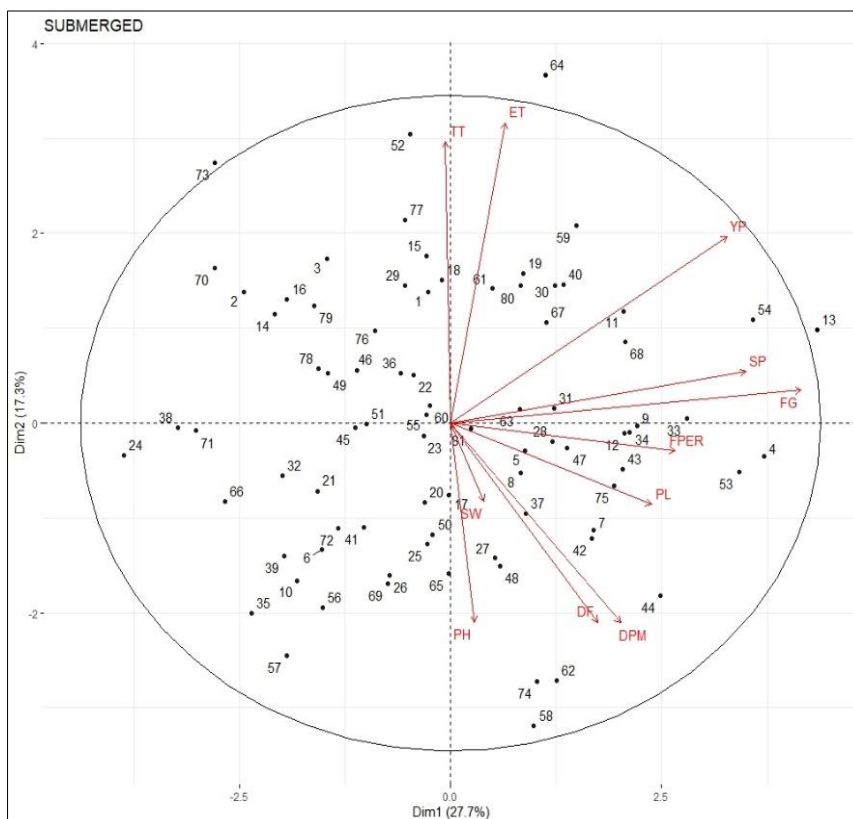
Table 1: Principal component analysis for eleven characters in rice genotypes of Manipur

Variables	PC1	PC2	PC3	PC4	PC5
Days to flowering	0.39	-0.47	0.74	-0.05	-0.13
Days to maturity	0.45	-0.47	0.70	-0.07	0.07
Plant height	0.06	-0.47	-0.30	0.47	0.53
Total Tillers per plant	-0.01	0.66	0.42	0.01	0.45
Effective tillers per plant	0.15	0.71	0.43	0.30	0.10
Panicle length	0.53	-0.19	-0.18	-0.31	0.61
Spikelet per panicle	0.79	0.12	-0.35	-0.37	-0.11
Filled grains per panicle	0.93	0.08	-0.23	-0.06	-0.13
Spikelet fertility percentage	0.60	-0.07	0.04	0.42	-0.12
Grain yield per plant	0.73	0.44	-0.10	0.24	-0.08
Test weight	0.09	-0.19	-0.12	0.77	-0.10

Eigen value	3.05	1.90	1.72	1.38	0.95
Percentage of variance	27.73	17.27	15.60	12.50	8.59
Cumulative % of variance	27.73	45.00	60.59	73.09	81.68
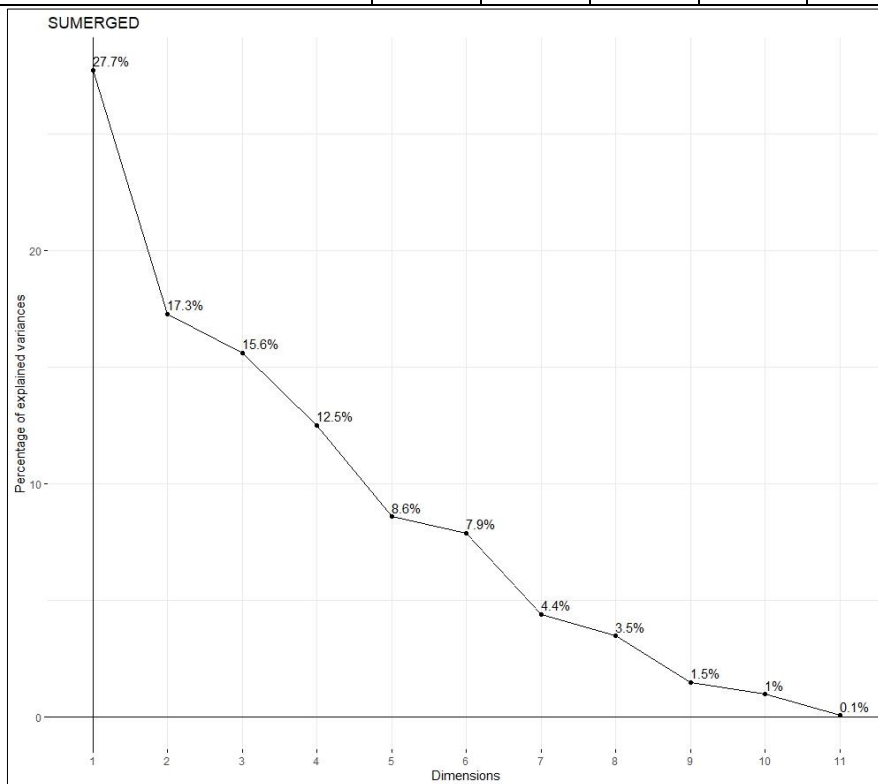
Fig 1: Scree plot graphical representation

Fig 2: Biplot of PC1 and PC2 in 80 rice genotypes for eleven quantitative characters

4. Conclusion

The principal component analysis revealed wide genetic variability in the rice genotypes under study. It also identified maximum contributing characters towards the total explained variability which were filled grains per panicle, spikelet per panicle, grain yield per plant and spikelet fertility percentage.

These characters that have high variability can be used in breeding programs for the development of submergence tolerance rice genotypes.

(DF-Days to 50% flowering, DPM-Days to maturity, PH-Plant height, TT-total tillers per plant ETH-Effective tillers per plant, PL-Panicle length, SP- Spikelet per panicle, FG-Filled grains per panicle, FPER- Spikelet fertility percentage, YP-Grain yield per plant, SW- Test weight).

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