



## Yield attributing traits of high zinc rice (*Oryza sativa* L.) genotypes with special reference to principal component analysis

**Partha Pratim Behera**

Department of Plant Breeding and Genetics, Assam Agricultural University, Jorhat, Assam, India.

**Shravan Kumar Singh**

Department of Genetics and Plant Breeding, Institute of Agricultural science, Banaras Hindu University, Varanasi, Uttar Pradesh, India.

**Kasireddy Sivasankarreddy**

Department of Plant Breeding and Genetics, Assam Agricultural University, Jorhat, Assam, India.

**Prasanta Kumar Majhi** ✉

Department of Plant Breeding and Genetics, Regional Research and Technology Transfer Station, Odisha University of Agriculture and Technology, Keonjhar, Odisha, India.

**Boddedula Jayasankar Reddy**

Department of Plant Breeding and Genetics, Assam Agricultural University, Jorhat, Assam, India.

**Dhirendra Kumar Singh**

Department of Genetics and Plant Breeding, College of Horticulture, Banda University of Agriculture and Technology, Uttar Pradesh, India.

ARTICLE INFO	ABSTRACT
<p>Received : 21 December 2021  Revised : 02 April 2022  Accepted : 12 April 2022</p> <p>Available online: 21 August 2022</p> <p><b>Key Words:</b>  Individual PCA  PCA biplot  Pooled environment  Rice</p>	<p>Total 21 high zinc rice genotypes were evaluated under five different locations for 14 different yield attributing traits, including grain yield/plant (gm) to determine the pattern of variation, the relationship among the individuals and their characteristics through Principal Component Analysis (PCA) during the <i>Kharif-2017</i>. PCA was done for all the locations individually as well as pooled analysis for all locations using R software. Out of the 14 PCs, the initial four PCs contributed more to the total variability. The highest cumulative variability of the first four PCs found at Bhikaripur (81.11%) followed by BHU Agriculture research farm-II (79.23%) etc. and Pooled variability was 76.61%. Pooled data analysis indicates PCA biplot or loading plot of first two principal components revealed that days to maturity, days to 1<sup>st</sup> flowering date and days to 50% flowering loaded more on the first component and number of spikelets per panicles, number of grains/panicles, grain weight per panicle, grain yield/plant accounted more variation in the second component compared to the other parameters. Thus, the pooled analysis of principal component analysis revealed the characters contributing to the variation and genetic variability that exists in these rice genotypes. This is because the genotypes BRRIdhan 72, Sambamahsuri and Swarna were identified in different principle components related to grain yield and grain quality, and were also located farthest away from biplot origin in individual PCA based biplot. So they may be employed to improve yield attributing factors like total effective tiller number. PC1, PC2 and PC3 have days to first flowering and days to 50% flowering, hence their genotypes may be valuable in producing early maturing cultivars. Thus, the results revealed that wide range of variability was shown by different traits of the genotypes which can be utilized in rice improvement programmes.</p>

### Introduction

Rice (*Oryza sativa* L.) is an important cereal crop that belongs to the family Gramineae. It delivers the daily intake of two-thirds of the world's population and about 20% of a human's calories intake (Wogu *et al.*, 2010). It is cultivated in more than 120 countries, largely in tropical and subtropical Asia (Mulyaningsih *et al.*, 2021). In Asia, rice accounts for 60-70% of energy consumption for over two

billion people (Tiruneh *et al.*, 2019). Rice grains hold 75-80% starch, 12% water, and 7% protein (Hossain *et al.*, 2015). Rice grain with good nutritional value contains vitamins like thiamine, riboflavin, niacin, and minerals like calcium, phosphorus, and magnesium (Negussie and Alemu, 2011). Rice plays a pivotal role in the food security of several countries. By 2050, the world population will reach 10 billion so the demand for rice will grow faster than other crops. To meet the demand for rice in the future development of high-yielding rice varieties is necessary. The successes of crop breeding programs are greatly dependent on the effective manipulation of the genetic variability and genotype selection utilizing all available desirable yields and quality contributing characteristics (Mignouna *et al.*, 1996). Zinc is one of the essential micronutrients, which serves as a co-factor for more than 300 enzymes involved in metabolism. Zinc deficiency is a serious health concern, especially in developing countries where many people rely on cereal-based foods for their daily diet and cannot afford to diversify their meals (Shahzad *et al.*, 2014). Moreover half of the world's population consumes rice as a staple diet and source of energy. Popular rice varieties are deficient in important minerals like zinc. Rice biofortification with higher amounts of zinc in its polished state could be a cost-effective and long-term option (Sharma *et al.*, 2013). In rice breeding programs identification of usable variability is possible through one of the multivariate techniques like Principal Component Analysis (PCA).

Rice breeders observe a number of different characters. Some of which may not be helpful in germplasm discrimination. PCA can be used in these situations to discover patterns and minimize redundancy in data sets (Maji and Shaibu, 2012). PCA is a classical statistical method for simplifying a multidimensional dataset to lower dimensions for analysis, visualization, or data compression. It involves the calculation of the Eigenvalue decomposition of a data covariance matrix or singular value decomposition of a data matrix, usually after mean centering the data for each attribute. It is the simplest of the true eigenvector-based multivariate analyses (Kambo and Yerpude, 2014). The crucial benefit of PCA arises from quantifying the significance of each

dimension for describing the variability of the data set. PCA can identify the minimal number of components that may represent the maximum amount of variation out of the overall variability (Morrison, 1978), as well as rank genotypes based on PC scores. Attributes with higher variability are more likely to provide high levels of gene transfer in breeding practices (Aliyu, 2000; Gana, 2006). The present experiment was carried out on rice germplasm to dissect yield-related traits at the individual and pooled environment to classify higher variability into total variability by taking into account many characters and relationships between the traits.

## Material and Methods

### Plant materials

A set of twenty-one genotypes and germplasm lines were used for the present study and are mentioned in (Table 1). The materials were collected from International Rice Research Institute (IRRI) South Asia Hub, Hyderabad, India. The experiment was conducted at five different locations (Table 2, Figure.1) in Uttar Pradesh, India during the *Kharif*-2017.

### Experimental Design

The experiment was laid out in a completely randomized block design with three replications. The weather conditions during the evaluations period from June 2017 to November 2017 were almost normal and favourable for crop growth. All the experiments of five different locations were carried out at irrigated ecosystem and medium upland with transplanted nursery establishment.

### Cultural Practices

The single seedling was transplanted at a 15 cm × 20 cm distance. All the standard recommended cultural practices were followed. Fertilizers were applied as 120 kg N, 60 kg P<sub>2</sub>O<sub>5</sub> and 60 kg K<sub>2</sub>O per hectare.

### Quantitative Data observations

Five competitive plants were selected randomly from each row of each genotype in each replication and observations were noted for all yield and yield attributing characters except for days to first flowering, days to 50% flowering, and days to maturity. The performance of the cultivars was judged by recording observations on the following attributes mentioned in Table.3. The depiction and

evaluation stage of the quantitative traits were as stated by the descriptor of Biodiversity International (IRRI and WARDA, 2007).

#### **Statistical analysis**

Multivariate Analysis was carried out in using R (4.0.5) software packages. Principal components analysis, eigenvectors, Eigen values, and 2D PCA gg-biplots were obtained using FactoMineR, factoextra, and psych packages. Multi-trait multi-environment analysis for PCA was analyzed using metan packages (Olivoto and Lúcio, 2020).

### **Results and Discussion**

#### **Pooled analysis of variance (ANOVA) of rice germplasm among morphological characters of five environments**

Pooled analysis of variance among morphological characters *viz.*, days to 1<sup>st</sup> flowering date, days to 50% flowering, days to maturity, total effective tiller number, plant height (cm), panicle length (cm), number of spikelets per panicles, number of grains/panicles, spikelets fertility percentage, grain weight per panicle, weight of 1000 seed (gm), grain length/breadth ratio, grain zinc content (ppm) and grain yield/plant (gm) were observed in the study was presented in the Table-3a and Table-3b. There were significant difference was present in the germplasm for all the traits at 5% level of probability, hence suitable for further genetic analysis. This significant difference among the genotypes explains the presence of dissimilarity in their genetic composition. However, this significant difference might be due to the influence of environment on the genotypes. High significant difference was recorded among the genotypes for all the observed traits which disclosed the presence of considerable variability among tested germplasm (Bharadwaj *et al.*, 2001; Maji and Shaibu, 2012; Tuhina-Khatun *et al.*, 2015; Pachauri *et al.*, 2017; Tiruneh *et al.*, 2019 and Kumari *et al.*, 2021).

#### **Principal Component Analysis (PCA)**

##### **Variable Principal Component Analysis (PCA) in the multi environment with special reference to the pooled environment**

The PCA described the proportion of the relative contribution of the different characters to the total variance of the rice genotypes under study. The

study of several morphological traits is important for the assessment of the variances between the genotypes and their breeding potential. PCA pools the capacity to provide a synthetic summary of the most relevant traits and assessment of the relative contribution of various characters to the total variability of the population. Data were measured in each component with Eigenvalues more than one as per the recommendations given by Brejda (2000). The genetic variation present in the genotypes was divided into principal components (PCs). Table 4a. and Table 4b. represent the principal components, Eigenvalues, and percentage contribution of each component to the total variation in the rice genotypes tested in the five different environments and pooled data of the same five environments.

The scree plot displayed in Figure 2. described the percentage of variation related to each principal component obtained by drawing a graph between Eigenvalues and principal component numbers. The PCA at five different environments and pooled data of five different environments indicated that among 14 principal components (PCs) primary four PCs contributed more to the total variability *viz.*, BHU Agriculture research farm-I (76.23%), BHU Agriculture research farm-II (79.23%), Bhikaripur (81.11 %), Karsada (72.55%), Rampur (76.23%) and Pooled data (76.61%).

In pooled data, the first principle component (PC1) added the highest proportion of the total morphological variation (31.90%) in the rice germplasm. Days to maturity (0.119) followed by days to 1<sup>st</sup> flowering date (0.115), days to 50% flowering (0.110), total effective tiller number (0.064), grain length/breadth ratio (0.054) contributed positively to the PC1 variation while other characters *viz.*, spikelets fertility percentage (-0.066), grain zinc content (-0.100), weight of 1000 seed (-0.268), panicle length (-0.278), plant height (-0.368), number of spikelets per panicles (-0.368), number of grains/panicles (-0.378), grain yield/plant (-0.421) and grain weight per panicle (-0.449) contributed negatively to the PC1 variation. Tuhina-Khatun *et al.* (2015) were not in support of this result as they reported that, plant height and panicle length were contributing more for PC1 in explaining total variability.

**Table 1: List of high zinc rice genotypes used for the experiment (Source: IRRI South Asia Hub, Hyderabad, India).**

Entry No.	Entry Name	Grain Zinc Content (ppm)	ENT RY No.	Entry Name	Grain Zinc Content (ppm)
1	IR 95044:8-B-5-22-19-GBS	20.6	12	BRRIdhan 64	24.97
2	IR 84847-RIL 195-1-1-1-1	21.8	13	BRRIdhan 72	20.7
3	IR 99704-24-2-1	14.67	14	DRR Dhan 45	18.13
4	IR 99647-109-1-1	23.7	15	DRR Dhan 48	19.2
5	IR 97443-11-2-1-1-1 -B	14.45	16	DRR Dhan 49	17.63
6	IR 97443-11-2-1-1-1-3 -B	23.47	17	IR 64	23.57
7	IR 82475-110-2-2-1-2	24.73	18	MTU1010	21.70
8	IR 96248-16-3-3-2-B	27.18	19	Sambamahsuri	24.47
9	R-RHZ-7	26.61	20	Swarna	18.89
10	CGZR-1	24.43	21	Local check(HUR3022)	16.9
11	BRRIdhan 62	23.33			

**Table 2: Five different locations used for the experiment**

Location Code	Location Name	Latitude	Longitude	Altitude
E1	BHU Agriculture Research farm –I	25.18° N	80.30° E	81M
E2	BHU Agriculture Research farm –II	25.18° N	80.30° E	81M
E3	Bhikaripur	25.26° N	82.83° E	87M
E4	Karsada	25.22° N	82.90° E	85M
E5	Rampur	25.23°N	82.89°E	80M

**Table 3a: Pooled mean square result of the five environments of morphological characters of rice**

Source	D.F	Fst DF	FDF	DM	ENT	PH	PL	NSP
Env	4	1364.82	1278.54	1851.51	17.83	7931.79	163.00	39182.85
Rep (Env)	10	2.52	1.11	1.89	1.42	65.31	5.30	160.21
Gen	20	1428.20	1160.65	1607.58	12.46	602.60	35.00	13053.30
Gen:Env	80	12.92	35.88	21.63	1.80	117.21	4.97	1258.23
Residuals	200	1.64	1.07	1.41	0.90	29.71	2.48	472.26
CV (%)	-	1.36	1.06	0.94	12.04	5.11	6.04	19.89
Overall mean	-	93.74	97.96	126.81	7.88	106.72	26.01	109.27

**Table 3b: Pooled mean square result of the five environments of morphological characters of rice**

Source	D.F	NGP	SFP	GWP	STW	GLBR	GZC	GYP
Env	4	25731.94	371.42	15.69	264.42	0.15	1362.36	1242.51
Rep (Env)	10	190.18	35.44	0.07	1.56	0.01	2.97	8.16
Gen	20	7084.18	155.48	1.81	107.38	1.07	143.28	36.30
Gen:Env	80	616.34	51.41	0.24	6.56	0.21	14.45	7.91
Residuals	200	236.92	21.66	0.08	1.13	0.02	3.92	2.40
CV (%)	-	18.52	6.09	18.76	5.82	3.37	8.93	13.34
Overall mean	-	83.12	76.37	1.51	18.26	4.00	22.16	11.62

Where, DF-Degree of freedom; Env-Environments; Rep-Replications; Gen-Genotypes; CV-Coefficient of variation; Fst DF-Days to 1<sup>st</sup> flowering date; FDF-Days to 50% flowering; DM-Days to maturity; ENT-Total effective tiller number; PH-Plant height (cm); PL-Panicle length (cm); NSP-Number of spikelets per panicles; NGP-Number of grains/panicles; SFP-Spikelets fertility Percentage; GWP-Grain weight per panicle; STW-Weight of 1000 Seed (gm); GLBR-Grain Length/Breadth ratio; GZC- Grain Zinc content (ppm); GYP-Grain yield/plant (gm)

About 25.12% of the morphological variation in the rice genotypes was reported by the second principle component (PC2) in the pooled data. Days to maturity (0.484) followed by days to 1<sup>st</sup> flowering date (0.483), days to 50% flowering (0.480), number of spikelets per panicles (0.250), number of grains/panicles (0.249), grain weight per panicle (0.120) and grain yield/plant (0.105) contributed positively to the PC2 variation while other characters *viz.*, grain length/breadth ratio (-0.020), spikelets fertility percentage (-0.027), plant height (-0.043), panicle length (-0.044), total effective tiller number (-0.054), weight of 1000 seed (-0.233) and grain zinc content (-0.299) contributed negatively to the PC2 variation. But Kumar *et al.* (2014) reported that yield related traits *viz.*, total spikelets/panicle and grain yield/plant were contributed more for PC1 rather than to PC2.

The third principle component (PC3) contributed about 11.86% of the total variation in the rice genotypes at the pooled data. The variation was due to traits *viz.*, total effective tiller number (0.618), grain length/breadth ratio (0.434), spikelets fertility percentage (0.389), grain yield/plant (0.215), plant height (0.205), grain zinc content (0.199), days to 1<sup>st</sup> flowering date (0.164), days to 50% flowering (0.146), days to maturity (0.133), panicle length (0.127), weight of 1000 seed (0.090) having higher positive values to the PC3 variation. While other characters *viz.*, grain weight per panicle (-0.088), number of grains/panicles (-0.115) and number of spikelets per panicles (-0.199) added negatively to the PC3 variation.

About 7.72% of the variability was contributed by the fourth principal component (PC4) in the rice genotypes at the pooled data with high positive values grain length/breadth ratio (0.415), number of grains/panicles (0.266), spikelets fertility percentage (0.228), number of spikelets per panicles (0.215), total effective tiller number (0.156), grain yield/plant (0.102), grain weight per panicle (0.032) and high negative values were found for other characters *viz.*, panicle length (-0.213), days to 1<sup>st</sup> flowering date (-0.231), days to maturity (-0.243), days to 50% flowering (-0.251), plant height (-0.276), weight of 1000 seed (-0.371) and grain zinc content (-0.435). The maximum collective variability of the initial four PCs was reported at Bhikaripur (81.11 %) followed by BHU Agriculture research farm-II (79.23%), BHU

Agriculture research farm-I (76.23%), Rampur (76.23 %), Karsada (72.55 %), and Pooled data was 76.61%. Tuhina-Khatun (2015) and Pachauri (2017) identified four principal components with Eigen value more than one (>1) and that explained 72.1% and 72.48% respectively of the total collective variance within the axes in an environment further strengthening current result.

The loading plot of pooled data component showed that the days to maturity, days to 1<sup>st</sup> flowering date, days to 50% flowering loaded more on the first component and accounted for more variation compared to the other parameters. Number of spikelets per panicles, number of grains/panicles, grain weight per panicle, grain yield/plant loaded more on the second component (Figure 3). The overall relationship among Eigen value with percentage variation with respect to PCA was presented in Figure-4. Kumari *et al.* (2021) in an environment identified days to 50% flowering, days to maturity, ear bearing tillers per plant, total grains and panicle length are important principal components that are in agreement with the present study except for panicle length.

#### Individual Principal Component Analysis (PCA) in the pooled environment

Principal components namely PC1, PC2, PC3 and PC4 of 21 genotypes contain positive PC scores (table 5a and 5b). Here in this pooled environment, genotypes with high PC scores (>1) have been taken under study. The range of positive PC scores for PC1 was from 4.38 (BRRIdhan 72) to 1.35 (Sambamahsuri). In PC2 the positive PC scores ranged from 3.65 (Swarna) to 1.64 (DRR Dhan 49). In PC3, the range of positive PC scores was from 1.96 (BRRIdhan 72) to 1.39 (BRRIdhan 64). In PC4 the positive PC scores ranged from 3.2 (IR 82475-110-2-2-1-2) to 1.02 (BRRIdhan 72). All the principal components contain the variable number of yield attributing traits and quality traits except PC2, because it has only yield and yield attributing traits. The highest number of traits were found in PC3 (10) followed by PC4 (7), PC2 (6) and least in PC1 (5). It indicates that the maximum variability of 21 genotypes was explained by the five traits which were present in PC1 (days to 1<sup>st</sup> flowering date, days to 50% flowering, days to maturity, Total effective tiller number and grain length/breadth ratio).

**Table 4a: Eigen value, percent of the total variation, and component matrix for the principal component axes in rice at different environments**

Parameters	BHU Agriculture research farm-I				BHU Agriculture research farm-II				Bhikaripur			
	PC1	PC2	PC3	PC4	PC1	PC2	PC3	PC4	PC1	PC2	PC3	PC4
Days to 1 <sup>st</sup> flowering date	0.339	0.328	-0.006	0.177	0.287	0.381	-0.195	0.139	0.316	0.299	0.242	-0.091
Days to 50% flowering	0.337	0.328	-0.005	0.186	0.290	0.376	-0.199	0.153	0.319	0.292	0.254	-0.094
Days to maturity	0.337	0.327	0.004	0.184	0.294	0.359	-0.235	0.156	0.322	0.291	0.252	-0.087
Total effective tiller number	-0.124	0.444	0.014	0.164	-0.223	0.386	0.078	0.061	-0.150	0.385	-0.091	0.173
Plant height	0.099	0.035	0.599	-0.139	0.092	-0.230	-0.336	0.472	0.093	-0.337	0.261	-0.134
Panicle length	0.076	-0.265	0.109	0.527	0.178	-0.075	0.420	0.014	0.051	-0.243	-0.336	0.102
Number of spikelets per panicles	0.355	-0.258	-0.200	0.098	0.391	-0.195	0.022	-0.206	0.391	-0.161	-0.143	0.021
Number of grains/panicles	0.395	-0.168	-0.164	-0.109	0.400	-0.115	0.154	-0.218	0.376	-0.170	-0.240	-0.158
Spikelets fertility Percentage	0.046	0.296	0.159	-0.576	-0.123	0.193	0.459	0.014	-0.130	0.023	-0.377	-0.742
Grain weight per panicle	0.321	-0.345	0.208	-0.077	0.341	-0.317	0.126	0.162	0.281	-0.387	0.032	-0.041
Weight of 1000 Seed	-0.171	-0.203	0.559	0.116	-0.175	-0.311	-0.035	0.570	-0.192	-0.334	0.277	0.277
Grain Length/Breadth ratio	-0.141	0.255	0.270	0.289	-0.120	0.270	0.419	0.362	0.094	0.182	-0.510	0.469
Grain Zinc content	-0.291	-0.012	-0.104	0.336	-0.286	-0.135	-0.141	0.041	-0.360	-0.135	0.124	-0.120
Grain yield/plant	0.325	-0.024	0.311	0.084	0.293	-0.034	0.353	0.363	0.310	-0.230	-0.031	0.167
Eigen value	2.250	1.719	1.279	1.008	2.239	1.779	1.305	1.102	2.300	1.931	1.112	1.047
Percentage of variance	36.16	21.12	11.69	7.26	35.80	22.60	12.16	8.68	37.80	26.64	8.83	7.84
Cumulative (%)	36.16	57.28	68.97	76.23	35.80	58.40	70.55	79.23	37.80	64.44	73.27	81.11

PC-1: First principle component; PC-2: Second principle component; PC-3: Third principle component; PC-4: Fourth principle component

**Table 4b: Eigen value, percent of the total variation, and component matrix for the principal component axes in rice at different environments.**

Parameters	Karsada				Rampur				Pooled data			
	PC1	PC2	PC3	PC4	PC1	PC2	PC3	PC4	PC1	PC2	PC3	PC4
Days to 1 <sup>st</sup> flowering date	0.239	-0.489	0.103	-0.056	0.249	0.455	-0.129	-0.121	0.115	0.483	0.164	-0.231
Days to 50% flowering	0.246	-0.485	0.101	-0.053	0.227	0.373	-0.283	0.030	0.110	0.480	0.146	-0.251
Days to maturity	0.233	-0.483	0.153	0.036	0.254	0.448	-0.135	-0.103	0.119	0.484	0.133	-0.243
Total effective tiller number	0.205	0.143	-0.373	-0.376	-0.189	0.345	-0.111	0.294	0.064	-0.054	0.618	0.156
Plant height	-0.108	0.036	0.390	-0.159	0.090	-0.223	-0.485	-0.178	-0.364	-0.043	0.205	-0.276
Panicle length	-0.031	-0.100	0.365	-0.540	0.180	-0.106	-0.367	-0.394	-0.278	-0.044	0.127	-0.213
Number of spikelets per panicles	-0.384	-0.277	-0.243	0.026	0.401	-0.140	0.276	-0.097	-0.368	0.250	-0.199	0.215
Number of grains/panicles	-0.414	-0.244	-0.194	-0.032	0.401	-0.135	0.298	-0.058	-0.378	0.249	-0.115	0.266
Spikelets fertility Percentage	-0.164	0.142	0.203	-0.354	0.150	0.057	0.112	0.561	-0.066	-0.027	0.389	0.228
Grain weight per panicle	-0.453	-0.193	0.022	0.003	0.412	-0.240	0.049	0.027	-0.449	0.120	-0.088	0.032
Weight of 1000 Seed	-0.231	0.087	0.481	0.101	0.075	-0.242	-0.498	0.236	-0.268	-0.233	0.090	-0.371
Grain Length/Breadth ratio	0.066	0.007	-0.250	-0.607	-0.067	0.184	0.243	-0.515	0.054	-0.020	0.434	0.415
Grain Zinc content	-0.027	0.165	0.291	-0.077	-0.249	-0.265	-0.112	-0.123	-0.100	-0.299	0.199	-0.435
Grain yield/plant	-0.404	-0.180	-0.123	-0.156	0.401	-0.105	-0.055	0.189	-0.421	0.105	0.215	0.102
Eigen value	2.054	1.712	1.246	1.205	2.250	1.719	1.279	1.008	2.113	1.8755	1.289	1.040
Percentage of variance	30.14	20.94	11.09	10.37	36.16	21.12	11.69	7.26	31.90	25.12	11.86	7.72
Cumulative (%)	30.14	51.09	62.18	72.55	36.16	57.28	68.97	76.23	31.90	57.02	68.88	76.61

Where, PC-1: First principle component; PC-2: Second principle component; PC-3: Third principle component; PC-4: Fourth principle component

**Table 5a: Scoring of 21 high zinc rice genotypes in different PC's in pooled environment.**

Sl. No.	Name of Genotypes	Code of genotypes	PC1	PC2	PC3	PC4
1	IR 95044:8-B-5-22-19-GBS	V1	-2.90	-0.17	-0.80	-0.62
2	IR 84847-RIL 195-1-1-1-1	V2	-1.77	-0.41	-0.14	0.74
3	IR 99704-24-2-1	V3	-0.52	-0.96	0.27	0.71
4	IR 99647-109-1-1	V4	-2.79	-0.64	0.83	-0.01
5	IR 97443-11-2-1-1-1-1 -B	V5	3.16	-0.96	-2.83	-0.18
6	IR 97443-11-2-1-1-1-3 -B	V6	3.84	-2.40	-2.50	-0.93
7	IR 82475-110-2-2-1-2	V7	-0.15	-1.45	-0.06	3.20
8	IR 96248-16-3-3-2-B	V8	-1.94	-0.56	0.26	0.15
9	R-RHZ-7	V9	-1.21	2.88	-0.45	0.45
10	CGZR-1	V10	-2.64	-1.74	-0.68	-0.25
11	BRRIdhan 62	V11	-3.83	0.53	-0.61	-0.52
12	BRRIdhan 64	V12	1.78	-3.56	1.39	-0.52
13	BRRIdhan 72	V13	4.38	-1.64	1.96	1.02
14	DRR Dhan 45	V14	0.36	-1.14	1.95	-1.19
15	DRR Dhan 48	V15	0.28	2.42	-1.25	-0.13
16	DRR Dhan 49	V16	1.96	1.64	-0.03	-1.36
17	IR 64	V17	-2.56	-0.35	0.31	-0.44
18	MTU1010	V18	-0.68	-0.52	-0.15	-0.03
19	Sambamahsuri	V19	1.35	3.62	0.17	1.08
20	Swarna	V20	2.87	3.65	0.55	0.44
21	Local check(HUR3022)	V21	0.99	1.77	1.83	-1.63

**Table 5b: Rice genotypes are selected on the basis of PC scores in each component having positive values & more than >1.0 in each PCs in pooled environment**

	PC1	PC2	PC3	PC4
Variable	DM, Fst DF, FDF, ENT, GLBR	DM, Fst DF, FDF, NSP, NGP, GWP, GYP	ENT, GLBR, SFP, GYP, PH, DM, Fst DF, FDF, PL, STW	GLBR, STW, ENT, GYP, PL, NSP
Genotype	BRRIdhan 72 (4.38)	Swarna (3.65)	BRRIdhan 72 (1.96)	IR 82475-110-2-2-1-2 (3.2)
	IR 97443-11-2-1-1-1-3 -B (3.84)	Sambamahsuri (3.62)	DRR Dhan 45 (1.95)	Sambamahsuri (1.08)
	IR 97443-11-2-1-1-1-1 -B (3.16)	R-RHZ-7 (2.88)	Local check(HUR3022)(1.83)	BRRIdhan-72 (1.02)
	Swarna (2.87)	DRR Dhan 48 (2.42)	BRRIdhan 64 (1.39)	
	DRR Dhan 49 (1.96)	Local check(HUR3022) (1.77)		
	BRRIdhan 64 (1.78)	DRR Dhan 49 (1.64)		
	Sambamahsuri (1.35)			

Where [ DF-Days to 1<sup>st</sup> flowering date; FDF-Days to 50% flowering; DM-Days to maturity; ENT-Total effective tiller number; PH-Plant height (cm); PL-Panicle length (cm); NSP-Number of spikelets per panicles; NGP-Number of grains/panicles; SFP-Spikelets fertility Percentage; GWP-Grain weight per panicle; STW-Weight of 1000 Seed (gm); GLBR-Grain Length/Breadth ratio; GZC-Grain Zinc content (ppm); GYP-Grain yield/plant (gm)]





Figure 1. The map showing all the five different experimental locations.

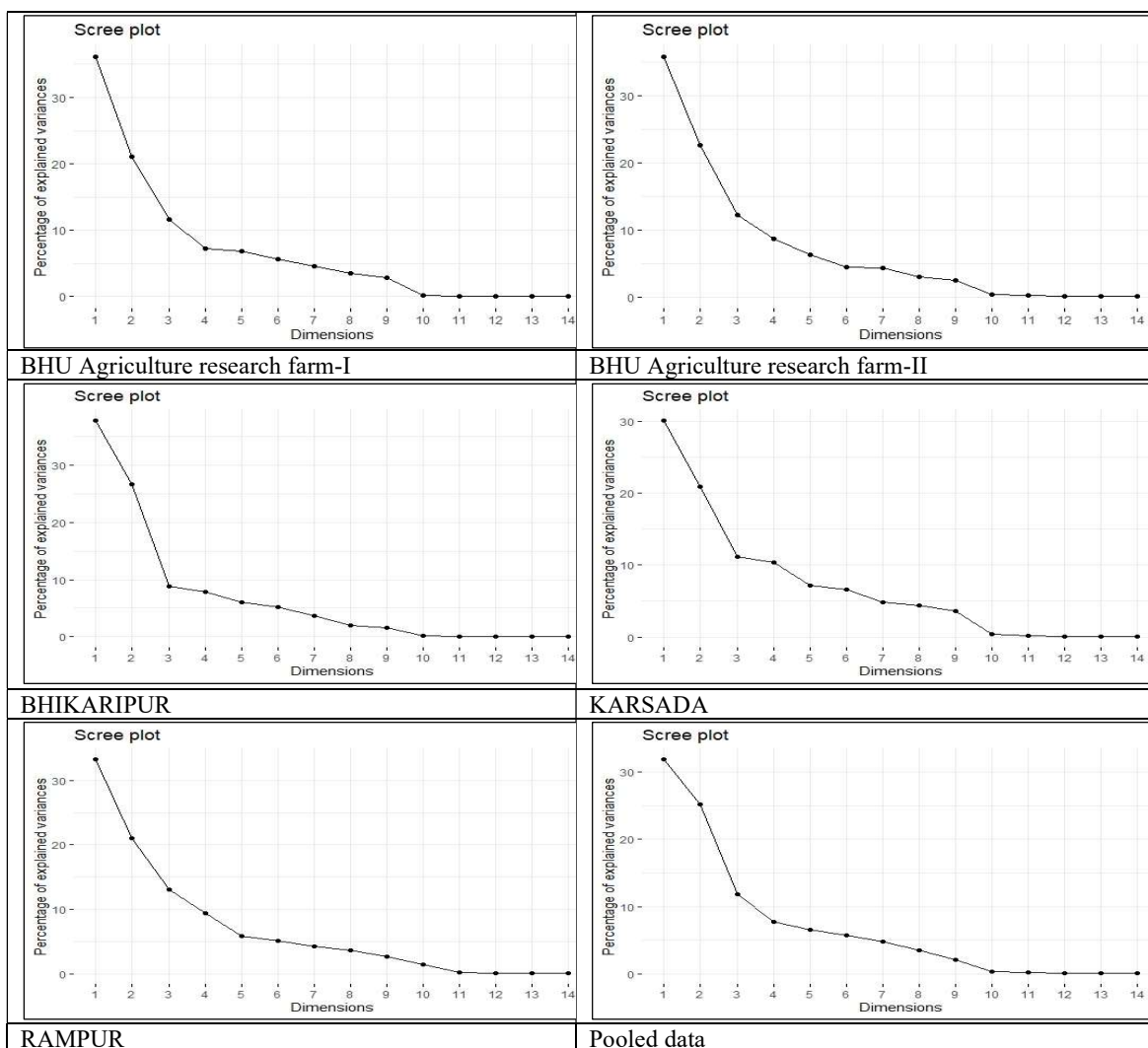


Figure 2: Scree plot of different environments of rice genotypes under multi-environment condition

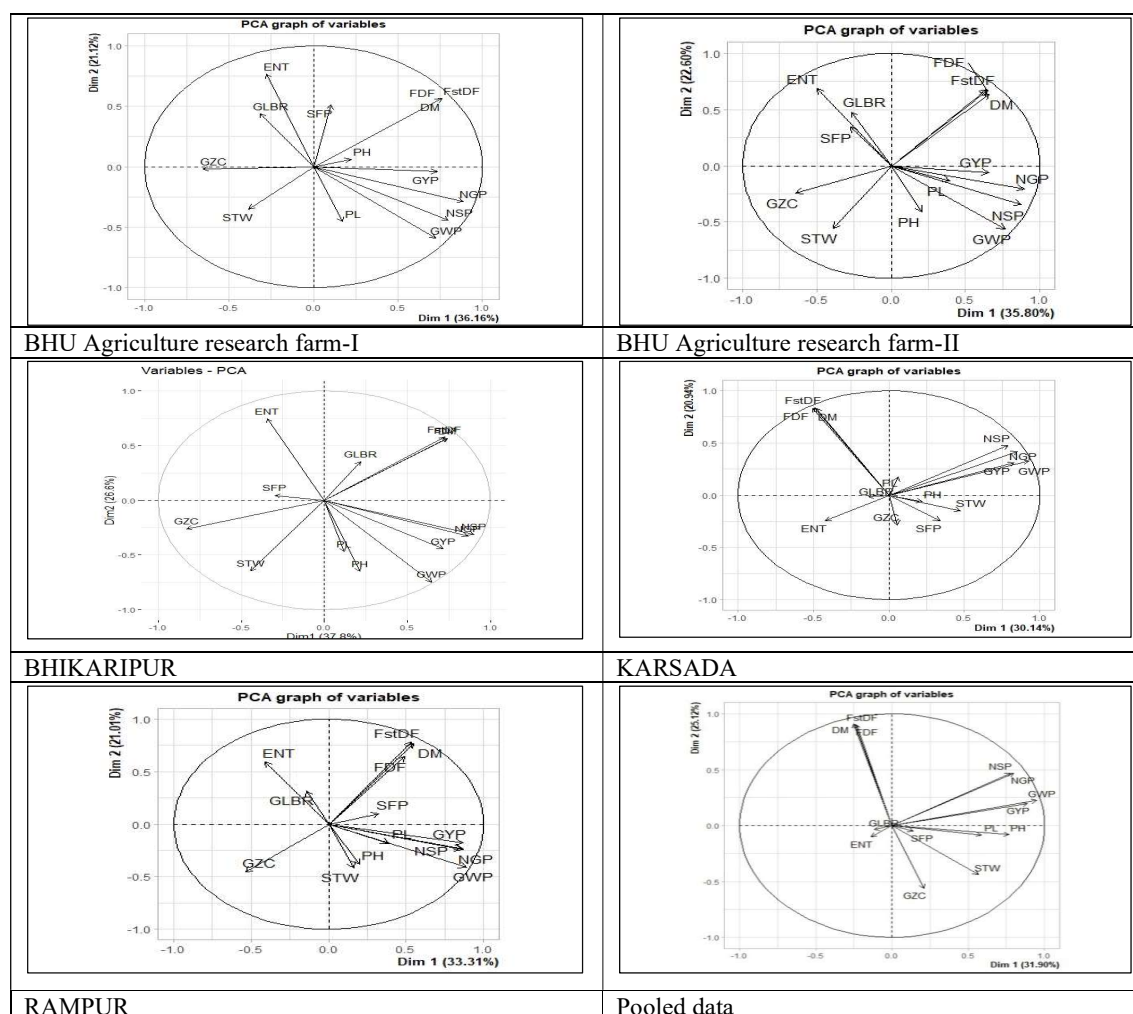


Figure 3: Loading plot of yield-related traits of rice genotypes at different environments

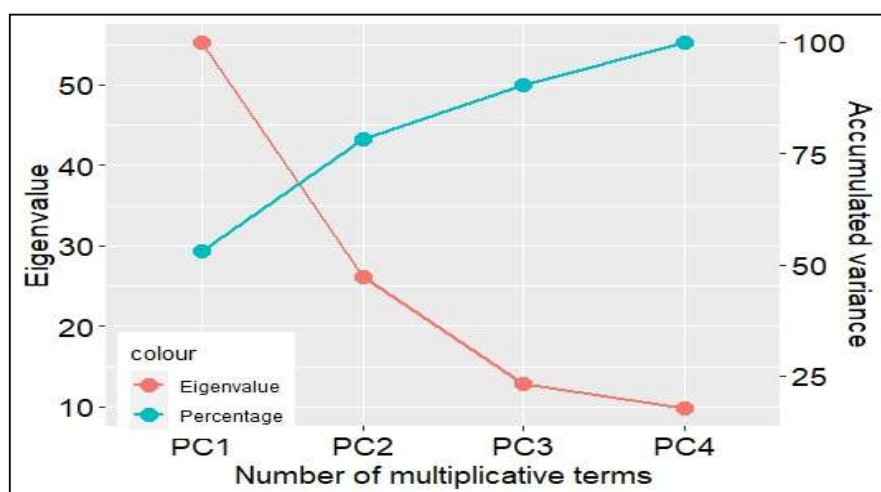
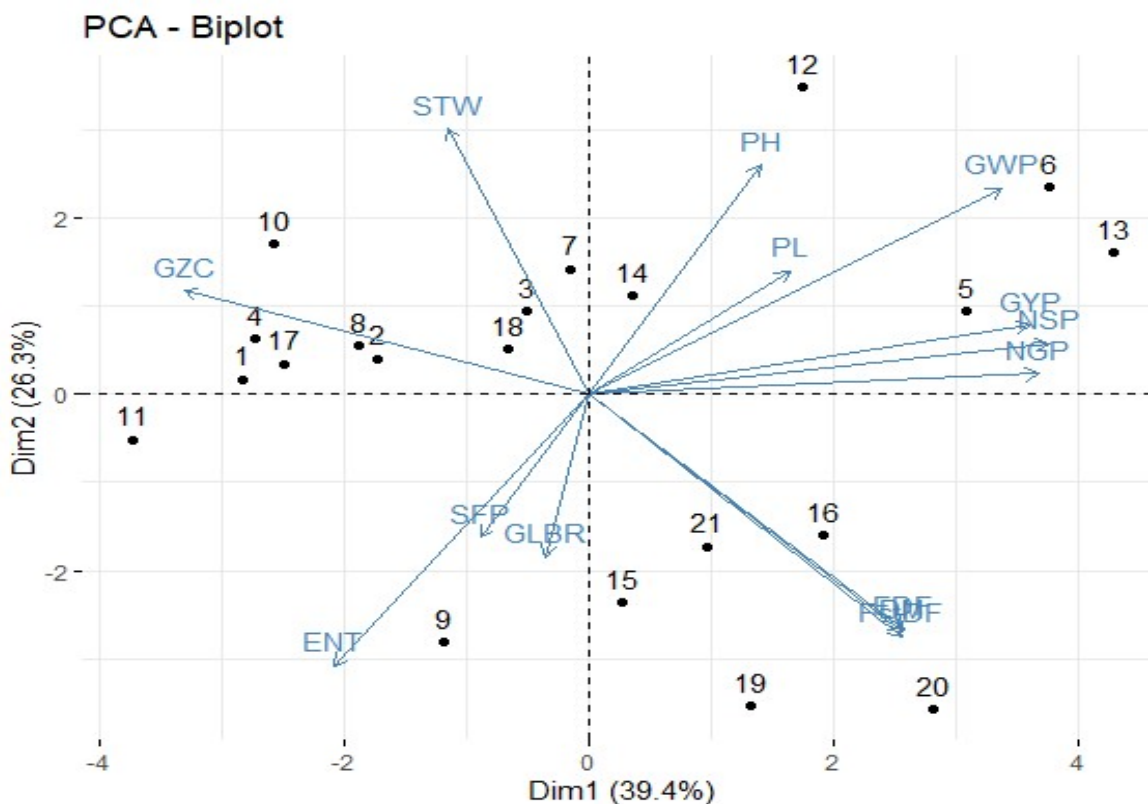


Figure 4: Overall relationship among Eigen value with percentage variation with respect to PCA.



**Figure 5: The bi-plot of 21 high zinc rice genotypes for PC1 and PC2 in pooled environment**

The highest number of genotypes were fallen under PC1 (7) followed by PC2 (6), PC3 (5) and PC4 (4). Some genotypes are found in more than one principal component. The genotype Sambamahsuri has fallen under 3 different PCs (PC1, PC2 and PC4) and the genotype BRRi dhan 72 also fallen under 3 different PCs (PC1, PC3 and PC4), whereas the Swarna genotype was found in PC1 and PC2. This explains the relationship of genotypes with different yield attributing traits and quality traits to express their variability. Therefore such genotypes may be recommended directly for cultivation (Gouret *et al.*, 2017). R-RHZ-7, DRR Dhan 48, Samba mahsuri and Swarna exhibited the highest score in PC2. Genotypes DRR Dhan 45 and Local check (HUR 3022) had the highest PC score in PC3 and IR 82475-110-2-2-1-2 had in PC4 (table 5a).

BRRi dhan 72, DRR Dhan 45, Local check (HUR 3022) and BRRi dhan 64 exhibited high scores in PC3. This means that selection of genotypes with high PC scores in PC3 can be improved with good

grain yield and grain quality traits. But Nachimuthu *et al.*, (2014) were not in agreement with this result as they reported that variability of PC3 was explained by some yield attributing traits only, viz., spikelet fertility, single plant yield, and number of productive tillers.

With the help of two main PCs (PC1 and PC2), bi-plot analysis was done. For better understanding through visualization both germplasm and traits studied were merged in a single bi-plot. PCA bi-plot for PC1 and PC2 explained the 65.7% of total variability and showed that number of spikelets per panicles, number of grains/panicles, grain weight per panicle, grain Zinc content (ppm) and grain yield/plant (gm) had shown high variability among all studied traits (Fig. 5). The genotypes; Swarna, BRRi dhan 62, BRRi dhan 64, BRRi dhan 72, IR 97443-11-2-1-1-3-B, Sambamahsuri and IR 97443-11-2-1-1-1-1-B were located far away from biplot origin indicating better performance in comparison with other genotypes. Aslam *et al.*, (2017) and Maqbool *et al.* (2015a, b), exploited bi-plot technique for evaluating crop genotypes in

diverse environments using first two principle components as they represent the most of data variability.

## Conclusion

The PCA analysis revealed that the rice genotypes used in this experiment do not have close genetic relationships and could serve as a good genetic source for improvement of several traits. Therefore, to exploit the tested genotypes in crop improvement, selection for the traits that show high variability has to be done. Characters with greater variability are likely to contribute more to the diversity and provide a high level of gene transfer in breeding programmes. The prime goal of crop improvement is the improvement of yield, so the morphological traits related to yield are used as the primary evaluation tool. Therefore, the results from

our study will be of greater benefit to select parents for improving various yield attributing traits analysed in this experiment for multi-environments.

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## Conflict of interest

The authors declare that they have no conflict of interest.

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