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Principal Component Analysis for Yield and Bacterial Leaf Blight (BLB) Disease Resistance in Rice (*Oryza sativa* L.) Genotypes

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ABSTRACT: The present investigation was carried out to determine variability among 184 rice genotypes using principal component analysis. First five principal components exhibited more than one Eigen values. PC1 accounted 28.29 % of the total variability contributed by the traits like panicle length, 1000-grain weight, grain weight per plant and AUDPC. The remaining variability of 20.40%, 14.16%, 10.91% and 10.03% was consolidated in component 2, component 3, component 4 and component 5 by various traits like days to 50% flowering, days to maturity, plant height, effective tillers per plant, panicle length, spikelets per panicle, grain weight per plant, 1000 grain weight, grain yield per plant and AUDPC. The first five axes accounted 84.33% of cumulative variance of total variance among 10 characters. Thus the results of principal component analysis revealed, vast genetic variation and the traits contributing for the variation in rice genotypes can be used for various breeding programmes for improvement in yield and disease resistance.

Keywords: Rice, Variability, Principal Component Analysis, Yield.

INTRODUCTION

Rice (*Oryza sativa* L.) is the most widely planted food crop grown across all the continents in the world, except Antarctica and it occupies approximately 11 % of cultivated land area and ranks second in production after wheat (Anis *et al.,* 2016; Tejaswini *et al*., 2018; Umesh *et al*., 2016). In Asia alone, more than 2 billion people obtain 60-70% of calories from rice and its derivatives and almost a billion families in Asia, Africa and America relies on rice based farming systems for their subsistence and principal means of income. According to Tenorio *et al*. (2013), Asia produces and consumes 90% of the world's rice, where as it providing nourishment to 50% of the total population. According to Wani and Sah (2014), by 2030, the globe will require around 25% more rice to meet the predicted demand of a rising world population. India produced 118.43 million tonnes of rice from an area of 43.78 mha at an average productivity of 2705 kg/ha. (Anonymous 2020-2021). Disease and pest are the most prominent biotic agents causing considerable yield reductions; an approximate 52% of the global production of rice is lost annually owing to the damage caused by these factors. Among the biotic factors disease of fungal, bacterial and viral origin are the most important factors which result in crop failure of $ 5 billion every year (Yarasi *et al*., 2008). *Xanthomonas oryzae* pv. Oryzae causes bacterial leaf blight (BLB), which is one of the most devastating diseases of cultivated rice in tropical and temperate locations around the world (Nino-Liu Do *et al*., 2006). It can lead to catastrophic yield losses of up to 80%, depending on the stage of the crop, cultivar susceptibility, and ambient circumstances (28 to 34°C) and genotype susceptibility (Srinivasan and Gnanamanickam, 2005; Noh *et al*., 2007; Mukul *et al*., 2019). Crop improvement programme and selection of efficient genotype is highly reliant on the efficient manipulation of genetic variability in germplasm and viable breeding strategies to improve yield with enhanced disease resistance. Multivariate approaches are commonly used in the statistical approach of categorization because they are useful in capturing and interpreting the innate disparity among genotypes. Multivariate approaches are commonly used in the statistical approach of categorization because they are useful in capturing and interpreting the innate disparity among genotypes. Principal Component Analysis (PCA) can be used to uncover commonalities between variables and categorize the genotypes; mean while cluster analysis on the other hand is concerned with classifying previously undeclared resources (Leonard and Peter, 2009; Mahendran *et al*., 2015). Therefore, this study was undertaken to determine level of germplasm variation and magnitude of genetic diversity among 184 rice genotypes for yield related traits and bacterial leaf blight resistance using Principal Component Analysis (PCA).

Table 1: List of Rice genotype collected from NBPGR, New Delhi and BHU, Varanasi.

Sr. No.	Genotype/Code	S. No.	Genotype/Code	S. No.	Genotype/Code
1.	IC 343395	63	IC 346927	125	IC 382629
2.	IC 343399	64	IC 346935	126	IC 382631
3.	IC 343990	65	IC 346936	127	IC 382632
4.	IC 343991	66	IC 334232	128	IC 382634
5.	IC 344660	67	IC 346942	129	IC 383396
6.	IC 344674	68	IC 346946	130	IC 383402
7.	IC 344726	69	IC 346947	131	IC 383404
8.	IC 283228	70	IC 346950	132	IC 383416
9.	IC 346004	71	IC 346952	133	IC 383418
10.	IC 346809	72	IC 346954	134	IC 383431
11.	IC 346811	73	IC 349680	135	IC 383441
12.	IC 346813	74	IC 349681	136	IC 383469
13.	IC 346817	75	IC 349682	137	IC 383473
14.	IC 346819	76	IC 349683	138	IC 383483
15.	IC 346821	77	IC 349686	139	IC 383558
16.	IC 346822	78	IC 349687	140	IC 383559
17.	IC 346823	79	IC 349689	141	IC 383564
18.	IC 346824	80	IC 353826	142	IC 383642
19.	IC 346826	81	IC 356101	143	IC 383682
20.	IC 346827	82	IC 356117	144	IC 384159
21.	IC 346829	83	IC 356419	145	IC 384162
22.	IC 346831	84	IC 356422	146	IC 384176
23.	IC 346835	85	IC 356429	147	IC 384178
24.	IC 346837	86	IC 356431	148	IC 384190
25.	IC 346838	87	IC 356432	149	IC384200
26.	IC 346841	88	IC 356437	150	IC 384201
27.	IC 346842	89	IC 356448	151	IC 384206
28.	IC 346844	90	IC 356449	152	IC 346941
29.	IC 346845	91	IC 356457	153	IC 384232
30.	IC 346846	92	IC 362108	154	IC 384235
31.	IC 346849	93	IC 362206	155	IC 384237
32.	IC 346852	94	IC 362210	156	IC 384243
33.	IC 346855	95	IC 362211	157	IC 384252
34.	IC 346857	96	IC 362269	158	IC 384255
35.	IC 346859	97	IC 363746	159	IC 384259
36.	IC 346863	98	IC 373131	160	IC 384260
37.	IC 346864	99	IC 373137	161	IC 384263
38.	IC 346869	100	IC 373205	162	IC 384266
39.	IC 346870	101	IC 373206	163	IC 384267
40.	IC 346873	102	IC 373211	164	IC 384271
41.	IC 346879	103	IC 373215	165	IC 384274
42.	IC 346880	104	IC 373217	166	IC 384275
43.	IC 346881	105	IC 373218	167	IC 384277
44.	I C 346887	106	IC 373220	168	IC 384279
45.	IC 346888	107	IC 373222	169	IC 384280
46.	IC 346890	108	IC 373225	170	IC 384284
47.	IC 346891	109	IC 373263	171	IC 384286
48.	IC 346892	110	IC 374720	172	IC 384290
49.	IC 346897	111	IC 382564	173	IC 384291
50.	IC 346899	112	IC 382568	174	IC 384292
51.	IC 346900	113	IC 382569	175	IC 384293
52.	IC 346902	114	IC 382572	176	IC 384295
53.	IC 346907	115	IC 382574	177	IC 384299
54.	IC 346911	116	IC 382575	178	IC 384303
55.	IC 346913	117	IC 382576	179	IC 384349
56.	IC 346916	118	IC 382592	180	IC 384350
57.	IC 346918	119	IC 382593	181	IC 384351
58.	IC 346919	120	IC 382604	182	IC 384354
59.	IC 346921	121	IC 382607	183	IC 384357
60.	IC 346922	122	IC 382625	184	IC 391524
61.	IC 346924	123	IC 382627		
62.	IC 282455	124	IC 382628		

MATERIAL AND METHODS

The present experiment was conducted at Agricultural Research Farm of Institute of Agricultural Sciences, Banaras Hindu University, Varanasi (U.P.), India. 184 rice germplasm collections were gathered from the National Bureau of Plant Genetic Resources in New Delhi via the Institute of Agricultural Sciences' Department of Genetics and Plant Breeding, Banaras Hindu University, Varanasi (U.P.) India evaluate with respect to yield attributes *viz.* days to 50% flowering, days to maturity, plant height, effective tillers per plant, panicle length, spikelets per panicle, grain weight per plant, 1000 grain weight, grain yield per plant and (Area under disease progress curve) AUDPC (Table 1). The nursery was seeded in the second week of August, and seedlings that were about 4 weeks old were transplanted in the second week of September, with a row-to-row × plant-to-plant spacing of 20 cm × 20 cm. Each plot comprises ten plants and symbolizes a single replication. To raise a decent crop, recommended agronomic strategies were followed. Analysis for principal components was done by using STAR software. The Department of Mycology and Plant Pathology IAS, BHU provided a culture of *Xanthomonas oryzae* pv. *Oryzae* (strain BX043 wild type) and subcultured on peptone sucrose agar medium and maintained it at pH 7.2-7.4 (Fahyand Persley, 1983) and in pathogenicity test, rice plants were inoculated with *Xanthomonas oryzae* pv. *Oryzae* using clipping method and plants were inspected every 24 hrs time intervals to note the onset of disease signs and lesion length were recorded at 8, 16, 24 and 32 days after inoculation (DAI). The area under disease progress curve (AUDPC) was computed using the Campbell and Madden (1990) formula.

RESULTS AND DISCUSSION

The result of the PCA explained the genetic variability of the rice collection. The five component viz., PC1, PC2, PC3, PC4 and PC5 showed 28.29%, 48.73%, 63.38%, 74.29% and 84.33% of variations among the characters respectively. The first five main PCAs are extracted from the complicated ten components, the total cumulative variance of these first five principal components (PC1, PC2, PC3, PC4, and PC5) accounted for 84.33% of the total variation (Table 2). Similar results were reported by Mahendran *et al.* (2015) and Ojha *et al.* (2017). The Eigen vectors decreased significantly from PC1 (28.29%) to PC5 (10.03 %). This suggests that after PC5 more principal components did not describe much variation. Thus, only the first five PCs were considered. Results (Table 3) revealed by rotated component matrix showed that the PC1 which accounted for the maximum variability (28.29%) and highly loaded with characters such as 1000 grain weight (0.301), grain weight per plant (0.274), panicle length (0.049) and AUDPC (0.037) made a tremendous contribution, while the rest made a negative contribution. It was obvious that yield features, with the exception of the number of effective tillers per plant and spikelet's per panicle, are the main contributors to PC1 variation. PC2 accounted 20.40% of the total variation and loaded positively with the AUDPC (0.037) and days to 50% flowering (-0.056), days to maturity (-0.061), plant height (-0.143), effective tillers per plant (-0.242), panicle length (-0.185), spikelets per panicle(-0.155), grain weight per plant (-0.402), 1000 grain weight (-0.349) and grain yield per plant (-0.573) contributed in negative direction. PC3 had the positive contribution from grain yield per plant (0.275) as compare to other traits and accounts 14.16%. of variation. In PC 4 accounts 10.91% of the total variation and positive factor loading observed with days to 50% flowering (0.124), days to maturity (0.118), effective tillers per plant (0.204), spikelets per panicle (0.416), grain weight per plant (0.301), 1000 grain weight (0.314), AUDPC (0.230) and negative contribution by rest of the traits. PC 5 reflected positive factor loading by all the traits other than days to 50% flowering, days to maturity, grain weight per plant, 1000 grain weight, grain yield per plant and out of total variability accounts 10.03%. As a result, strong features congregate in different principle components, contributing to the explanation of variability and tending to stick together. This may be kept into consideration during utilization of these characters in future breeding program.

Table 2: Eigen values, Proportion of Variance and cumulative variability of different rice genotypes.

Statistics	PC1	PC2	PC3	PC4	PC5
Standard deviation	1.682	1.429	1.210	1.044	1.001
Proportion of Variance	28.29	20.40	14.16	10.91	10.03
Cumulative Proportion	28.29	48.73	63.38	74.29	84.33
Eigen Value	2.829	2.043	1.465	1.090	1.003

Table 3: Eigen vectors or component loading in different PCs for yield and related traits in Rice genotypes.

Variables	PC1	PC2	PC3	PC4	PC5
Days to 50% Flowering	-0.5549	-0.0560	-0.1240	0.1240	-0.2125
Days to Maturity	-0.5557	-0.0619	-0.1359	0.1182	-0.2085
Plant Height cm	-0.4300	-0.1430	-0.3694	-0.0805	0.1151
Effective Tillers/Plant	-0.1114	-0.2424	-0.0568	0.2043	0.7297
Panicle Length (cm)	0.0496	-0.1859	-0.3643	-0.6788	0.3232
Spikelets/ Panicle	-0.1087	-0.1555	0.3775	0.4164	0.3849
Grain Weight/ Plant	0.2748	-0.4024	-0.3773	0.3016	-0.0893
1000 Grain Weight	0.3016	-0.3495	-0.3750	0.3143	-0.2280
Grain Yield/Plant	-0.0630	-0.5733	0.2758	-0.1970	-0.1553
AUDPC	0.0370	0.4922	-0.4384	0.2305	0.1703

The percentage of variation associated from each principal component was derived by constructing a graph between Eigen values and principal component numbers, as shown in Fig. 1 via Scree plot.PC1 has a variance of 28.29% and an Eigen value of 2.82. PC2, PC3, PC4, and PC5 have eventually reduced Eigen values of 2.04, 1.46, 1.09, and 1.00, respectively. After PC5 started to straighten, an elbow type line was created with minute differences seen in each PC, clearly demonstrating that PC1 had the most variation. It was further reported by Fenty (2004); Guei *et al.* (2005) that PCA condenses a large number of variables into a smaller number of components that summarise the interactions.

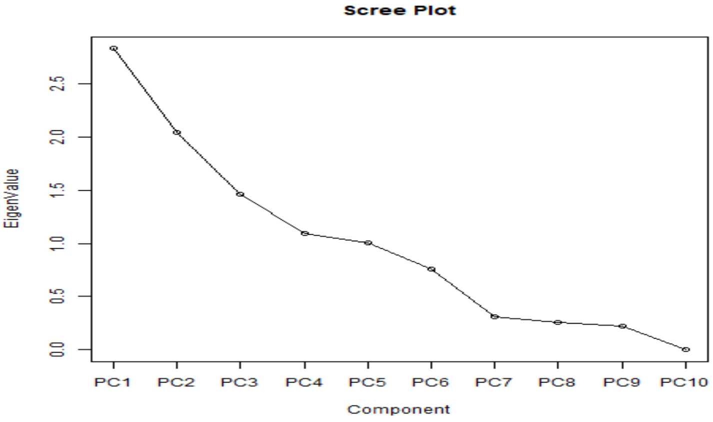

Fig. 1. Scree plot showing eigen value variation of rice germplasm.

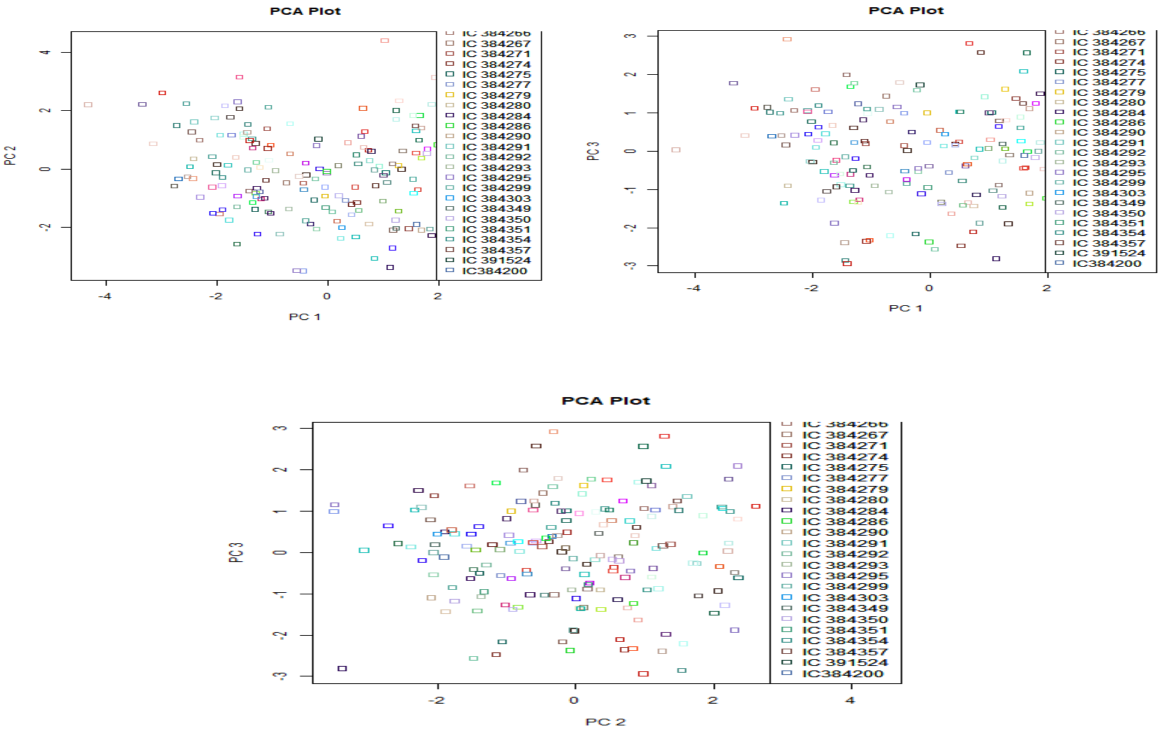

Fig. 2. Distribution of rice genotypes across the various components.

CONCLUSION

Each coefficient of proper vectors expresses the degree of contribution of independent figure with which each primary component is associated, whereas the phenotypic value of each variable gauges the importance and contribution of each component to total variance. Thus, the prominent variables forming different main components and contributing to the interpretation of variability and having a higher retention rate together may be taken into account when using these variables in breeding programmes for yield and bacterial blight resilience. On the basis of result it had concluded that five component *viz.,* PC1, PC2, PC3, PC4 and PC5 contributed 84.33 per cent of total variation.

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Conflict of Interest. None.

REFERENCES

Anis, G., Sabagh, A. E. L., Ghareb, A. and Rewainy, A. E. (2016). Evaluation of promising lines in rice (*Oryza sativa* L.) to agronomic and genetic performance under Egyptian conditions. *Int. J. Agron. Agric. Res*., *8*(3): 52–57.

Anonymous (2020-21). Agriculture Statistics at a Glance, Directorate of Economics & Statistics, Department of Agriculture & Cooperation, Ministry of Agriculture. Government of India.

Campbell, C. L. and Madden, L. V. (1990). Introduction to Plant Disease Epidemiology. John Wiley and Sons. New York.

Fahy, P. C., and Persley, G. J. (1983). Plant bacterial diseases: A diagnostic guide, Academic Press, New York, 393.

Fenty, J. (2004). Analysing distances. *The Strata Journal*., *4*: 1– 26.

Guei, R. G., Sanni, K.A. and Fawole, A. F. J. (2005). Genetic diversity of rice (*Oryza sativa*). *Agron Africaine*., *5*: 17–28.

Leonard, K. and Peter, R. J. (2009). Finding Groups in Data: An Introduction to Cluster Analysis. pp.344.

Mahendran, P., Veerabadhiran, P., Robin, S., and Raveendran, M. (2015). Principal component analysis of rice germplasm accessions under high temperature stress. *Intl. J. of Agric. Sci. and Res., 5*(3): 355-360.

Mukul, Sandhya, Singh, P. K., Singh, S. P. and Aprajita (2019). Analysis of Genetic Variability to Improve Yield and Resistance to Bacterial Leaf Blight in Rice (*Oryza sativa* L.) Germplasm. *Int. J. Curr. Microbiol. App. Sci. 8*(04): 52-58.

Nino-Liu, D. O., Ronald, P. C., and Bogdanove, A. J. (2006). *Xanthomonas oryzae* pathovars: model pathogens of a model crop. *Mol. Plant Pathol*., *7*(5): 303-324.

Noh, T. H., Lee, D. K., Park, J. C., Shim, H. K., and Choi, M. Y. (2007). Effect of bacterial leaf blight occurrence on rice yield and grain quality in different rice growth stage. *Res Plant Dis., 13*: 20-23.

Ojha, G. C., Sarawgi, A. K., Sharma, B. and Parikh, M. (2017). Principal component analysis of morphophysiological traits in rice germplasm accessions (*Oryza sativa* L.) under rainfed condition, *Int. J. Chem. Stud*., *5*(5): 1875-1878.

Srinivasan, B. and Gnanamanickam, S. (2005). Identification of a new source of resistance in wild rice, Oryzarufipogon to bacterial leaf blight of rice caused by Indian strains of *Xanthomonas oryzae* pv. oryzae. *Curr. Sci*., *88*: 1229-1231.

Tejaswini, K. L. Y., Manukonda, S., Kumar, B. N. V. S. R., Rao, P. V. R., Ahamed, L. M., and Raju, S. K. (2018). Application of principal component analysis for rice f5 families characterization and evaluation. *Emer. Life Sci. Res*., *4*(1): 72-84.

Tenorio, F.A., Ye, C., Redona, E., Sierra, S. and Laza, M. (2013). Screening rice genetic resources for heat tolerance. *SABRAO J. Breed. Gene*., *45*(3): 371–381.

Umesh, J., H. K., Sravan, T. and Waza, S. A. (2016). Genetic divergence analysis for yield and quality traits in some indigenous genotypes of basmati rice (*Oryza sativa* L). *Green Farming*, *7*(2): 345-348.

Wani, S. H. and Sah, S. K. (2014). Biotechnology and Abiotic Stress Tolerance in Rice. *J. Rice Res., 2*:e105.

Yarasi, B., Sadumpati, V., Immanni, C. P., Vudem, D. R., and Khareedu, V. R. (2008) Transgenic rice expressing *Allium sativum* leaf agglutinin (ASAL) exhibits high-level resistance against major sap-sucking pests. *BMC Plant Biol*., *8*: 102.

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