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Assessing the Genetic Diversity for Yield Attributing Traits in Aromatic Rice Landraces Using Multivariate Analysis

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ABSTRACT

The present investigation was carried out in *kharif* 2020 (July to November) to explore the genetic diversity for yield and its attributing traits. Genetic diversity can directly provide information on germplasm richness and the extent of their genetic amelioration. Multivariate statistical techniques analyze multiple measurements on each individual under study and are widely used in the analysis of genetic diversity. Here, multivariate analysis techniques like principal component analysis was used to assess genetic diversity in 90 aromatic rice genotypes along with six checks for 24 yield attributing traits. Analysis of variance revealed significant and ample amount of variation for all the studied traits. High magnitude of coefficient of variation was observed for number of effective tillers plant^{-1}, panicle weight, number of filled grains panicle^{-1}, total grains panicle^{-1}, grain yield plant^{-1} (g), 1000 grain weight and biological yield plant^{-1} (g) indicating the existence of significant variability among the yield traits and offers the opportunities of improvement through desirable selection techniques. Results of principle component analysis revealed that out of twenty-four traits studied, only seven principal components (PCs) exhibited more than 1.00 eigen value and showed about 77.39% cumulative variability among the traits and are given due importance in this study. Here PC1 had the highest variability followed by PC2, PC3 and so on. Top ranking accessions identified in PC1 are Sukra Phool, Tendu Phool, Banspatri and Chinnour. Consequently, the results of the current study can be taken into account while developing new rice varieties.

KEYWORDS: Aromatic rice, genetic diversity, principal component analysis, rice landraces

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1. INTRODUCTION

Rice (*Oryza sativa* L.) is one of the leading staple foods, feeding over half of the world's population (Ricepedia, 2020; Anonymous, 2020a). From ancient times cultivation of rice extensively occurs near the river valleys of South and Southeast Asia (Rathna-Priya et al., 2019) and it is believed to have originated probably in India. Chhattisgarh is the mono cropped state dominated by paddy with over 80 percent of the cultivable land under paddy (Anonymous, 2019). It is well known that the traditional rice varieties and their wild relatives constitute an invaluable gene pool in terms of resistance/tolerance to biotic and abiotic stresses, which can be exploited for developing modern new-generation rice varieties having enough resilience to sustain adverse climatic changes (Beena et al., 2017, 2018; Naresh et al., 2018; Manikanta et al., 2020; Nithya et al., 2020). In recent years, premium grain quality has become an essential requirement for producers and consumers, thus significantly affecting global rice trading (Panda et al., 2020). Rice aroma is a highly heritable trait as reported by Wakte et al. (2017). Aromatic rice is sold at premium prices in the National as well as in the International market, because of having a specific aroma and supreme rice grain (Verma et al., 2014, 2015). India had exported 4.415 million tonnes of Basmati to the global market valued at US$ 4722 million, and 7.6 million tonnes of non-Basmati rice valued at US$ 3,048 million between April 2018 and March 2019 (Anonymous, 2020b).

For selection, conservation, characterization, and proper utilization of germplasms, genetic diversity is the primary component of any agricultural production system (Emon and Ahammed, 2020). The characterization directly provides the information about germplasm richness there by giving a better insight about germplasm composition and presence of genetic diversity (Breseghello, 2013; Ahmed et al., 2016). Adequate knowledge of genetic variation in different genotypes is a preliminary step in breeding programs for the selection and production of new varieties (Kumbhar et al., 2015). Plants with genetic diversity have the potential to respond to rapid changes in environmental circumstances (Raza et al., 2019). The success of any plant breeding programme is dependent on the presence of sufficient variability in the breeding material (Rauf et al., 2016). In the development of new high-yielding varieties, genetic resources play an important role (Piradi et al., 2016). To maintain current food self-sufficiency and fulfil future food and export demands, production must increase roughly at a rate of 1.5 mt per year by 2050, and productivity must increase by about 30% i.e., from current level of 2.56 t ha^{-1} to 3.25 t ha^{-1}. (Pathak et al., 2021). Genetic diversity is considered as a major component of germplasm and is important for breeding and improving rice lines and varieties to meet the current and future food requirements (Reig-Valiente et al., 2016; Tu-Anh et al., 2018). To expand the genetic base of a breeding program, it is necessary to use a population with a high level of genetic variance (Nachimuthu et al., 2015).

Multivariate analysis is a set of statistical techniques used for analysis of data that contain more than one variable. This technique simultaneously analyses multiple measurements on each individual under investigation and is widely used in analysis of genetic diversity. Principal Component Analysis (PCA) is one of the tools of multivariate technique that analyzes a data table in which observations are described by several inter correlated quantitative dependent variables (Nachimuthu et al., 2014). The main advantage of PCA is that it quantifies the value of each dimension in characterizing the variability of a data set (Raj et al., 2020). Principal component analysis (PCA) based on phenotypic attributes can be used to assess genetic variability (Islam et al., 2018; Bhattarai et al., 2019). Principal component analysis (PCA) is an effective approach to measure genetic divergence between germplasm genotypes with respect to their characteristics (Beena et al., 2021). So, the present research was therefore undertaken to assess the genetic diversity for yield attributing traits in aromatic rice landraces using multivariate analysis.

2. MATERIALS AND METHODS

2.1. *Experimental site and materials used*

This experiment was carried out at Research cum Instructional Farm, Department of Genetics and Plant Breeding, College of Agriculture, Indira Gandhi Agricultural University, Raipur (Chhattisgarh), India during *kharif* (July-November, 2020). The experimental material consists of 90 aromatic rice landraces belonging to IGKV gene pool along with six checks. These six checks include one non-aromatic check Mahamaya and five aromatic checks namely, Tarun Bhog Selection 1, Chhattisgarh DevBhog, Badshah Bhog Selection 1, Vishnu Bhog Selection 1 and Dubraj Selection 1.

2.2. *Planting pattern, observations recorded and statistical analysis*

Nursery sowing was done in well prepared raised seed bed in first week of July 2020. Twenty-eight days old seedlings were transplanted in well puddle field in Augmented Block Design as suggested by Federer, 1956. The plant to plant and row to row distance was maintained 15 cm and 20 cm, respectively. The distance between each block was maintained at 50 cm. The randomization of check varieties was done within each block. Observations were recorded for 24 quantitative traits viz., days to 50% flowering, plant height (cm), number of effective tillers plant^{-1}, length of leaf blade (cm), width of leaf blade (cm), panicle length (cm), panicle weight (g), panicle harvest index, filled grains panicle^{-1}, unfilled grains panicle^{-1}, total grains panicle^{-1}, spikelet fertility %, grain yield plant^{-1} (g), thousand grain weight (g), grain length (mm), grain breadth (mm), grain length/breadth ratio, decorticated grain length (mm), decorticated grain breadth (mm), decorticated grain length/breadth ratio, biological yield plant^{-1}, harvest index, hulling % and milling % at particular stages of rice plant following the minimal descriptor of rice. The observations recorded were statistically analyzed using PAST v3.14 software.

3. RESULTS AND DISCUSSION

The analysis of variance revealed highly significant differences among the genotypes for all grain yield and its attributing traits. Singh et al. (2010) also observed highly significant differences among the genotypes for studied traits which are in agreement with the present study. The presence of a wide range of variability might be due to diverse sources of the materials having high natural recombination and mutations (Table 1).

3.1. Mean performance and assessment of variability parameters

The data on descriptive statistics *viz*., mean, range, standard error, standard deviation and coefficient of variation are illustrated in Table 2. In the present investigation, a wide range of genetic variability was observed for most of the yield and yield attributing traits. High magnitude of coefficient of variation (more than 20%) in the entire accessions was observed for effective tillers plant^{-1} (22.47%), length of leaf blade (21.45%), panicle weight (24.27%), number of filled grains panicle^{-1} (27.05%), number of unfilled grains panicle^{-1} (51.75%), total grains panicle^{-1} (23.47%), grain yield plant^{-1} (g) (24.41%), 1000 grain weight (21.32%) and biological yield plant^{-1} (g) (20.21%). High magnitude of coefficient of variation for effective tillers plant^{-1} was also observed by Singh et al. (2010). The presence of high magnitude of coefficient of variation indicates the existence of significant variability among the yield traits and offers the opportunities of improvement through desirable selection techniques.

3.2. Principal component analysis

The outcome of principal component analysis described the genetic diversity among rice genotypes for the studied traits.

Table 1: Analysis of variance for yield and its attributing traits

Sources of Variation	Degrees of freedom	Days to 50% flowering	Plant height	Effective tillers plant^{-1}	Length of leaf blade	Width of leaf blade	Panicle length
		Mean sum of squares					
Blocks (eliminating treatments)	5	5.238	2.501	4.333	0.521	0.005	1.406
Treatments (ignoring blocks)	95	23.747**	302.312**	7.375**	51.902**	0.047**	9.208**
Checks	5	13.228	2669.784**	28.133**	207.14**	0.195**	49.696**
Varieties	89	23.084**	109.939**	2.684	41.733**	0.025**	6.251**
Checks Vs Varieties	1	135.372**	5586.158**	321.029**	180.814**	1.315**	69.954**
Error	25	7.012	7.854	2.187	1.842	0.005	1.494

Table 1: Continue..

Sources of Variation	Degrees of freedom	Panicle weight	Panicle harvest index	Filled grains panicle^{-1}	Unfilled grains panicle^{-1}	Total grains panicle^{-1}	Spikelet fertility %
		Mean sum of squares					
Blocks (eliminating treatments)	5	1.369	0.001	112.984	35.933	189.445	3.809
Treatments (ignoring blocks)	95	44.665**	0.002**	2724.873**	480.771**	2740.344**	111.694**
Checks	5	287.85**	0.001	4789.028**	1178.467**	4704.561**	184.635**
Varieties	89	26.021**	0.001**	1750.813**	408.470**	2103.544**	87.526**
Checks Vs Varieties	1	488.068**	0.021**	79095.467**	3427.051**	49594.464**	1897.989**
Error	25	1.26	0	88.063	14.36	106.544	1.79

Table 1: continue...

Sources of variation	Degrees of freedom	Grain yield plant^{-1}	1000 grain weight	Grain length	Grain breadth	Grain L/B ratio	Decorticated grain length
		Mean sum of squares					
Blocks (eliminating treatments)	5	1.599	0.468*	0.032	0.012	0.007	0.01
Treatments (ignoring blocks)	95	37.723**	27.541**	1.438**	0.0340**	0.323**	0.961**
Checks	5	256.656**	335.371**	6.791**	0.220**	1.702**	4.277**
Varieties	89	19.681**	8.755**	1.154**	0.023**	0.249**	0.773**
Checks Vs Varieties	1	548.841**	160.292**	0.006	0.003	0.03	1.093**
Error	25	0.644	0.131	0.014	0.008	0.009	0.01
Total	125						

Table 1: Continue...

Sources of variation	Degrees of freedom	Decorticated grain breadth	Decorticated grain L/B ratio	Biological yield plant^{-1}	Harvest index	Hulling %	Milling %
		Mean sum of squares					
Blocks (eliminating treatments)	5	0.013*	0.013	4.422	1.083	1.852	3.368
Treatments (ignoring blocks)	95	0.040**	0.309**	246.856**	46.892**	55.459**	59.164**
Checks	5	0.265**	1.496**	123.225**	455.335**	264.211**	257.749**
Varieties	89	0.027**	0.244**	256.571**	14.440**	34.359**	47.506**
Checks Vs Varieties	1	0.007	0.135**	0.38	892.837**	889.661**	103.818**
Error	25	0.005	0.007	3.736	1.298	2.676	2.394
Total	125						

**: Significant at (p=0.01) level of significance; *: Significant at (p=0.05) level of significance

The PCA analysis reduces the dimensions of a multivariate data to a few principal axes, generates an Eigen vector for each axis and produces component scores for the characters (Leonard and Peter, 2009). Principal components with eigen values more than 1 and variation more than 4% were considered as main PC (Brejda et al., 2000). In the present investigation, principle component analysis revealed that out of twenty four characters studied, only seven principal components (PCs) exhibited more than 1.00 eigen value and showed about 77.39% cumulative variability among the traits studied while the other components were rejected because they have eigen values less than one. So, these seven PCs were given due importance for further explanation. Out of the seven principal components (PCs) exhibiting more than 1.00 eigen value PC1 had the highest variability (23.647%) followed by PC2 (14.328%), PC3 (11.823%), PC4 (8.403%), PC5 (7.235%), PC6 (6.075%) and PC7 (5.877%) as illustrated in Table 3.

Scree plot explained the variation associated with each principal component obtained by drawing a graph between eigen values and principal component numbers. PC1 showed highest variability of 23.647% which then declined gradually (Figure 1). The first PC accounts for as much of the variability in the data as possible, and each succeeding component accounts for as much of the remaining variability as possible.

The results of the present analysis as illustrated in Table 4 revealed that the first principal component PC1 mainly

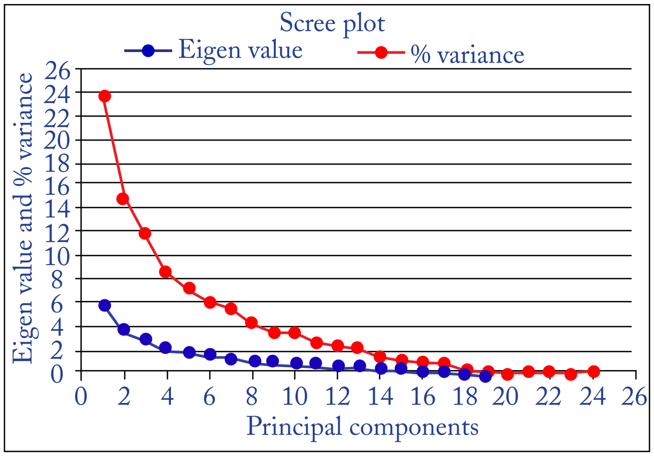

Figure 1: Scree plot diagram of eigen values constructed on twenty four traits recorded in 96 rice genotypes

Table 2: Descriptive statistics for quantitative traits in 96 rice genotypes

Characters	Mean	Range		Standerd error	Standard deviation	Coefficient of variation (%)
		Min	Max			
Days to 50% flowering	100.66	90.31	109.47	0.50	4.95	4.91
Plant height	138.06	93.58	164.76	1.21	11.82	8.56
Effective tillers plant^{-1}	9.19	6.17	16.00	0.21	2.06	22.47
Length of leaf blade	29.94	21.50	40.76	0.66	6.42	21.45
Width of leaf blade	1.31	1.06	1.78	0.02	0.17	12.90
Panicle length	26.47	21.26	31.56	0.26	2.59	9.77
Panicle weight	21.81	14.51	37.40	0.54	5.29	24.27
Panicle harvest index	0.88	0.80	0.95	0.00	0.04	4.26
Number of filled grains panicle^{-1}	160.81	87.31	275.47	4.44	43.51	27.05
Number of unfilled grains panicle^{-1}	39.32	10.67	83.00	2.08	20.35	51.75
Total grains panicle^{-1}	200.13	101.97	303.47	4.79	46.96	23.47
Spikelet fertility %	80.19	61.34	94.39	0.97	9.46	11.80
Grain yield plant^{-1}	19.14	12.49	34.47	0.48	4.67	24.41
1000 Seed weight	15.53	11.53	32.52	0.34	3.31	21.32
Grain length	7.25	5.60	8.80	0.11	1.06	14.61
Grain breadth	2.28	1.97	2.72	0.02	0.16	7.00
Grain L/B ratio	3.19	2.30	4.21	0.05	0.50	15.75
Decorticated grain length	5.38	4.15	6.60	0.09	0.87	15.95
Decorticated grain breadth	2.04	1.53	2.43	0.02	0.17	8.45
Decorticated grain L/B ratio	2.69	1.81	3.97	0.05	0.49	18.40
Biological yield plant^{-1}	77.14	55.77	117.57	1.59	15.59	20.21
Harvest index	24.93	19.75	45.29	0.45	4.41	17.67
Hulling %	73.45	58.89	86.38	0.59	5.81	7.91
Milling %	62.38	45.27	76.79	0.686	6.72	10.77

Table 3: Eigen values, proportion of variation % and cumulative variation % of analyzed components

Principal components	Eigen value	Proportion of variation %	Cumulative variation %	Principal components	Eigen value	Proportion of variation %	Cumulative variation %
PC1	5.675	23.647	23.647	PC13	0.479	1.995	95.602
PC 2	3.559	14.328	37.975	PC14	0.322	1.342	96.944
PC 3	2.838	11.823	49.798	PC15	0.245	1.020	97.963
PC 4	2.065	8.403	58.201	PC16	0.210	0.873	98.836
PC 5	1.736	7.235	65.436	PC17	0.187	0.778	99.613
PC 6	1.458	6.075	71.511	PC18	0.065	0.270	99.882
PC 7	1.242	5.877	77.388	PC19	0.017	0.072	99.953
PC8	0.988	4.198	81.586	PC20	0.004	0.018	99.971
PC9	0.859	3.580	85.166	PC21	0.003	0.013	99.984
PC10	0.820	3.418	88.584	PC22	0.002	0.009	99.993
PC11	0.637	2.655	91.238	PC23	0.001	0.004	99.997
PC12	0.569	2.369	93.607	PC24	0.001	0.003	100

Table 4: Contribution of each trait towards each of the major principal components

Traits	PC 1	PC 2	PC 3	PC 4	PC 5	PC 6	PC 7
Days to 50% flowering	-0.099	-0.170	0.333	0.037	-0.009	0.020	-0.127
Plant height	-0.155	0.024	-0.021	0.257	-0.166	**0.430**	0.153
Effective tillers plant^{-1}	0.035	0.173	0.238	0.009	-0.137	-0.146	-0.291
Length of leaf blade	0.213	-0.055	0.045	-0.352	0.263	0.117	-0.010
Width of leaf blade	0.158	-0.042	0.270	-0.305	0.109	-0.079	0.034
Panicle length	0.043	0.142	-0.054	**0.483**	-0.039	**0.449**	-0.049
Panicle weight	0.252	0.271	0.268	**0.435**	0.015	0.014	-0.175
Panicle harvest index	0.029	0.042	-0.032	-0.160	-0.260	0.167	-0.165
Filled grains panicle^{-1}	0.149	0.163	**0.459**	-0.127	-0.064	0.015	**0.449**
Unfilled grains panicle^{-1}	-0.009	-0.245	0.155	0.228	0.330	-0.200	0.083
Total grains panicle^{-1}	0.142	0.045	**0.437**	0.067	0.083	-0.072	**0.452**
Spikelet fertility %	0.052	0.280	0.029	-0.440	-0.316	0.156	0.138
Grain yield plant^{-1}	0.398	0.278	0.265	0.168	0.140	0.239	0.256
1000 grain weight	**0.465**	0.196	-0.018	-0.063	0.054	0.014	0.052
Grain length	**0.488**	-0.049	-0.119	0.012	0.028	0.007	0.191
Grain breadth	0.011	**0.440**	-0.188	-0.084	**0.427**	0.022	-0.041
Grain L/B ratio	0.355	-0.197	-0.029	0.041	-0.162	-0.009	0.193
Decorticated grain length	**0.485**	-0.049	-0.087	0.032	0.019	-0.002	0.217
Decorticated grain breadth	0.048	**0.420**	-0.134	-0.065	**0.477**	0.015	0.114
Decorticated grain L/B ratio	0.357	-0.195	-0.022	0.047	-0.202	-0.017	0.120
Biological yield plant^{-1}	0.228	0.123	0.231	0.136	0.105	**0.430**	-0.061
Harvest index	0.104	0.252	0.101	0.073	-0.172	-0.455	-0.236
Hulling %	0.007	**0.409**	-0.155	0.173	-0.200	-0.249	**0.407**
Milling %	0.037	**0.401**	-0.269	0.230	-0.140	-0.132	0.185
Eigen value	5.675	3.558	2.837	2.064	1.736	1.457	1.242
Proportion of variation%	23.647	14.828	11.823	8.603	7.234	6.074	5.177
Cumulative variation%	23.647	38.475	50.298	58.901	66.135	72.209	77.386

Values in bold represent highly weighted factors in respective PC

comprises genotypes with increased grain length (0.488) followed by increased decorticated grain length (0.485) and thousand grain weight (0.465). It was found that yield attributing traits i,e grain length, thousand grain weight positively affects PC1. The second principal component PC2 was highly loaded with increase grain breadth (0.440) followed by increased decorticated grain breadth (0.420), hulling % (0.409) and milling % (0.401). The third principal component PC3 comprises genotypes with higher number of fertile grains panicle^{-1} (0.459) and total grains panicle^{-1} (0.437). The fourth principal component PC4 was highly related with panicle length (0.483) and panicle weight (0.435). The fifth principal component PC 5was found positively related with grain breadth (0.427) followed by decorticated grain breadth (0.477). The sixth principal component PC6 was found highly related with panicle length (0.449), plant height (0.430) and biological yield plant^{-1} (0.430). Similarly, the seventh principal component PC7 was highly related with total grains panicle^{-1} (0.452), fertile grains panicle^{-1} (0.449) and hulling % (0.407).

Therefore, results revealed that all the seven principal components are associated with yield attributing traits. Hence, a good breeding program for increased yield can be initiated by selecting top accessions from PC1 to PC7. PCA has been used by various researchers like Gana et al. (2013), Sinha and Mishra (2013), Yugandhar et al. (2018), Ilieva et al. (2019), Sao et al. (2019) and Salem et al. (2021) for

Table 5: Contribution of each genotype towards the major principal components

Accession Name	PC 1	PC 2	PC 3	PC 4	PC 5	PC 6	PC 7
AamaGohi	-0.254	2.274	0.446	0.014	1.841	1.015	-1.096
Aatma Shital	-0.967	1.054	1.990	0.486	-0.014	1.248	-0.579
Atma Shital	-0.875	-0.022	0.472	-0.071	1.611	0.684	0.232
Akbar Badshah	-0.784	-0.422	0.793	-1.304	-0.718	1.843	-0.013
Bag Muchh	0.717	-1.842	0.063	-0.719	1.056	0.068	0.068
Wasmati	-0.445	-1.070	0.570	0.736	-1.570	1.502	1.498
Banspatri	1.821	0.097	0.972	1.066	2.232	0.779	0.148
Barang	-1.587	0.636	-0.419	-0.227	-0.006	0.531	1.142
Badshah Bhog	-1.317	-0.490	0.370	0.257	-0.197	0.477	0.138
Badshah Bhog	-0.946	0.368	-1.254	-0.770	-0.154	-0.436	-0.306
Badshah Bhog	-0.784	-1.424	-0.077	0.050	1.156	0.351	-1.731
Basha Bhog	-0.280	-0.169	0.754	0.051	0.974	1.728	-2.339
BassaBhog	-0.579	0.678	1.310	-0.415	-1.419	-0.158	-1.436
BisnuBhog	-0.511	-0.684	0.669	-1.480	1.425	0.980	-0.464
Muni Bhog	0.867	-1.490	-0.582	0.267	1.282	0.094	-1.025
Chini Kapoor	-0.932	-0.405	0.521	0.936	0.889	-0.592	-0.855
Chini Kapoor	-1.377	0.274	0.067	-0.906	0.540	1.003	0.900
Chinnur	0.645	-2.034	0.062	-0.040	1.332	-0.443	1.165
Chinnour	1.638	-0.751	0.557	1.174	0.623	0.431	-0.044
ChiraiNakhi	-0.643	0.097	1.467	1.162	-0.184	-0.510	-0.511
Dubraj	1.277	-0.662	-0.184	-0.389	-0.639	1.216	-0.813
Dubraj	0.516	-1.386	0.003	-0.891	0.595	-0.580	0.962
Dubraj	0.673	-0.897	0.056	0.257	0.633	-0.211	0.783
Dubraj	1.142	-0.627	-0.327	0.604	-0.438	-0.434	-0.587
Dubraj	1.391	-0.060	1.792	-0.273	0.550	0.514	0.346
Dubraj Dhan Deshi	1.301	-1.220	0.481	-0.181	-0.452	0.132	-1.280
MajhaliDubraj	0.468	-0.575	-0.205	0.262	0.655	0.128	0.657
Ganga Balu	-0.695	0.058	0.205	0.406	-1.121	-0.172	-0.764
Bam Baijira	0.067	-1.068	0.099	-0.569	0.464	0.401	1.598
Bhanta Phool	-0.878	0.174	0.782	-0.310	-0.269	1.524	2.484
Jui Phool	1.090	0.863	1.026	-0.657	0.717	0.811	-0.977
Ramkali	-1.079	-0.546	-0.448	-1.314	0.431	0.108	-0.898
Dubraj	1.460	-2.433	0.825	-0.218	0.270	-0.996	-0.559
SamundChini	-1.087	-0.026	0.989	-0.473	0.097	1.332	-0.577
Samudra Fen	-0.390	0.305	2.310	0.892	-1.789	1.522	-0.922
Sansari	-0.997	-1.184	0.732	0.133	-2.160	-0.078	-1.585
Sarsariya	0.424	-1.882	0.323	0.931	-0.909	-1.680	-1.621
Jira Shankar	-0.994	-0.163	0.229	-0.522	0.541	0.454	-0.728
Til Kasturi	-0.713	-0.170	-0.696	0.042	-0.197	0.423	-0.749

Table 5: Continue...

Accession Name	PC 1	PC 2	PC 3	PC 4	PC 5	PC 6	PC 7
Tulsi Amrit	-0.403	-0.063	1.214	0.960	-1.169	0.963	-0.714
Tulsi Bas	1.342	0.148	0.436	-0.633	-0.418	0.653	0.086
Tulsi Mala	-0.596	-0.634	-0.017	-0.064	-1.055	0.046	-0.418
TulsiManjari	-1.415	0.433	-1.148	0.471	-0.487	-0.512	-0.044
Badshah Bhog	-0.799	0.847	-1.154	-0.214	-1.490	0.499	-0.703
Badshah Bhog	-0.636	0.016	-0.947	1.433	-0.367	-1.035	-1.774
Chhatri Bhog	0.785	0.929	-1.661	0.134	-0.874	-1.141	0.429
Gobind Bhog	-1.479	-0.427	0.442	0.138	-0.505	-0.187	0.857
Raja Bhog	-0.409	-0.116	-0.277	-1.584	0.242	0.577	-0.903
Kali Muchh	0.560	-0.455	-1.564	-0.420	-1.985	1.271	0.533
Kali Muchha	0.515	-0.697	-1.986	0.180	-1.904	-0.160	0.094
LoktiMachhi	-0.434	0.273	-1.853	-0.102	2.110	1.596	-1.446
Sukra Phool	2.061	1.517	-1.051	0.202	-0.945	2.010	0.027
Tendu Phool	1.917	2.394	0.508	-0.275	0.173	2.163	1.974
Basmati I	1.599	0.661	-0.695	1.635	-0.374	1.372	-0.379
Chhatri	0.563	-0.745	-2.112	-0.786	-0.259	-0.285	-0.342
Chhatri	0.550	0.924	-1.924	0.146	-0.694	-0.488	0.271
Bhatta Phool	-1.112	1.700	0.486	0.488	-0.058	-1.167	0.213
Til Kasturi	-0.387	1.213	-0.733	-0.719	-0.235	-1.091	-0.486
Kubri Mohar	0.312	0.345	-1.513	0.939	-0.462	-0.851	-0.426
Lalloo	0.450	-0.292	-2.203	-1.475	-0.478	-0.894	-0.402
Angar Moti	-0.394	1.435	-0.786	-1.867	1.940	-2.069	-0.482
Kadam Phool	-0.601	1.170	0.702	-1.656	0.213	-0.465	-0.570
Laichi Phool	-0.161	0.579	-0.764	-2.229	0.960	-0.454	1.817
Lallu	-0.120	1.208	-1.623	-1.440	0.732	-1.022	-0.338
Chini Kapoor	0.963	2.111	-1.473	1.087	-1.053	0.669	-0.153
Bag Muchh	0.753	0.803	0.463	-0.710	0.337	0.048	0.933
TulsiManjari II	-0.633	0.485	0.786	1.169	0.517	-1.209	1.670
Sukla Phool	1.045	1.774	-0.121	2.972	0.998	-0.121	-0.210
Ganga Baru	-1.014	1.119	0.971	1.013	-0.261	-1.668	1.229
Jai Gundi	-1.711	-0.217	0.238	1.166	0.445	-1.354	1.503
BayasaBhog	0.868	-0.610	1.109	0.344	2.131	-0.385	0.968
BisnuBhog	-1.275	-0.513	-0.091	0.835	0.649	0.168	0.360
Raja Bhog	-1.437	-0.943	0.258	0.529	-0.124	-0.641	0.542
VishnooBhog	-0.327	0.310	-0.724	-1.368	0.203	0.339	0.400
Vishnu Bhog	-1.029	-1.404	0.131	-0.461	-0.367	-1.690	-0.640
Bikoni	-0.487	0.608	-1.755	-0.485	0.755	1.084	-0.564
UraiButa	-0.668	0.932	-0.803	2.285	1.445	0.000	-1.597
ChendaraChhal	-1.452	0.086	-0.892	1.079	0.597	-0.528	1.403
Chinnour	0.803	-1.231	-0.168	0.064	0.523	0.559	0.548

Table 5: Continue...

Accession name	PC 1	PC 2	PC 3	PC 4	PC 5	PC 6	PC 7
Duban Mua	0.891	-1.426	-0.922	-0.663	-0.918	0.017	0.734
Badshah Bhog	-1.206	-0.804	-0.081	0.067	-1.049	-0.672	0.962
Basa Bhog	-0.464	-0.306	-0.321	2.197	0.614	0.676	-0.974
Dubraj	1.125	-0.104	0.495	1.176	-0.307	-0.667	0.364
Dubraj	0.676	-0.757	-1.308	-0.291	0.181	-0.016	0.601
Dubraj	1.303	-0.184	0.905	-0.406	-1.135	-0.065	1.344
Dubraj	0.946	-0.107	0.223	-0.704	-0.994	-0.318	-0.245
Dubraj	0.575	-0.774	-0.100	-0.705	0.240	0.442	1.215
Dubraj (Deshi)	1.321	0.106	0.198	-0.601	-1.221	0.661	0.496
Dudh Nag	0.793	-0.515	-0.016	1.372	1.476	-1.370	1.806
Bhanta Phool	-0.139	-0.070	-1.044	2.743	0.037	-0.690	0.706
Mahamaya	2.290	2.863	1.218	-0.627	0.594	-2.900	-0.842
TarunBhog Selection 1	-0.559	0.754	1.159	-2.123	0.545	-0.231	-0.957
Chhattisgarh Dev Bhog	1.379	-0.081	1.175	-0.829	-0.616	-2.784	-1.072
Badshah Bhog Selection 1	-1.248	0.629	0.107	0.649	-1.328	0.551	1.666
Vishnu Bhog Selection 1	-0.858	1.263	1.243	-1.160	-0.664	-0.821	1.567
Dubraj Selection 1	0.884	0.667	1.417	-0.873	-2.535	-1.420	-0.568

characterization of different rice landraces lines. Yugandhar et al. (2018) also observed 71% cumulative variance of the total variability by first six principal component axes which is in agreement with the present study.

PCA helps us to identify the characters which have great impact in phenotype of different landraces of rice, and this is very much important in the selection procedure. Top 5 principal component scores (PC scores) for all the accessions were estimated in seven principal components and presented in Table 6.

Table 6: List of superior genotypes in 7 principal components on the basis of top 5 PC score

Sl. No.	PC1	PC2	PC3	PC4	PC5	PC6	PC7
1.	Mahamaya (Check)	Mahamaya (Check)	Samudra Fen	Sukla Phool	Banspatri	Tendu Phool	Bhanta Phool
2.	Sukra Phool	Tendu Phool	Aatma Shital	Bhanta Phool	Bayasa Bhog	Sukra Phool	Tendu Phool
3.	Tendu Phool	Chini Kapoor	Dubraj	UraiButa	Lokti Machhi	Akbar Badshah	Laichi Phool
4.	Banspatri	Sukla Phool	ChiraiNakhi	Basa Bhog	Angar Moti	Basha Bhog	Dudh Nag
5.	Chinnour	AamaGohi	Dubraj Selection 1 (Check)	Basmati I	AamaGohi	LoktiMachhi	TulsiManjari

4. CONCLUSION

The accessions Sukra Phool, Tendu Phool, Banspatri and Chinnour contributed maximum in yield improvement. The information, thus obtained, will be helpful in selecting genetically diverse genotypes for rice improvement programme.

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