Biological Forum – An International Journal **14(2): 1273-1276(2022)**

ISSN No. (Print): 0975-1130
ISSN No. (Online): 2249-3239

Principal Component analysis of Yield and its attributing Traits in advanced Inbred Lines of Rice under Sodicity condition (*Oryza sativa* L.)

Sameer Upadhyay*, Sanket Rathi, Madhu Choudhary, Sanchika Snehi, Vishal Singh, P.K. Singh and R.K. Singh
Department of Genetics and Plant Breeding, Institute of Agricultural Sciences,
Banaras Hindu University, Varanasi (Uttar Pradesh), India.

(Corresponding author: Sameer Upadhyay)*

(Received 04 April 2022, Accepted 06 June, 2022)
(Published by Research Trend, Website: www.researchtrend.net)

ABSTRACT: Sodicity is one of the prima facie concerns among salt stress that a rice crop comes across throughout its vegetative and reproductive phases, restricting its output and productivity. Since yield under salt stress depends on a number of attributing traits, PCA helps reduce these variables in terms of a small number of variables with no loss in the original data set. Therefore, a study was conducted using 250 Recombinant Inbred Lines (F_7) in the natural sodic conditions of ANDUAT, Kumarganj, Ayodhya with nine agro-morphological traits and a principal component analysis was carried out. Out of nine principal components, three exhibited Eigenvalue more than one governing 91.68% variance. The highest positive Eigenvalue was observed for panicle length and test weight in PC1, indicating their pronounced effect on the overall variation in the lines.

Keywords: Rice, Sodicity, RILs, PCA, Eigenvalues, Yield.

INTRODUCTION

Rice (*Oryza sativa* L.) is the world's most extensively farmed cereal grain, providing sustenance to one-third of the world's population. India, behind China, has the world's largest rice-growing area, with 44 million hectares (Mha) under cultivation. The Kharif rice production in India during 2021–22 is estimated to be 107.04 million tonnes (Mt) (Anonymous, 2021). Rice yield increase of 1.0–1.2% per year beyond 2020 will be required to feed the world's still-growing population while keeping prices low (Anonymous, 2013).

Sodicity is one of the most pressing concerns among all the abiotic issues that rice, a salt-sensitive cereal, faces during its vegetative and reproductive stages, limiting its production and productivity (Sheoran *et al.*, 2021; Liang *et al.*, 2015). It causes phosphorus, zinc, and potentially iron insufficiency, as well as boron toxicity. Plants are less able to acquire crucial nutrients from the soil when they are affected by sodicity (Upadhyay *et al.*, 2020). Reduced germination rate, stunted plant growth, limited root development, low tillering, spikelet sterility and number, low test weight, low yield, uneven field growth, poor root growth, leaf rolling, low harvest index, leaf browning, delayed flowering, reduced seed set due to lower pollen viability and mortality are some of the pertinent morphological signs a plant shows when grown in sodic soil. Alkalization of soil due to $NaHCO_3$ and Na_2CO_3 might be a more severe problem than soil salinisation caused by neutral salts, such as NaCl and Na_2SO_4, in certain respects (Li *et al.*, 2017). Furthermore, extensive field testing revealed production losses ranging from 36 to 69% in rice grown on sodium salt-affected soils versus normal soils. (Upadhyay *et al.*, 2022; Qadir *et al.*, 2014). The use of sodic lands for agricultural yield improvement is anticipated to increase to meet the desired yield gain, and the long-term sustainability of sodic soils for food and feed production will become a major problem. The selection of those features that are yield determiners under sodic circumstances should be examined in this context.

Plant breeders frequently measure a vast number of traits, some of which may lack adequate discriminating power for germplasm assessment, characterization, and management (Maji and Shaibu 2012). In this situation, Principal Component Analysis (PCA) can be used to uncover patterns in data sets and reduce redundancy. It is a multivariate statistical approach that attempts to simplify and evaluate the interrelationship between a large number of variables in terms of a small number of variables or components without sacrificing any of the original data set's key information. Clifford and Stephenson (1975) reported that the first three principal components are frequently the most essential in representing variation patterns.

With the above argument, an experiment was conducted to evaluate the Principal Components Analysis of the traits in Recombinant Inbred Lines (RILs) obtained from a cross of PUSA 44 (Susceptible) and CSR 43 (Tolerant) cultivated under sodicity conditions.

MATERIALS AND METHODS

The genetic materials consisted of two parents *viz.*, PUSA 44 (Sodicity susceptible) as female and CSR 43 (Sodicity Tolerant) as male parents. In *Kharif* 2016, at the Agricultural farm of the Institute of Agricultural Sciences, Banaras Hindu University (BHU), Varanasi, a cross was established between the parents, and F_{1s} were obtained. These F_{1s} were validated using SSR markers. Single F_1 plant was selfed, and 250 RILs were generated in *Kharif* 2019 following off-season sowing at ICAR-National Rice Research Institute and main-season sowing at BHU utilising the Single Seed Descent (SSD) technique up to F_7 generation. The phenotypic evaluation was performed in *Kharif* 2020 at NSP-6 Agricultural Research Farm of Acharya Narendra Dev University of Agriculture and Technology (ANDUAT), Kumarganj, Ayodhya.

ANDUAT is located in the Gangetic alluvium of Eastern Uttar Pradesh, with a latitude of $26^{o}47'$ North and a longitude of $81^{o}12'$ East, at the height of 113 meters above mean sea level. It lies in the semi-arid zone, with the monsoon supplying 80% of total precipitation. The soil samples were taken randomly from various locations, followed by mixing in equal proportions. Later the mixture was subjected to pH and EC meters following standard protocol. Post Analysis, the location was found to have a pre-transplanting and post-harvest pH of 9.6 and 9.2, respectively, while the EC (at 25^{o}C) and ESP were 0.65 dSm^{-1} and 75.57, respectively. Accordingly, the soil was classified as moderately sodic.

Ten seedlings (F_7) per line of 21 days old were transplanted following alpha lattice design of experiment with two replications of 20 × 20 cm spacing. Recommended package of practices were followed and data was recorded on five randomly selected plants for the quantitative traits *viz.*, Days to 50% Flowering, Days to Maturity, Plant Height (cm), Effective Tillers per plant, Panicle Length, Filled Grains Per Panicle, Test Weight (g), SPAD and Grain Yield Per Plant (g). Principal Component Analysis was performed on the mean data collected concerning all of the aforesaid quantitative traits using *STAR v.2.0.1* of IRRI.

RESULT AND DISCUSSION

By evaluating the dependency among the characteristics, principal component analysis (PCA) is used to reduce big data sets into smaller principal components with no loss of detail. Table 1 depicts Eigenvalues, Variance Percentage and Cumulative Percentage. Three of the eight components evaluated in the current study had Eigenvalues more than one. The components having Eigenvalue more than one together controlled 91.68 % variance among the selected traits. PC1, PC2 and PC3 controlled 75.02, 12.99 and 3.66 % variability among the RILs for the traits under study. The contributions of nine quantitative traits to the principal components are shown in Table 2. The same principal component showed an Eigenvalue of 5.752, 2.169 and 1.33, respectively. PC1 showed panicle length (0.3554) and test weight (0.3486) as the relatively higher contributors. Similar findings were reported by Manohara *et al.* (2020); Sahu *et al.* (2016). No negative relation among traits was found for PC1. The highest positively correlated variables for PC2 were Filled Grains per Panicle (0.4800) and Grain Yield per Plant (0.4195). The component PC3 had Effective Tillers per plant, and Panicle Length displayed the highest contributions. Christina *et al.* (2021) reported similar observations. The scree plot showed the variance percentage between Eigenvalues and the Principal Components (Fig. 1). PC1 exhibited 75.02 % variability with an Eigenvalue of 5.752. The graph depicts that maximum variation was contributed by PC1. A similar report was shown by Shivani *et al.* (2021).

Table 1: Eigenvalues, Variance Percentage and Cumulative Percentage of Principal Components.

Principal Components	Eigenvalues	Percentage of Variance	Cumulative Percentage
PC1	5.752	75.02	75.02
PC2	2.169	12.99	88.02
PC3	1.33	3.66	91.68
PC4	0.218	2.42	94.10
PC5	0.156	1.74	95.84
PC6	0.126	1.40	97.24
PC7	0.105	1.17	98.41
PC8	0.082	0.92	99.33
PC9	0.06	0.67	100

Table 2: Contributions of first three principal component to variations among RILs.

Traits	PC1	PC2	PC3
Days to 50% Flowering	0.3386	-0.3066	0.2002
Days to Maturity	0.3254	-0.4320	-0.1056
Plant Height	0.2512	-0.2255	-0.2304
Effective Tillers per plant	0.3302	0.2394	0.4657
Panicle Length	0.3554	0.0665	0.4305
Filled Grains Per Panicle	0.2982	0.4800	-0.5364
Test Weight	0.3486	0.1969	0.2241
SPAD	0.3201	-0.4020	-0.3251
Grain Yield Per Plant	0.3284	0.4195	0.2234

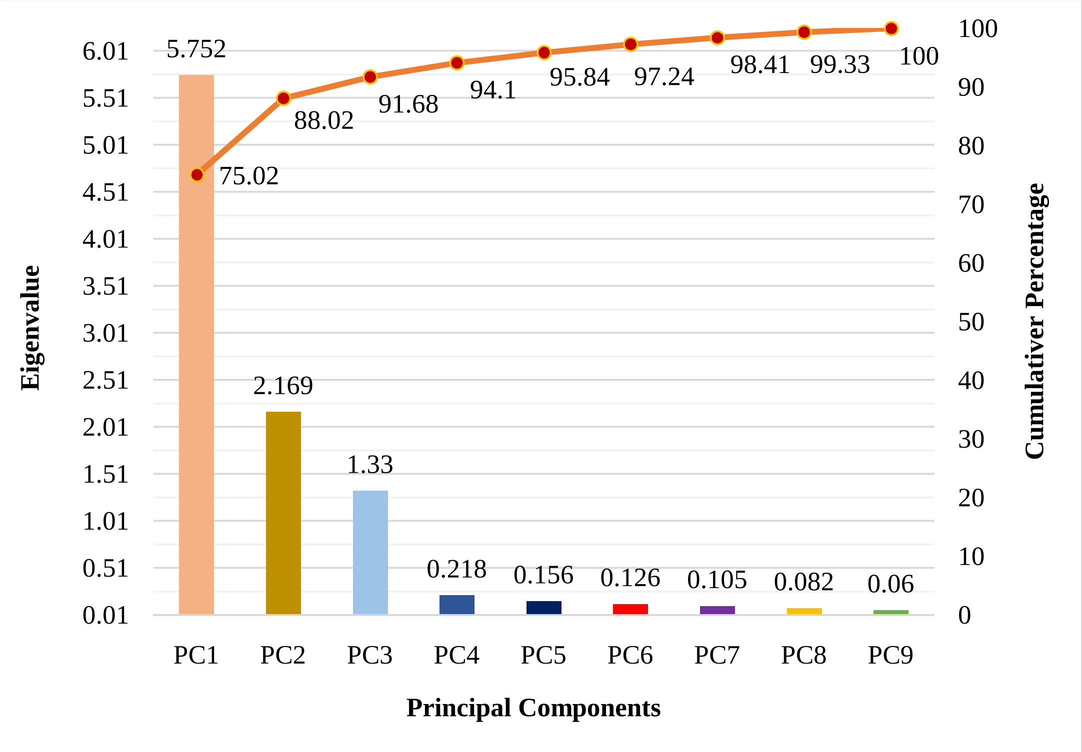

Fig. 1. Scree Plot diagram of Principal Components of Recombinant Inbred Lines.

CONCLUSION

PCA can be used to extract all of the relevant components and emphasize their contributions to overall variability, making it an excellent tool for speeding up the breeding process. Genotypes selected for Panicle Length and Filled Grains per Plant would be useful in plant breeding programs since these component traits significantly control the overall performance of lines. The PCA also revealed that test weight and effective tillers per plant played a prominent role in classifying the variation in the population. These RILs could be further used as a mapping population for identifying genomic regions (QTLs) conferring tolerance towards sodicity at the seedling or reproductive stages. Furthermore, these RILs can be utilized as germplasm to exploit the variability required to improve or develop tolerant genotypes.

Acknowledgement. The authors acknowledge the support Institute of Agricultural Sciences, Banaras Hindu University, Varanasi, and Acharya Narendra Dev University of Agriculture and Technology, Ayodhya, for providing necessary resources for the smooth conduct of the experiment. They further express their heartfelt regards to Dr. Rameswar Prasad Sah, Senior Scientist, Crop Improvement Division, ICAR-NRRI, Cuttack, for providing resources to conduct off-season trails and value to the manuscript.

Conflict of Interest. None.

REFERENCES

Anonymous (2021). Second Advanced Estimates of Production of Major crops for 2021-22 Press Information Bureau, Delhi https://static.pib.gov.in/WriteReadData/specificdocs/documents/2021/may/doc202152541.pdf. Accessed in January, 2022.

Anonymous (2013). GRiSP (Global Rice Science Partnership 2013). *Rice almanac, 4th edition*. International Rice Research Institute, Los Baños, Philippines, p.283.

Christina, G. R., Thirumurugan, T., Jeyaprakash, P. and Rajanbabu, V. (2021). Principal component analysis of yield and yield related traits in rice (*Oryza sativa* L.) landraces. *Electronic Journal of Plant Breeding*, *12*(3): 907–911.

Clifford, H. T. and Stephenson, W. (1975). An Introduction to Numerical Classification. Academic Press, London. p. 229.

Li, N., Sun, J., Wang, J., Liu, H., Zheng, H., Yang, L., and Zou, D. (2017). QTL analysis for alkaline tolerance of rice and verification of a major QTL. *Plant Breeding*, *136*(6): 881–891.

Liang, J. L., Qu, Y. P., Yang, C. G., Ma, X. D., Cao, G. L., Zhao, Z. W., and Han, L. Z. (2015). Identification of QTLs associated with salt or alkaline tolerance at the seedling stage in rice under salt or alkaline stress. *Euphytica*, *201*(3): 441–452.

Maji, A. T. and Shaibu, A. A. (2012). Application of principal component analysis for rice germplasm characterization and evaluation. *Journal of Plant Breeding and Crop Science*, *4*(6): 87–93.

Manohara, K. K., Morajkar, S. and Shanbagh, Y. (2020). Genetic analysis of grain yield and its associated traits in diverse salt-tolerant rice genotypes under coastal salinity condition. *Journal of Cereal Research*, *12*(3): 290–296.

Sahu, H., Saxena, R. R., Verulkar, S. B. and Rawte, S. (2016). Association, Principal Component and Genetic Divergence Study in Recombinant Inbred Lines (RIL's) Population of Rice. *International Journal of Bio-resource and Stress Management*, *7*(4): 673–681.

Sheoran, P., Kumar, A., Sharma, R., Barman, A., Parjapat, K., Singh, R. K., and Singh, R. K. (2021). Managing sodic soils for better productivity and farmers' income by integrating use of salt tolerant rice varieties and matching agronomic practices. *Field Crops Research*, *270*(108192): 1-15.

Shivani, D., Neeraja, C. N., Cheralu, C. and Shankar, V. G. (2021). Multivariate analysis and character association studies for yield and nutritional characters in swarna and type 3 RIL population of rice (*Oryza sativa* L.). *Journal of Cereal Research*, *13*(2): 180–187.

Upadhyay, S., Rathi, S., Choudhary, M., Singh, P. K., Loitongbam, B., Bisen, P., and Singh, R. K. (2022) Genetic Architecture and Association Studies for Grain Yield and its attributing Traits in Recombinant Inbred Lines for Sodicity Tolerance in Rice (*Oryza sativa* L.). *International Journal of Bio-resource and Stress Management*, *13*(5): 519–526.

Upadhyay, S., Singh, P. K., Rathi, S. R., Bisen, P. and Loitongbam, B. (2020). Sustainable Production of Rice under Sodicity Stress condition. In: Rakshit, A., Singh, H., Singh, A.K., Singh, U.S., and Fraceto, L. (Eds.) *New Frontiers in Stress Management for Durable Agriculture* (pp. 65–74). Springer, Singapore.

How to cite this article: Sameer Upadhyay, Sanket Rathi, Madhu Choudhary, Sanchika Snehi, Vishal Singh, P.K. Singh and R.K. Singh (2022). Principal Component Analysis of Yield and its Attributing Traits in Advanced Inbred Lines of Rice under Sodicity condition (*Oryza sativa* L.). *Biological Forum – An International Journal*, *14*(2): 1273-1276.