



P-ISSN: 2349-8528

E-ISSN: 2321-4902

IJCS 2019; 7(3): 4184-4187

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Received: 22-03-2019

Accepted: 24-04-2019

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Principal component analysis of rice varieties under bacterial leaf blight incidence

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Abstract

Present investigation was carried out to determine the relationship and genetic diversity among thirty six rice genotypes using Principal Component Analysis (PCA); The data was collected from Experimental Block 1, Department of Plant Breeding and Genetics, Odisha University of Agriculture and Technology, Bhubaneswar and were characterized using ANOVA model. This study gave empirical evidence on eleven yield and agro-morphological characters from which data were recorded. In this study, Component 1 had the contribution from the traits viz., Days to 50% flowering, Effective tillers per hill and Panicle length which accounted 43.84% to the total variability. Harvest index, Grain yield per plant, Chlorophyll content index at tillering stage have contributed 20.52% to the total variability in component 2. The remaining variability of 12.50% and 7.20% was consolidated in component 3 and component 4 by various traits like Panicle length and Grain yield per plant. The cumulative variance of 83.99% of total variation among 11 characters was explained by the first four axes. Thus the results of principal component analysis revealed wide genetic variability in this rice germplasm accessions. High BLB resistant trait with high genetic variability is expected to provide high level of gene transfer. These results can now be used by breeders to develop high yielding rice varieties and new breeding protocols for rice improvement during breeding programs.

Keywords: Principal component analysis, rice, bacterial leaf blight resistance

Introduction

Bacterial Leaf blight (BLB) in rice, caused by *Xanthomonas oryzae* pv. *Oryzae* (Xoo) was first observed in 1884 by the farmers of Japan, it is one of the primitive known diseases. Consequently, its prevalence been reported from altered parts of Asia, Northern Australia, Africa and USA. This disease is epidemic in many parts of the world, causing severe crop loss up to 50%. Evaluation studies have revealed that this disease reduces different levels of grain yield, depending on the stage of the crop, degree of cultivar susceptibility and to a great extent, the conduciveness of the environment in which it occurs. Based on the sternness of the damages caused by infection have demanded the development of strategies to control and manage the disease, so as to reduce crop loss and to avert an epidemic. Plant Breeders measures large number of variables, among them few cannot be adequate inequitable power for germplasm evaluation, characterization, and management. In this regard, Principal Component Analysis (PCA) may be used to disclose motifs and reduce redundancy in data sets (Adams, 1995; Amy and Pritts, 1991) [2, 3] as morphological and physiological variations consistently occur in crop species. Awareness with the nature, extent and union of this variation could be useful for genetic advancement of crop species. Unless a compilation has been accurately evaluated and its attributes become known to breeders, it has little realistic use. Looking in a broad sense at Germplasm evaluation and in the perspective of genetic resources is the portrayal of the material in a collection that covers the whole array of activities starting from collection of germplasm characterization, preliminary evaluation and also for further evaluation. Rice is considered as staple food crop in India and many people depend on it for their livelihood (Anonymous, 2000) [4]. Advancement in varieties made to be continuous process and further accomplishment in the plant breeding programme aimed at the evaluation of high yielding, better quality, fertilizer responsive, disease and insect resistance varieties depends upon the selection of suitable plants to be utilized in breeding programme. The effectiveness of selection depends primarily upon the extent of genetic variability in the breeding material at hand. A organized evaluation is required after collection of germplasm, sequentially to know its different morphological, physiological and developmental characters

including some special features i.e., biotic and abiotic stress tolerance, pest and disease resistance. Such methodical and thorough evaluation operations, though expensive and time consuming, are of immense worth. The primary goal in exploiting useful genes from germplasm collections fluctuate significantly between crops and for altered ecological zones within a crop. Viz., stable resistance to different races of rusts, semi-dwarfness, better quality, drought tolerance and wider adaptability with higher yield potential, better quality and compound resistance to pests and diseases in rice, resistance to viruses, nematodes and bacterial diseases. Appropriate and most efficient method should be used for germplasm evaluation and characterization, and while further detailed evaluation is mostly done by the breeders for taking additional information. Hotelling (1933) indicated that principal component analysis (PCA) is an exploratory tool designed by Karl (1901) to identify unknown trends in a multi-dimensional data set. However, in a typical micro-array experiment, the expression of thousands of genes is measured across many conditions such as treatments or time points. Therefore, it becomes impossible to make a visual inspection of the relationship between genes or conditions in such a multi-dimensional matrix. One way to make meaning of this data is to reduce its dimensionality (Hotelling, 1933). Several data decomposition techniques are available for this purpose and multivariate data analysis (Cooley and Lohnes, 1971) [5]. PCA is among these techniques that reduced the data into two dimensions (Smith, 2002; Rao, 1964; Raychaudhuri *et al.*, 2000) [16, 13, 14]. Multivariate statistical techniques which at the same time analyze multiple measurements on each individual under study, are widely used in analysis of genetic diversity irrespective of whether it is morphological, biochemical or molecular marker-based and subsequently, classification of germplasm collections. Among the multivariate techniques,

cluster analyses, PCA, principal co-ordinate analysis (PCoA) are remarkable. The study was undertaken to run a classificatory analysis on the rice genotypes by means of PCA, which would enable us to classify the available germplasm into distinct groups on the basis of their genetic diversity. The information, thus obtained, would be helpful to develop an effective rice-breeding programme and as such a quantification of the degree of divergence would be helpful in choosing suitable genotypes and traits of interests for ongoing breeding programmes.

Principal component analysis is one of the important tools of diversity analysis. This technique is very helpful for identification of plant characters that categorize the distinctiveness among promising genotypes. Considering the importance of PCA, this study is conducted on rice germplasm accessions with an objective to identify of the Morpho-physiological traits responsible for the yield differences among the rice genotypes.

Materials and Methods

Thirty genotypes of Rice were investigated during 2015-2016. The experiment was conducted in an RBD replicated 3 times by adopting a spacing of 20x20cm. All the agronomic package of practises were carried out for healthy plant growth. Observations were recorded on eleven yield related traits viz., Days to fifty percent flowering, Plant height, Flag leaf area, Chlorophyll content index (CCI) at maximum tillering stage, CCI at 50% flowering stage, Panicle length, Effective tillers per hill, Fertility percentage, 100 grain weight, Harvest index, and Grain yield per plant. The PCA analysis reduces the dimensions of a multivariate data to a few principal axes, generate an Eigen vector for each axis and produces component score for the character, (Sneath *et al.*, 1973 and Ariyo *et al.*, 1991) [1].

Table 1: List of traits measured

S. No	Traits	Method of measurement
1.	Days to 50% Flowering (Days)	The number of days from sowing to 50% flowering days
2.	Plant Height (cm)	The average of height from the base to the tip of last leaf.
3.	Flag Leaf Area(cm)	Length x Width x k (Factor 0.75)
4.	CCI At Maximum Tillering (No)	Chlorophyll meter (SPAD-502-plus, Minolta France SA, Currieressur-Seine, France.
5.	CCI At 50% Flowering (No)	Chlorophyll meter (SPAD-502-plus, Minolta France SA, Currieressur-Seine, France.
6.	Panicle Length (cm)	From the panicle base to the tip of last spikelet of panicle.
7.	Effective Tillers/ Hill (No)	Counting of the tillers from one hill
8.	Fertility percent (%)	(Number of fertile spikelets /Total Number of spikelets) × 100
9.	100 Grain Weight (gm)	One hundred seeds were counted and weighed
10.	Harvest Index	(Economic yield/ Biological yield) x 100
11.	Grain Yield Per Plant (gm)	Weighing the total grains per m2

Results and Discussions

The results of the PCA explained the genetic diversity of the rice varieties under study. There are no standard tests to prove significance of proper values and the coefficients. Principal component analysis has shown the genetic diversity of the varieties; The cumulative variance of 83.99% (Table 2) by the first four axes with Eigen value > 1.0 except for fourth axes indicating that within first three axes exhibited great influence on the phenotype of rice varieties under study. All the varieties were widely scattered across different quarters (Fig 1). In this study, we choose to follow the criterion used by Clifford and Stephenson (1975) [6] and result was corroborated with findings of Guei *et al.*, (2005) [9], which suggested that the first three principal components are often the most important in reflecting the variation patterns among varieties, and the characters associated with these are more useful in

differentiating characters. According to this criterion, the first three components account for more than 76.79% of the total variation giving a clear idea of the structure underlying the variables analyzed. However, the criterion of Raji (2002) [12] was chosen to determine the cut-off limit for the coefficients of the proper vectors; this criterion treated coefficient greater than 0.3 as having a large enough effect to be considered important, while traits having a coefficient less than 0.3 were considered not to have important effect on the overall variation observed in the present study.

The distribution of varieties based on the first and second principal component exhibited the phenotypic variation among the population and explains how these widely dispersed along both the axes (Fig 1). PCA of quantitative traits found that, the first principal component accounted 43.79% to the total variability, whereby days to 50%

flowering (0.39), effective tillers per hill (0.38), panicle length (0.34), plant height (0.295), flag leaf area (0.323), Chlorophyll content index at maximum tillering stage (0.263), effective tillers per hill (0.386), fertility percentage (0.326), 100 grain weight (0.221) and harvest index (0.255) were contributed positively. The second principal component accounted 20.492% to the total variability. The variable contributing most positively were days to 50% flowering (0.091), Chlorophyll content index at maximum tillering stage (0.382), Panicle length (0.046), harvest index (0.452) and grain yield per plant (0.356). The third component accounted 12.50% to the variance in which the variable Days to 50% flowering (0.049), Flag Leaf Area (0.013), Panicle Length (0.293), and Harvest Index (0.078) contributed positively. The fourth component accounted for 7.20% to the variance in which the variables Days to 50% flowering (0.222), Plant Height (0.111), Effective Tillers/ Hill (0.330) and 100 Grain Weight (0.236) contributed positively. Harvest index contributed the highest in variation. Thus, the predominant character coming together in different principal components and contributing towards explaining the variability and have the tendency to remain together. This may be taken into consideration during utilization of these characters in breeding programme. Significance of Eigen value determines the direction of the new feature space and eigen value determines the magnitude of the PCA components. The higher the eigen value is, the higher will be the variance along a co-variance matrix in the eigen vector direction (Principle component). The phenotypic value of each trait measured the importance and contribution of each component to the total variation, where as each coefficient of proper vectors indicates the degree of contribution of every original variables with which each principal component is associated. The first 4

components accounted for 83.995% of the total variance. Characters with high variability are expected to provide high level of gene transfer during breeding programmes (Gana, 2006, Gana, 2013, Varthini, 2014) [7, 8].

Conclusion

Harvest index has contributed positively in three components of variation followed by panicle length. Similarly, chlorophyll content index at maximum tillering stage and effective tillers per hill have contributed the most in two components of variation, so, these characters spread over different principal component and contributing most to explain the variability should be taken into consideration for their utilization in breeding programme.

Table 2: Eigen value, contribution of variability and Eigen vectors for the principal component axes in Bacterial leaf blight infected condition

Parameter	PC1	PC2	PC3	PC4
Days to 50% Flowering (Days)	0.397	0.091	0.049	0.222
Plant Height (cm)	0.295	-0.395	-0.134	0.111
Flag Leaf Area(cm)	0.323	-0.317	0.013	-0.085
CCI At Maximum Tillering (No)	0.263	0.382	-0.192	-0.047
CCI At 50% Flowering (No)	-0.106	-0.452	-0.247	-0.529
Panicle Length (cm)	0.340	0.046	0.293	-0.484
Effective Tillers/ Hill (No)	0.386	-0.117	-0.048	0.330
Fertility percent (%)	0.326	-0.175	-0.105	-0.317
100 Grain Weight (gm)	0.221	-0.035	-0.586	0.236
Harvest Index (No)	0.255	0.452	0.078	-0.309
Grain Yield Per Plant (gm)	-0.021	0.356	-0.580	-0.216
Eigen Value (Root)	5.255	2.459	1.501	0.865
% Var. Exp.	43.794	20.492	12.505	7.205
Cum. Var. Exp.	43.794	64.286	76.791	83.995

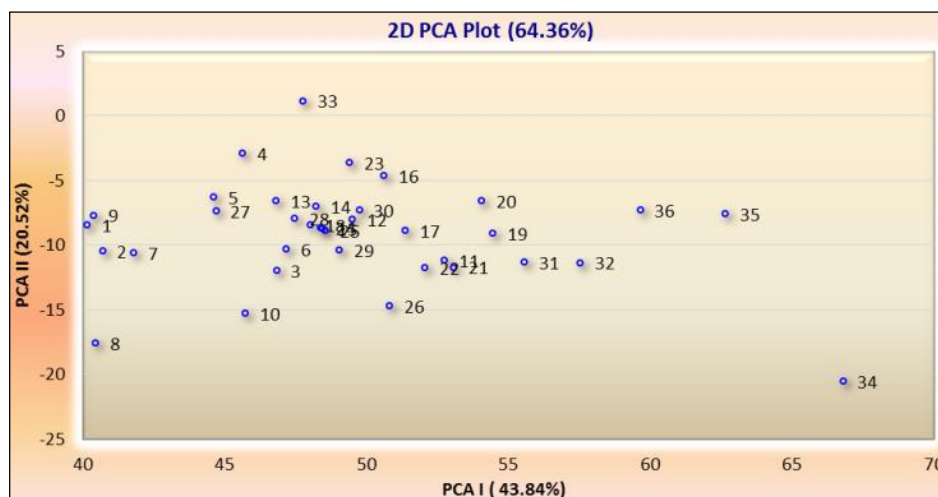


Fig 1: Distribution and grouping of 36 rice genotypes across first two components based on PCA

References

- Ariyo QJ, Odulaja A. Numerical analysis of variation among accessions of Okra. *Abelmoschus esculentus*. *Annals of Botany*. 1991; 67:527-531.
- Adams MW. An estimate of homogeneity in crop plants with special reference to genetic vulnerability in dry season. *Phseolus vulgaris*. *Ephytica*. 1995; 26:665-679.
- Amy EL, Pritts MP. Application of principal component analysis to horticultural research. *Hortscience*. 1991; 26(4):334-338.
- Anonymous. Economic survey, Government of Pakistan, Economic advisory wing, Finance Division, Islamabad, 2000-2001, 16-17.
- Cooley WW, Lohnes PR. *Multivariate Data Analysis*. John Wiley & Sons, Inc., New York, 1971.
- Clifford HT, Stephenson W. *An Introduction to Numerical Classification*. Academic Press, London, 1975, 229.
- Gana Varthini. Evaluation of Rice Genetic Diversity and Variability in a Population Panel by Principal Component Analysis *Indian Journal of Science and Technology*. 2006, 2013 and. 2014; 7(10):1555-1562.
- Gana AS, Shaba SZ, Tsado EK. Principal component analysis of morphological traits in thirty-nine accessions of rice (*Oryza sativa*) grown in a rainfed lowland ecology

- of Nigeria. *J Plant Breeding and Crop Science*. 2013; 5:120-126.
9. Guei RG, Sanni KA, Fawole AFJ. Genetic diversity of rice (*Oryza sativa*). *Agron Africaine*. 2005; 5:17-28.
 10. Hotelling H. Analysis of a complex of statistical variable into principal components. *J Educ. Psych.* 1993; 24:417-441.
 11. Pearson K. On lines and planes of closest fit to system of point in space, *philosophical Magazine*. 1901; 6:559-572
 12. Raji AA. Assessment of genetic diversity and heterotic relationships in African improved and local cassava germplasm. PhD thesis. University of Ibadan, Nigeria, 2002.
 13. Rao. The Use and Interpretation of Principal Component Analysis in Applied Research. *Indian Journal of Statistics*. 1964; 26(4):329-358.
 14. Raychaudhuri S, Stuart JM, Altman RB. Principal components analysis to summarize microarray experiments: Application to sporulation time series. *Pacific Symposium on Biocomputing*, 2000.
 15. Sneath, Ariyo *et al.* Multivariate analysis of genetic divergence in twenty to genotypes of Ground nut. *Journal of plant Breeding and Crp. Science*. 1991; 2(7):192-204.
 16. Smith LI. A tutorial on Principal Components Analysis, 2002.
http://www.cs.otago.ac.nz/cosc453/student_tutorials/principal_components.pdf.
 17. Vishnu Varthini N, Robin S, Sudhakar D, Raveendran M, Rajeswari S, Manonmani S. Evaluation of Rice Genetic Diversity and Variability in a Population Panel by Principal Component Analysis. *Indian Journal of Science and Technology*. 2014; 7(10):1555-1562.