Indian J. Genet. Plant Breed., (2022) 82(1): 94-98
doi: 10.31742/IJGPB.82.1.13

ISSN: 0975-6906
www.isgpg.org

SHORT RESEARCH ARTICLE

Principal component analysis and genetic divergence studies for yield and quality-related attributes of rice restorer lines

Shweta Tiwari*, Yogendra Singh, P.K. Upadhyay[1] and G.K. Koutu

Abstract

A study on genetic diversity and principal component analysis (PCA) in a set of 90 fertility restorer lines of rice was conducted to identify potential parents for producing high-yielding hybrids. The D^2 statistics uncovered the maximum inter-cluster distance between the clusters having different genotypes. The genotypes PS 2, PRR 828, JR-4322-2, and JR-4322-2 belonging to these diversified gene pools may produce heterotic hybrid combinations involving the most suitable parents mentioned above. The PCA reduces dimensional complexity into nine principle axes with PC1 account maximum variable genotypes, namely, JR-1009, ANP-553, JR-1062-1, JR-1103-1, JR-1023-1, JR-1054-4, IR09N 261, JR-1008, NPT-3806, and JR-81. Considering the magnitude of genetic distance, the per cent contribution of traits towards divergence (fertile spikelet/plant and total spikelet/plant) along with the highest cluster means of these traits reflected by the genotypes belonging to clusters, IX and X. The most quality attributes were included in PC4 and PC5 containing genotypes NPT 10, R710, and JR1301. The diversified gene pool and intensive selection designed for varietal development followed by molecular characterization give a precise idea about the upcoming utilization of existing genetic diversity.

Keywords: D^2 statistics, genetic divergence, principal component analysis, restorer lines

Rice is the daily food supplement of millions of families in Asia and thus acts as a plate filler crop. Per capita consumption in the rice-dependent nation is 62-192 kg of rice per year, providing about 20% of the per capita energy and 13% of dietary protein by Bollinedi et al. (2020). The demand for rice grain draws the attraction of many breeders to enhance its quantity and quality. At present, the total rice production in India is estimated to be 122.27 m t compared to 118.87 m t in 2019-2020 (economictimes.indiatimes.com, 2022). The main focus of breeders is on increasing yield and adopting novel breeding approaches in constant fluctuating climatic conditions that demand new biotic and abiotic resistance genes from hidden diversity. Genetic divergence among genotypes may arise due to geographical separations or genetic barriers to crossability. In rice breeding, hybrids produced from genotypes of diverse origin display greater heterosis and produce novel high-yielding varieties. Diverse germplasms are an excellent source of developing varieties for crop improvement. The grouping or classification of genotypes based on a suitable divergent scale is imperative to obtain progeny superiority. The maximum inter-cluster distance indicated wide diversity, while the minimum suggested a close relationship between the groups (Devi et al. 2019). The relative contribution of each character to total divergence is considered for assessing polygenic variation. Principal component analysis (PCA) is a non-parametric, multivariate technique that analyzes a data table in which several inter-correlated quantitative dependent variables describe observations to extract the important information (Nachimuthu et al. 2014). Fertility restorer lines of rice are utilized in hybrid breeding programs to enhance

Department of Plant Breeding and Genetics, College of Agriculture, Jawaharlal Nehru Krishi Vishwa Vidyalaya, Jabalpur 482 004, Madhya Pradesh, India; [1]Department of Genetics and Plant Breeding, R.B.S. College, Bichpuri Campus, Dr. B.R. Ambedkar University, Agra, U.P., India

Corresponding Author: Shweta Tiwari, Department of Plant Breeding and Genetics, College of Agriculture, Jawaharlal Nehru Krishi Vishwa Vidyalaya, Jabalpur 482 004, Madhya Pradesh, India, E-Mail: geneticistnbreedershweta@gmail.com

How to cite this article: Tiwari S., Singh Y., Upadhyay P. K., Koutu G. K. 2022. Principal Component Analysis and Genetic Divergence Studies for Yield and Quality-related Attributes of Rice Restorer Lines. Indian J. Genet. Plant Breed., **82**(1): 94-98.

Source of support: Nil

Conflict of interest: None.

Received: Aug. 2021 **Revised:** Dec. 2021 **Accepted:** Jan. 2022

productivity through variability assessment. Therefore, a study was conducted to identify the elite genotypes among the varied population and utilize the diversified fertility restorers in the hybridization program.

The experiment was conducted during *kharif* seasons 2018 and 2019 under Rice Improvement Project at Seed Breeding Farm, JNKVV, Jabalpur (MP). A set of 90 fertility restorer lines of rice were sown in a Randomized Block Design (RBD) with three replications. The plots consisted of four rows of each genotype with a spacing of 15cm between plants and 20 cm between rows. Recommended agronomic practices were followed to raise a good crop. Twenty-nine agronomic attributes, namely, days to fifty per cent flowering **(**DFF), days to maturity (DTM), flag leaf length (FLL), flag leaf width (FLW), total tillers per plant (TT/P), productive tillers per plant (PT/P), stem thickness (ST), stem length (SL), plant height in cm (PH), number of panicles per plant (Pa/P), panicle length (PL), biological yield per plant (BY/P), panicle weight per plant (PaWt/P), no. of fertile spikelets per panicle (Fsp/pa), total number of spikelets per panicle (TSp/pa), spikelet fertility in percent (SF), spikelet density in percent (SD), thousand seed weight in g (ThSWt), panicle index (PI -, harvest index (HI), grain length (GL), grain width (GW), decorticated grain length (DGL), decorticated grain width (DGW), length to breadth ratio (L/B), hulling percentage (H), milling percentage (M) and head rice recovery percentage (HRR) were taken based on DUS guidelines to assess the genetic diversity and rank the variability of restorer lines. The observations were recorded on 10 randomly taken plants from each replication as per the standard procedure, and the data were subjected to statistical analysis using mean values. The data were analyzed in conformity with multivariate analysis of genetic divergence using D^2 statistics by Mahalanobis (1936). The average inters- and intracluster D^2 mean values were estimated according to the procedure given by Singh and Chaudhary (1977), and grouping of genotype was done following the Tocher's method, while the methodology followed for PCA analysis was given by Massay (1965) and Jolliffie (1986).

Table 1. Contribution of different characters towards genetic divergence

S. No	Character	Times ranked 1^{st}	Per cent contribution of traits towards divergence
1	No. of fertile spikelets/plant	1297	32.38
2	No. of total spikelets/plant	1262	31.51
3	Thousand-grain weight	299	7.47
4	Grain length	294	7.34
5	Decorticated grain length	227	5.67
6	Days to maturity	208	5.19
7	Days to 50% flowering	103	2.57
8	Harvest index	71	1.77
9	Spikelet fertility in percent	65	1.62
10	Stem length	63	1.57

Assessment of genetic divergence

Results of analysis of variance indicated that the mean sums of squares due to genotypes were highly significant for all the 29 traits under study, which articulated the existence of variability. All the characters contributed to genetic divergence except the total number of tillers/plant, productive tillers/plant, stem thickness, the total number of panicles/plant, panicle length, spikelets density %, and panicle index. The characters contributed the maximum to the genetic divergence, as given in Table 1. Several researchers have reported divergence for the total number of spikelets/ panicles and the number of fertile spikelets/ panicles (Prasad et al. 2018).

The 90 genotypes were grouped into 10 clusters following Tocher's method (Table 2). Among them, three clusters are poly-genotypic, i.e., Cluster 1, Cluster III, Cluster IV, while Cluster II, V, VI, VII, VIII, IX, and X were mono-genotypic and predicting uniqueness in genes. The formation of distinct, solitary clusters maybe since their ancestor's geographic barriers prevented the gene flow or intensive natural and human selection for diverse and adaptable gene complexes must be the reason for this genetic diversity Ranjith et al. (2018)

The descending order of intracluster distance was reported in clusters III, IV, and I concluded divergence within these clusters. The genotypes belonging to different clusters separated by high statistical distance could be used in hybridization programs for obtaining a wide spectrum of variation among the segregates. In this context, PRR 828 (Cluster IX) with JR 4322-2 (Cluster X) and PS 2 (Cluster VIII) with PRR 828 (Cluster IX) may result in to heterotic combinations.

The cluster means of grain yield/plant, panicle length, panicle weight/plant, thousand-grain weight, harvest index, decorticated grain length and decorticated grain width were detected at crest in cluster VIII discloses that PS 2 commits its share in major yield and its associated traits (Table 3). Nayak et al. (2004) concluded selection and choice of parents mainly depend upon the contribution of characters towards divergence. Thus the preponderance of no. of fertile spikelets/plant and a number of spikelets/ plant in divergence (Table 1) discerns clusters IX and X, with genotypes, PRR 828, JR-4322-2. In addition to these fertility-related traits, panicle index, percent spikelet fertility, and percent spikelet density (Table 3) may prove useful for hybrid breeding. The genotypes in cluster VII exhibited the peak mean value for most of the quality traits like hulling, milling, and head rice recovery percentage, indicating that JR-1326 may be a useful source of genes for quality breeding approaches.

Table 2. Distribution of fertility restorer lines in different clusters

Cluster No.	No. of genotype	Genotypes
1	68	MAHAMAYA, R 548, R 650, R 704, ABHYA, R 321, R 294, R 712, R 710, R 304, JR 503, SUGHANDA 3, NPT 10, NPT 13-01, NPT 15, NPT 29, NPT 35-01, NPT 37, NPT 70, NPT (S) 8-1, NP 72, NP 1024, NP 8421, NPT 31, LAXMI 144, IR 79854-38-2-4, IR 79854-48-2-1, AD 02207, JR-1004, JR-1009, JR-1103, JR-1103-1, JR-1204, JR 1301, JR-1309, JR-1312, JR-1327, JR-4319-1, RP 5911-52-13-3-2-2-1, CR 2829-PLN 32, CANP 318, ANP 526, NPT 32, JR 1302, IR 838614-673-13, JR 1322, NPT 89* IR64, ,NPT 14-12,NPT 40-018 PUSA BASMATI,JR 81,NPT 3804,NPT-3805, ,NPT 3817,NPT 3820,NPT-3821,JR-1001,JR-1008, JR-1014, JR-1021,JR-1023-1,JR-1054- 4,JR-1062-1, JR-1064-1, JR-1101-6, JR-1124-4,RT CNP 28, PRR 801, PRR 805, PRR 828, RPHR 619
2	1	NPT 65
3	8	CBSN 168, PRR 78, JR-1306, RPHR 2, JR-1018, PSP 456, SPS 71 X NPT 80, NPT 3806
4	7	NPT-3810, RPHR 1005, NPT 3803, RT CNP 28, JR-1019, NPT 89 X IR36, R 710
5	1	ANP 553
6	1	IR 09 N 261
7	1	JR-1326
8	1	PS 2
9	1	PRR 828
10.	1	JR-4322-2

Table 3. Cluster mean values for yield and yield attributing traits of fertility restorer lines

Cluster	Characters	Type of traits
II	Biological yield per plant, flag leaf width, grain width	Y
IV	Flag leaf length	Y
V	Flag leaf width, total tillers per plant, productive tillers per plant, days to fifty percent flowering	Y
VI	Days to maturity, panicle weight per plant, grain length, decorticated grain length, length/breath ratio	QY
VII	Hulling percent, milling percent, head rice recovery	Q
VIII	Panicle length, panicle weight per plant, thousand seed weight, harvest index, decorticated grain length, decorticated grain width, grain yield per plant	QY
IX	Stem thickness, fertile spikelet per panicle, spikelet fertility percent	Y

*Significant at probability level at 0.05 and **significant at probability level 0.01; Y=Yield attributing; QY= Quality and yield attributing and Q = Quality

Principal component analysis (PCA) rotational component matrix (RCM)

Out of the 29 traits studied, only nine principal components (PCs) exhibited more than 1.00 Eigenvalue and showed about 80.449% total cumulative variability among the traits (Fig. 1). The Scree plot exhibited the percent of variation by each PCs and deduced that PC1 has a preponderance of maximum variability of about 16.04% with the highest Eigenvalue. Further, the progressive decrease in variability was found in PC2, PC3, PC4, PC5, PC6, PC7, PC8, and PC9 with values 14.02, 10.64, 8.94, 8.60%, 7.58, 5.87, 4.53, and 4.24 percent, respectively. Fig. 2 indicated that the maximum variation was observed in PC1 compared to the other 29 PCs. So, the selection of lines and traits from this PC will be useful (Fig. 1). The analogous results were observed in new plant type (NPT) rice lines by Shivangi et al. (2021).

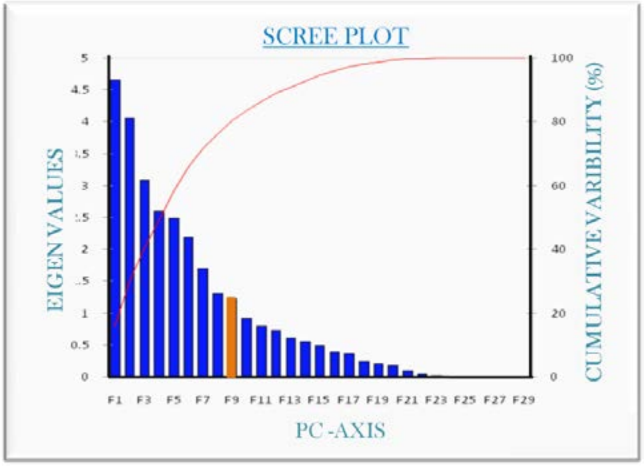

Fig. 1. Scree plot of principal component analysis of rice restorer lines

The results presented in Table 4 revealed the yield-related traits of PC1 donate a maximal share to the total variation thus Fig. 2 portrayed the rotational component matrix between variable traits and PC1. A similar verdict of variability was obtained for total tiller number/plant,

Table 4. Interpretation of rotated component matrix for the traits having highest value (>1.0) in each PCs

Traits	PC 1	PC 2	PC 3	PC 4	PC 5	PC 6	PC 7	PC 8	PC 9
	TT/pl	FSP/pa	FLL	TGW	H%	PT/pl	ST	DTM	DFF
	Pa/pL	TSP/pa	FLW	DGW	M%		BY/pL		SF(%)
	PL	SD%	SL		HRR%				GL
	PW/pL	PI	PH						
	HI		PW/pL						
	GL		GY/pL						
	DGL								
	L/B ratio								

Table 5. List of fertility restorer limes common in each Principal Component

Genotype	PCs	Genotype	PCs
R 321	PCA 1, PCA 5, PCA 8	JR 1004	PCA 8, PCA 4
NPT 65	PCA 2, PCA 3, PCA 7	AD 02207	PCA 5, PCA 6, PCA 8
R 704	PCA3, PCA4, PCA5, PCA6, PCA9	JR 1009	PCA 1, PCA 3
R 712	PCA 4, PCA 6	R 710	PCA 4, PCA 6
MAHAMAYA	PCA 4, PCA 9	PRR 78	PCA 1, PCA 2
IR 79854-38-2-4	PCA 1, PCA 6, PCA 7	RP 5911-52-13-3-2-2-1	PCA 5, PCA 8
R 548	PCA 4, PCA 6	LAXMI 144	PCA 7, PCA 9
NPT 35-01	PCA 3, PCA 8	R 304	PCA 6, PCA 7, PCA 8, PCA 9
JR- 1309	PCA 1, PCA 5	NPT 10	PCA 3, PCA 4, PCA 6, PCA 7
CANP 318	PCA 3, PCA 9	JR-1021	PCA 1 , PCA 5
NP 72	PCA 2, PCA 5	JR- 1103-1	PCA 1 PCA 6
AD 02207	PCA 5, PCA 6	JR- 1204	PCA 3, PCA 4, PCA 5
NPT 13-01	PCA 4, PCA 8	NPT 35-01	PCA 3 PCA 6
JR- 1064-1	PCA 2 PCA 8	RPHR 2	PCA 2, PCA 7
JR 1001	PCA 1, PCA 2, PCA 5, PCA 6	JR 4322-2	PCA 2, PCA 3, PCA 6
RPHR 619	PCA 5, PCA 6, PCA 7, PCA 9	ANP 526 ANP 553	PCA 1, PCA 6
NPT 3803	PCA 3, PCA 4, PCA 6, PCA 8	ANP 526	PCA 1, PCA 2, PCA3, PCA 5, PCA 6
JR 1014	PCA 1, PCA 2, PCA 5	JR- 1327	PCA 4, PCA 5
NPT 3821	PCA 1, PCA 2, PCA 5, PCA 7	NPT 40-018 Pusa Basamti	PCA 1, PCA 3
JR 1001	PCA 1, PCA 2, PCA 5, PCA 6	NPT 70	PCA 3, PCA 4, PCA 7
JR 1014	PCA 1, PCA 2, PCA 5, PCA 7	SPS*NPT 80	PCA 3, PCA 6
JR 1018, JR 1019, NPT 3806	PCA 1 PCA 2	JR 1054-1, JR 1304	PCA 1 PCA 3

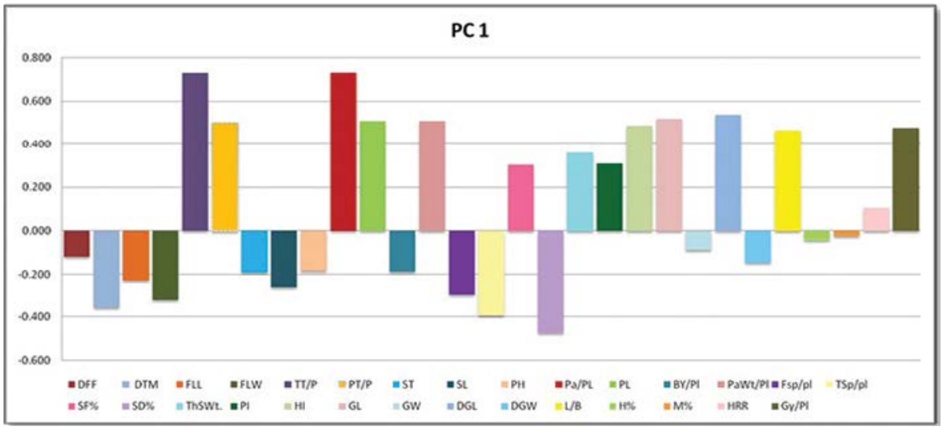

Fig. 2. Average Inter and Intra cluster D2 value for fertility restorer line

panicle length, grain length panicle length, and harvest index (Tiruneh et al. 2019; Nachimuthu et al. 2014). The PC score manifested that JR 1009, ANP-553, JR-1062-1, JR-1103-1, JR-1023-1, JR-1054-4, IR09N 261, JR-1008, NPT-3806, and JR-81 genotypes belong to PC1 and devote supreme genetic variability for almost eight traits. Table 5 indicated that most of the important yield and quality attributing traits were present in PC1, PC9 but the result may not be in propinquity with other researchers that only a single PC as in present case the PC1 contributed for most of the yield attributing traits. The germplasm lines demonstrating maximum positive PC scores and common in PC1, PC2, PC 3, and PC5 illustrating relation with yield and quality attributes are ANP 526, NPT-3821, JR-1001, JR 1014, and JR-1062-1. The PC4 and PC5 accommodate the common quality line is JR 1326 as presented in Table 5. Based on yield and quality traits, these superior lines could be utilized as a donor in crop improvement programs.

Authors' Contribution

Conceptualization of research (PKU, GK, YS); Designing of the experiments (PKU, GK, ST); Contribution of experimental materials (GK, YS); Execution of field/lab experiments and data collection (ST, YS, GK); Analysis of data and interpretation (PKU, GK, ST); Preparation of a manuscript (ST, GK, YS).

References

Bollinedi H., Vinod K. K., Bisht K., Chauhan A., Gopala Krishnan S., Prolay K., Bhowmick M., Nagarajan D., Rao S., Ellur R. K. and Singh A. K. 2020. Characterising the diversity of grain nutritional and physico-chemical quality in Indian rice landraces by multivariate genetic analyses, Indian J. Genet. Plant Breed., **80**(1): 26-38. doi: 10.31742/ISGPB.80.1.4.

Devi M., Jyothulal D.P.B., Krishnaveni1 B. and. Rao V.S. 2019. Genetic Divergence Studies in Rice (*Oryza sativa L.*) Hyrids for Yield, Yield Component Traits and Quality Parameters. Int. J. Curr. Microb. Appl. Sci., **8**(6): 1577-1583.

http:economictimes.indiatimes.com, 2022

Jolliffie I.T. 1986. Principal Component Analysis. Springer, New York. Mahalanobis PC 1936. On the generalized distance in statistics. Proc. Nat. Inst. Sci., **2**: 49-55.

Massay W.F. 1965. Principal components regression in exploratory statistical research. J. Amer. Statistics Assoc., **60**: 234-246

Nachimuthu V.V., Robin S., Sudhakar D., Raveendran M., Rajeswari S. and Manonmani S. 2014. Evaluation of rice genetic diversity and variability in a population panel by principal component analysis. Indian J. Sci. Technol., **7(**10**)**: 1555–1562.

Nayak A.R., Chaudhury D. and Reddy J. N. 2004.Genetic divergence in scented rice. Oryzae., **41(**384**)**: 79-82.

Rahangdale S., Singh Y., Upadhyay P. K. and Koutu G. K. 2020. Principal component analysis of JNPT lines of rice for the important traits responsible for yield and quality. Indian J. Genet. Plant Breed., **81(1)**: 127-131. doi: 31742/ISGPB.81.1.14.

Singh R.K. and Chaudhary B.D. 1977. Biometrical methods in quantitative genetics analysis, Kalyani Publishers, New Delhi., 318.

Tiruneh A., Gebrselassie W. and Tesfaye A. 2019. Genetic diversity study on upland rice (*Oryza sativa* L.) genotypes based on morphological traits in south western Ethiopia. Asian J. Crop Sci., **11(1)**: 17-24.