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Research Article

Evaluation of nutritional and grain quality diversity in rice (*Oryza sativa* L.) germplasm based on multivariate analysis

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Abstract
Two hundred traditional landraces and exotic genotypes from 12 countries were assessed for variability for eight-grain quality traits by UPGMA cluster analysis, Pearson's correlation coefficient and principal component analysis. Analysis by the UPGMA method clustered 200 genotypes into two clusters. In PCA analysis, the first five principal components explained about 74.19 % of the total variation among the eight characters. Component 1 had contributions from all the traits and it accounted for 22.46 % of the total variability. Component 2 had the contribution from Grain width and Zinc content which accounted for 15.75% of the total variability. Component 3 had a contribution from grain length and amylose with a variability of 13.11%. Component 4 contributed from ASV and amylose and component 5 for ASV and GC with a variability of 11.63 per cent each. Thus, the results indicate a high level of genetic variation in the rice germplasm.

Keywords: Rice genetic variation, Principal component analysis, multivariate

INTRODUCTION

Rice (*Oryza sativa* L.) is the most important cereal crop grown worldwide, covering 162.76 million hectares and yielding 495.87 million tonnes with a productivity of 4.55 t/ha. India has the largest area under rice cultivation in the world with 43.86 million hectares and ranks second in production with 99.24 million tonnes with a productivity of 2.49 t/ha next to wheat. (Ministry of Agriculture, Government of India, 2018-19). Rice has one of the world's most extensive germplasm collections. Rice breeding has benefited greatly from the availability of various cultivated and wild rice germplasm. To develop an effective and valuable breeding method, sufficient knowledge of genetic diversity in the gene pool is required. Characterization of existing variability and realignment of features in them through selective breeding could go a long way towards addressing current and emerging threats to global food security (Vanaja and Babu., 2006). Landraces provide an important gene pool for future breeding programmes (Patra.,2000). Genetic distance estimates for population grouping can be done by different methods and it is crucial to understand the usable variability existing in the population panel (Nachimuthu *et al*., 2014). Apart from improving productivity, rice quality is also given top priority as it is of great importance to millers and consumers. (Koutroubas *et al*., 2004). Though many reports on the morphological characterization of germplasm are available, the reports on the assessment of grain quality variations are scanty.

Multivariate analysis is the most commonly used method for estimating genetic variability in germplasm collections to illustrate patterns of variation. For morphological characterization of genotypes and grouping based on similarities, PCA and cluster analysis are favoured multivariate approaches (Mohammadi and Prasanna 2003). The combination of these two approaches yields comprehensive information on the traits that contribute significantly to genetic variability in crops. PCA can be used to detect similarities between variables and classify the genotypes, while cluster analysis on the other

hand is concerned with classifying previously unclassified materials. In the present study level of germplasm variation on grain properties was determined and classified using multivariate approaches.

MATERIALS AND METHODS

Two hundred germplasm lines maintained at Tamil Nadu Rice Research Institute, Aduthurai, Tamil Nadu were utilized for grain quality analysis. All the genotypes were raised in the field for seed multiplication during *Kharif* 2019 at the research farm of TRRI, Aduthurai. The study material comprised of landraces and varieties collected from different states of India as well as from different countries (**Table 1**). The panicles of individual genotypes were bagged upon flowering and the collected seeds were subjected to grain quality analysis. For easy identification and retrieval, each accession was named AD-G1 to AD-G 200.

The grain quality traits *viz*., grain length(GL), grain width(GW), L/B ratio, Alkali spread value (ASV), gel consistency (GC), Amylose content were estimated as per Juliano (1979) and iron and zinc content using ED- XRF (X Supreme 8000). The Principal Component Analysis was used to find the plant attributes that account for the majority of the observed differences between genotypes. PCs with Eigenvalues greater than one were chosen in the manner proposed by Jeffers., 1967. Mean values of 200 genotypes for nine traits were used. Principal components are typically estimated using a correlation or covariance matrix. The analysis was carried out using the STAR software.

RESULTS AND DISCUSSION

The gene pool of rice studied for grain quality traits manifested a wider range in the expression of the traits. The largest variation was observed for Amylose % (CV= 54.8) followed by zinc content (35.8), ASV (34.6), Iron content (32.8) and GC (32.2), grain breadth (7.17) and grain length-width ratio (8.82). Grain length has shown the least variation with the CV of 5.4%. The accession with the longest grain was 6.9 mm in AD-G-094 (T 1143) and the shortest grain was measured in the genotype AD-G-185 (Singanskayama) from Africa. The overall mean for grain length in germplasm accessions was 6.03mm. The largest grain width of 3.1 mm was recorded in the genotype AD-G-081 (Hunan sien collected from China) Slender grain type with lowest grain width (2.0 mm) was noticed in the genotype AD-G120 (Puthuvitha). The mean grain width was 2.47 mm. The mean alkali spreading value was 3.43 with a minimum of 2.0 AD-G-027(Aramalachorma) and a maximum in the genotype AD-G-197(Sadrumuradavali) collected from Cuttack. The grain length width ratio was highest for the genotype AD-G-153 (B.112) (5.6) and lowest for the genotype AD-G-004 (T58) (1.9). The mean ratio was 2.45. The genotype AD-G-156 (R. vshimbaearly), a rare collection from Iraq, recorded a hard gel consistency of 22 mm, whereas the genotype AD-G-139 (T1504) had a maximum gel consistency of 115mm. The amylose content has shown a wide range of variation with a mean of 13.42. The genotype AD-G-065 (V.Vurgariskom) collected from Russia recorded the highest per cent of amylose content (47.4%) and the genotype AD-G-090 (Wangchochao) from china had the lowest amylose content o3.1%). The zinc content ranged from 3.8 ppm in the genotype AD-G-149 (Palmansuff no.24) to 70.01 ppm in the genotype AD-G-195 (Banaspatri). The mean zinc content was observed as 25.81 ppm. The maximum iron content (19.0) was recorded in the genotype AD-G-001(Myla) and the minimum (3.0 ppm) in the genotype AD-G-179(Bhurarata).

Analysis by the UPGMA method clustered 200 genotypes into two clusters (**Fig. 1**). Cluster 1 consisted of 82 genotypes in which 9 entries were from Tamil Nadu, 57 entries which were collected from different states of India and 16 exotic collections (**Table 2**). Cluster 2 consisted of 118 genotypes in which 12 entries were from Tamil Nadu, 84 were from other states of India and 22 were exotic collections.

Pearson's correlation coefficient (r) is a measure of the strength of a two-variable linear association. **Table 3** shows the correlation coefficient among rice grains.

Table 1. Characteristic means and variation of 200 accessions of rice landraces.

Variable	Mean	SD	CV	Min		Max	
				Value	Accession	Value	Accession
Grain Length	6.039	0.330	5.460	5.2	AD-G-185	6.9	AD-G-094
Grain width	2.472	0.177	7.177	2	AD-G-120	3.1	AD-G-081
L/B ratio	2.4559	0.217	8.823	1.9	AD-G-04	3.14	AD-G-153
ASV	3.43	1.188	34.646	2	AD-G-027	7	AD-G-197
Gel consistency (mm).	45.785	14.751	32.218	22	AD-G-156	115	AD-G-139
Amylose (%)	13.425	7.364	54.850	3.1	AD-G-090	47.4	AD-G-065
Zinc (ppm)	25.81575	9.246	35.817	3.8	AD-G-149	70.01	AD-G-195
Iron (ppm)	7.7795	2.558	32.877	3	AD-G-179	19	AD-G-001

Table 2. Genotypes information with clustering pattern

S. No.	Genotype	Parentage	Origin	Membership
1	AD-G-01	Myla	Travancore	1
2	AD-G-02	Cheerachampan	Malabar	2
3	AD-G-03	Sakulathisannabhtta	Mysore	2
4	AD-G-04	T58	Tamil Nadu	2
5	AD-G-05	Sornavarai	Tirunelveli	2
6	AD-G-06	Manavari	Tirunelveli	2
7	AD-G-07	Kodaikuluthan	South Arcot	2
8	AD-G-08	Kodaikuluthan	Tamil Nadu	1
9	AD-G-09	Thattan samba	Tamil Nadu	2
10	AD-G-010	Thattan samba	Tamil Nadu	2
11	AD-G-011	Thattan samba	Tamil Nadu	2
12	AD-G-012	Ambadai	South canara	1
13	AD-G-013	Rasangi	Godowari	2
14	AD-G-014	Mundan	Malabar	2
15	AD-G-015	Poonooran	Malabar	2
16	AD-G-016	Red sirumani	Thanjavur	1
17	AD-G-017	Chanmamulu.H.PY	Malabar	2
18	AD-G-018	Elavan hill paddy	Malabar	2
19	AD-G-019	Elavan hill paddy	Malabar	2
20	AD-G-020	Vallayan	Malabar	2
21	AD-G-021	Vallayan	Malabar	1
22	AD-G-022	Kozallan	Malabar	2
23	AD-G-023	Vachan	Malabar	2
24	AD-G-024	Salem thamban	Malabar	2
25	AD-G-025	Aramalachormali	Malabar	2
26	AD-G-026	Aramalachormali	Malabar	2
27	AD-G-027	Aramalachorma	Malabar	1
28	AD-G-028	Aramalachorma	Malabar	2
29	AD-G-029	Navaranellu	Malabar	2
30	AD-G-030	Yah.zamit B. 56	Burma	2
31	AD-G-031	Hoire c. 106	Burma	2
32	AD-G-032	Kameeno	Japan	1
33	AD-G-033	Sekiton	Japan	2
34	AD-G-034	Samangai	Mangalore	2
35	AD-G-035	Peria samba	Madurai	2
36	AD-G-036	Peria samba	Madurai	1
37	AD-G-037	T396/2-	Tamil Nadu	2
38	AD-G-038	Thavalaikannan	Malabar	2
39	AD-G-039	Palodellariyan	Coorg	2
40	AD-G-040	Surli (Black)	South Canara	1
41	AD-G-041	T2285	Tamil Nadu	1
42	AD-G-042	T492	Tamil Nadu	2
43	AD-G-043	Manavari	Tirunelveli	2
44	AD-G-044	Mikuruvai	Tirunelveli	1
45	AD-G-045	Thooyala	Tirunelveli	2
46	AD-G-046	Thooyala	Tirunelveli	1
47	AD-G-047	T527/1-	Tamil Nadu	1
48	AD-G-048	Derabat	Ceylon	1
49	AD-G-049	Derabat	Ceylon	2

S. No.	Genotype	Parentage	Origin	Membership
50	AD-G-050	Kooda No. 1	Ganjam, india	1
51	AD-G-051	T573	Tamil Nadu	1
52	AD-G-052	Boroponbi	Ganjam, india	1
53	AD-G-053	Nanekram	Hyderabad	2
54	AD-G-054	Kolamba strain	Kharjat	1
55	AD-G-055	TepiDumai	Assam	1
56	AD-G-056	Hybrid 2 S.C 54	Assam	1
57	AD-G-057	PatnaiGajaba – type No. 225	Bengal	2
58	AD-G-058	Pre vittoria	Bulgaria	2
59	AD-G-059	Thitattmata A 22- 53	Burma	2
60	AD-G-060	Parunellu	Madurai	1
61	AD-G-061	Pluestrick	British Guinia	1
62	AD-G-062	Pluestrick	British Guinia	1
63	AD-G-063	Baghar	Assam	2
64	AD-G-064	Vialinica gust	Russia	2
65	AD-G-065	V .Vurgariskom	Russia	2
66	AD-G-066	V.Vurgariskom	Russia	1
67	AD-G-067	V .Vurgariskom	Russia	1
68	AD-G-068	V. Vurgariskom	Russia	2
69	AD-G-069	V. Vurgariskom	Burma	2
70	AD-G-070	C . 102	Extracted	2
71	AD-G-071	Lst. Gold clust	Extracted	1
72	AD-G-072	Lst. Gold clust	W.Africa	1
73	AD-G-073	Kesse – Koyama (m)	W.Africa	2
74	AD-G-074	Giddakaruvadlu	Chittoor	1
75	AD-G-075	Baiairu	Chittoor	2
76	AD-G-076	T990	Tamil Nadu	2
77	AD-G-077	Aruam samba	Selam	1
78	AD-G-078	Dalva T.35	Cuttack	2
79	AD-G-079	C.suniv no.12	China	1
80	AD-G-080	Aunan IEA	China	2
81	AD-G-081	Hunan sien	China	2
82	AD-G-082	Hunan sien	China	1
83	AD-G-083	Ichaotei	China	2
84	AD-G-084	Lanshien tan	China	1
85	AD-G-085	Mantehao	China	2
86	AD-G-086	Deikoonw no.2	China	2
87	AD-G-087	Seusentsau	China	2
88	AD-G-088	Siappwkuo	China	1
89	AD-G-089	Talichao(2)	China	2
90	AD-G-090	Wangchochao	China	2
91	AD-G-091	T102/t311 dark	Tamil Nadu	1
92	AD-G-092	T1065	Tamil Nadu	1
93	AD-G-093	T1093/1	Tamil Nadu	1
94	AD-G-094	T1143	Tamil Nadu	1
95	AD-G-095	Pottinallavari	Rajampet	2
96	AD-G-096	Type 9 deep water	Pusa	2
97	AD-G-097	A14 teelavadl	Karmool,AP	2
98	AD-G-098	A21 venkatu	Karmool,AP	2
99	AD-G-099	Moddoi	Ganjem,india	2
100	AD-G-0100	T1301/1-	Tamil Nadu	1

S. No.	Genotype	Parentage	Origin	Membership
101	AD-G-0101	Keitiachompa	Berhampur ,India	1
102	AD-G-0102	Velutharikazhama	Malabar	2
103	AD-G-0103	Rajah kazhama	Malabar	2
104	AD-G-0104	Rajah kazhama	Malabar	1
105	AD-G-0105	Vellaikazhama	Malabar	2
106	AD-G-0106	Vellaikazhama	Malabar	2
107	AD-G-0107	Amakari	Malabar	2
108	AD-G-0108	Vattan	Malabar	1
109	AD-G-0109	Annachampan	Malabar	2
110	AD-G-0110	Kothamchuma	Malabar	2
111	AD-G-0111	Thekkancheera	Malabar	2
112	AD-G-0112	Kolakkadoddari	Southkanada	1
113	AD-G-0113	Veluthankuthiy	Malabar	2
114	AD-G-0114	Kuthikayama	Malabar	1
115	AD-G-0115	Karuthalli	Malabar	1
116	AD-G-0116	Kuthikayama	South kanada	1
117	AD-G-0117	Vadakkan	Malabar	1
118	AD-G-0118	Japan 32	Japan	2
119	AD-G-0119	Puthuvitha	Malabar	1
120	AD-G-0120	Puthuvitha	Malabar	1
121	AD-G-0121	Onarathan red	Malabar	2
122	AD-G-0122	Thavalaikannan	Malabar	1
123	AD-G-0123	Thavalaikannan	Malabar	2
124	AD-G-0124	Veluthakannan	South Canara	2
125	AD-G-0125	Thadvvan brown	South Canara	1
126	AD-G-0126	Thadvvan brown	South Canara	2
127	AD-G-0127	Thadvvan brown	South Canara	1
128	AD-G-0128	T1460-	Tamil Nadu	1
129	AD-G-0129	Veluthan	Malabar	2
130	AD-G-0130	Baragaibelliri	South Canara	2
131	AD-G-0131	Baragaibelliri	South Canara	1
132	AD-G-0132	Surli(black)	South Canara	1
133	AD-G-0133	T144/1-	Tamil Nadu	1
134	AD-G-0134	Nirkayama	South Canara	2
135	AD-G-0135	Karthigai samba	Thirunelveli	2
136	AD-G-0136	Karthigai samba	Thirunelveli	1
137	AD-G-0137	Kathi samba	Thirunelveli	1
138	AD-G-0138	Kur 19 p.pirathi	Thirunelveli	2
139	AD-G-0139	Kur 19 p.pirathi	Thirunelveli	1
140	AD-G-0140	Oryzaelchinger	Belguinlonge	2
141	AD-G-0141	Oryzaelchinger	Belguinlonge	2
142	AD-G-0142	BT2 summer paddy	Berhampur	2
143	AD-G-0143	BT2 summer paddy	Berhampur	2
144	AD-G-0144	Kotiparusannam	Berhampur	1
145	AD-G-0145	DC.sierrileone	Africa	2
146	AD-G-0146	T1521/2-	Tamil Nadu	2
147	AD-G-0147	Prong 36	Larkanasindpakirtan	2
148	AD-G-0148	T1661/1-	Tamil Nadu	2
149	AD-G-0149	palmansuff no.24	Kodaikanal	2
150	AD-G-0150	T1725	Tamil Nadu	2
151	AD-G-0151	T1725/1	Tamil Nadu	2

S. No.	Genotype	Parentage	Origin	Membership
152	AD-G-0152	T1725/2	Tamil Nadu	2
153	AD-G-0153	B.112	Orrisa	1
154	AD-G-0154	Kodai	Udumalaipat, Tamil Nadu	1
155	AD-G-0155	T1770/1-	Tamil Nadu	2
156	AD-G-0156	R .vshimba early	Censul IRAQ	2
157	AD-G-0157	Vadakanadanj 114	Berhampur	2
158	AD-G-0158	Goddvahanam 15	Berhampur	2
159	AD-G-0159	Dhanvasulva	Berhampur	1
160	AD-G-0160	T1846-	Tamil Nadu	1
161	AD-G-0161	Nayppusannam	Berhampur	2
162	AD-G-0162	Bangaragaddi	-	2
163	AD-G-0163	Japan.3	Japan	2
164	AD-G-0164	Japan-12	Japan	1
165	AD-G-0165	Japan-32	Japan	2
166	AD-G-0166	Japan-32	Japan	2
167	AD-G-0167	Japan-38	Japan	1
168	AD-G-0168	T1531-	Tamil Nadu	1
169	AD-G-0169	Vachan	Malabar	2
170	AD-G-0170	N.22	Uttar pradesh	2
171	AD-G-0171	T3	Uttar Pradesh	2
172	AD-G-0172	T3	Uttar Pradesh	1
173	AD-G-0173	T.17 NAG.20	Uttar Pradesh	2
174	AD-G-0174	AD.CAR.(1XAR28)A6	Korimgaing, Assam	2
175	AD-G-0175	Kakalatha	Kolata,Bombay	2
176	AD-G-0176	AD.CAR.(1XAR28)A6	Korimgaing,Assam	2
177	AD-G-0177	Kakalatha	Kolata,Bombay	2
178	AD-G-0178	Kakalatha	Kolata,Bombay	1
179	AD-G-0179	Bhurarata	Kolata,Bombay	2
180	AD-G-0180	Bhurarata	Kolata,Bombay	1
181	AD-G-0181	Mahadi raja	Kolata,Bombay	2
182	AD-G-0182	Mahadi raja	Kolata,Bombay	2
183	AD-G-0183	Kaunganpoothala	North Malabar	2
184	AD-G-0184	NAO.T.L Nanking	China	2
185	AD-G-0185	Singanskayama	Africa	1
186	AD-G-0186	T21343	Tamil Nadu	1
187	AD-G-0187	T2149	Tamil Nadu	2
188	AD-G-0188	Ks4139(KSD)TLL	Cuttak	1
189	AD-G-0189	Poungrgearm	Cuttak	1
190	AD-G-0190	Palasannam	Kisna	2
191	AD-G-0191	Np.137	Karnal,	1
192	AD-G-0192	Np 137	Karnal,	1
193	AD-G-0193	Bhimiuri	Bengal	2
194	AD-G-0194	Asahi	Japan	1
195	AD-G-0195	Banaspatri	Laskari, Gurabar	1
196	AD-G-0196	Mugad 161	Dharklar	1
197	AD-G-0197	SadrumuraDavali	Cuttack	1
198	AD-G-0198	Phaurelgt	Kalintong, Assam	1
199	AD-G-0199	Phaurelgt	Kalintong, Assam	1
200	AD-G-0200	champasan	Kalintong, Assam	1

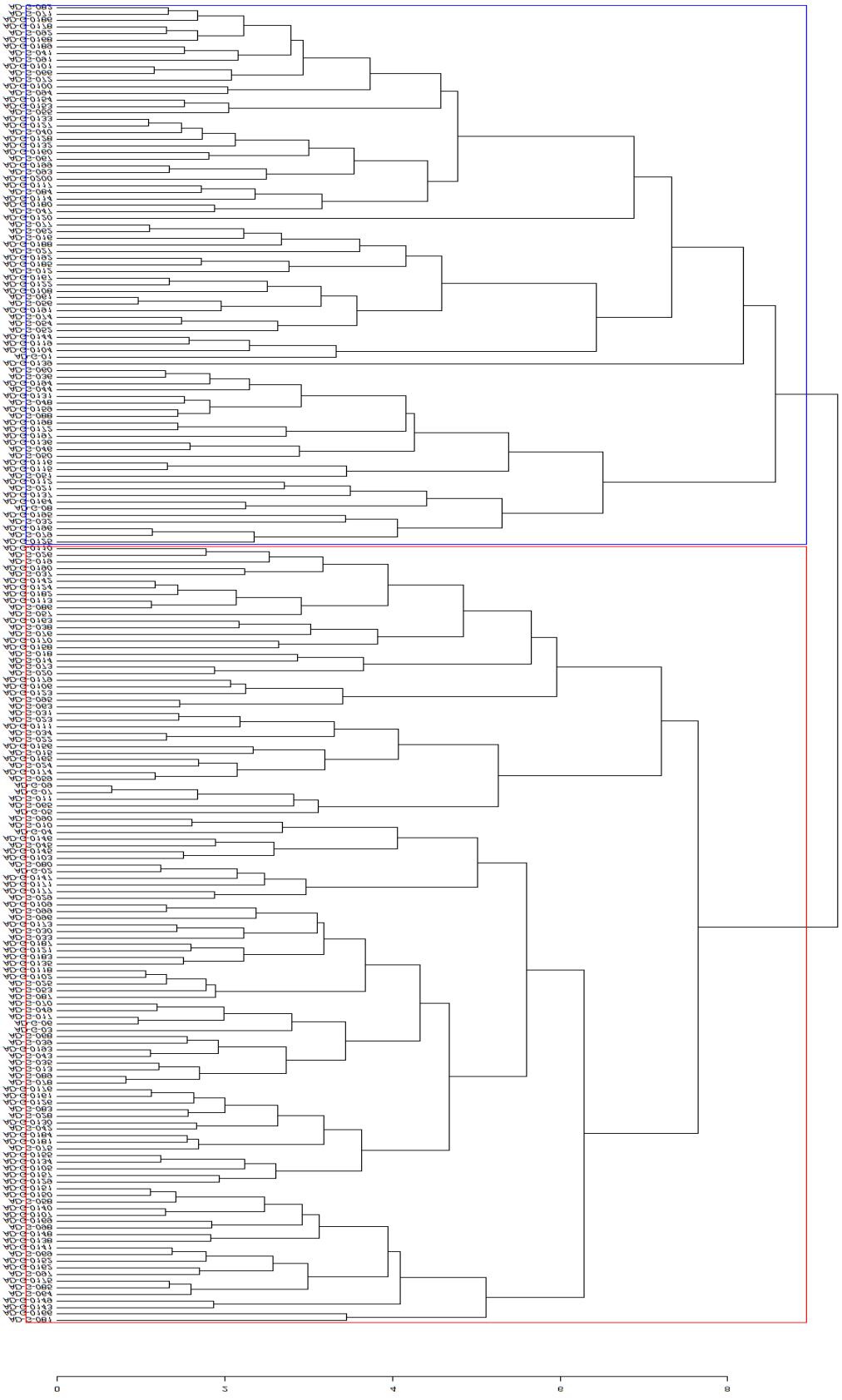

Fig. 1. Clustering pattern and dendrogram of rice germplasam

Table 3. Correlation matrix of eight characters used in characterizing the rice collection

	Grain Length	Grain width	L/B ratio	ASV	GC	Amylose	Zinc	Iron
Gain Length	1	0.061714	0.571064**	-0.03788	0.029318	0.078305	0.159746*	-0.18418*
Grain width		1	-0.77652**	0.012109	0.03686	0.095859	-0.06284	-0.03339
L/B ratio			1	-0.04367	-0.01792	-0.04815	0.145192*	-0.0787
ASV				1	0.034541	0.067792	0.069073	-0.06636
GC					1	-0.07981	0.029268	-0.02494
Amylose						1	-0.02139	-0.06551
Zinc							1	-0.27465**
Iron								1

*P<0.05, **P<0.01

Grain length was found to have a positive and significant relationship with Kernel length and Zinc content. Grain width showed a negative and significant association with the L/B ratio. Zinc content showed a positive and highly significant association with iron content. These findings were in agreement with those of (Danbaba *et al*., 2011, Mathure *et al*., 2011 and Singh *et al*., 2012)

The purpose of the PCA is to obtain a small number of factors that account for maximum variability out of the total variability. Proper values quantify the importance and contribution of each component to the total variance, whereas proper vector coefficients indicate the degree of contribution of each original variable with which each principal component is associated. The greater the coefficients, regardless of sign, they can distinguish between accessions. There are no inferential tests that may be used to demonstrate the significance of appropriate values and coefficients (Sanni *et al*., 2012). The current study was based on the Proportion of Variance Criterion by (Hatcher and O'Rourke, 2014). According to this criterion, five principal components with a cumulative variance of 74.19% were extracted. The purpose of the PCA is to obtain a small number of factors that account for maximum variability out of the total variability. Eigenvector values, percentage of variance and the cumulative percentage are presented in **Table 4**. Five components had Eigenvalues greater than 1.0. Scree plot explained the percentage of variation by a graph between Eigen Values and Principal Components (**Fig. 2**). The graph clearly shows that the greatest variation was observed in PC1, PC2, PC3, PC4, and PC5

Table 4. Eigen value and percent of total variation and component matrix for the principal component axes

PC	1	2	3	4	5	6	7	8	9
Eigen values	2.021	1.417	1.180	1.046	1.010	0.915	0.765	0.636	0.005
% of variance	22.46	15.75	13.11	11.63	11.23	10.17	8.50	7.07	0.06
Cumulative %	22.46	38.22	51.33	62.96	74.19	84.36	92.86	99.94	100.00

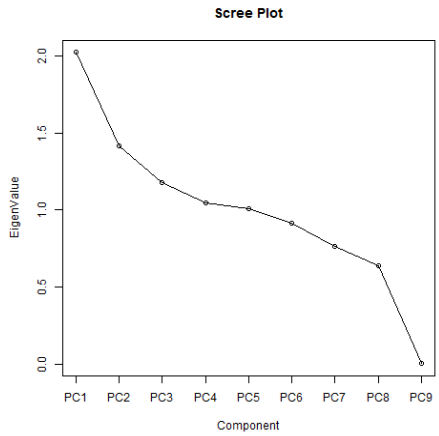

Fig. 2. Eigen value for the corresponding principal components

Table 5. Coefficients and vectors associated with the first three principal components.

	PC1	PC2	PC3	PC4	PC5
Grain Length	-0.4223	0.2725	**0.3343**	-0.2803	-0.2219
Grain Width	**0.5036**	**0.4285**	0.1586	-0.2341	-0.2213
L/Bratio	-0.6759	-0.1917	0.0725	0.0094	0.0310
ASV	0.0162	0.2663	-0.1686	**0.5105**	**0.6156**
GC	0.0054	0.1000	-0.1767	-0.6769	**0.5785**
Amylose	0.0553	0.1654	**0.6910**	**0.3132**	0.1632
Zinc	-0.2480	**0.4251**	-0.0505	-0.0485	0.1456
Iron	0.1902	-0.5831	0.0337	-0.0336	0.0837

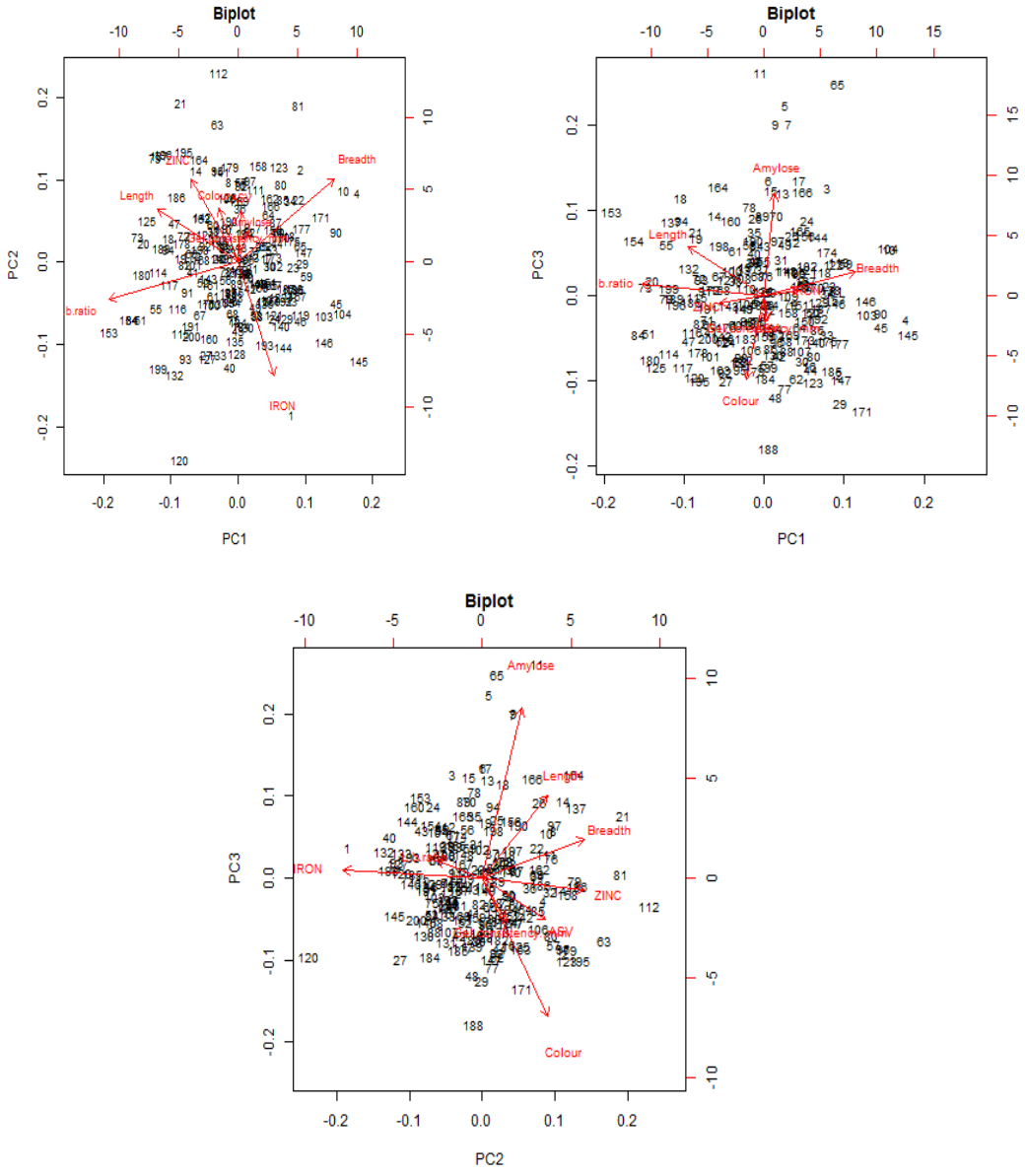

Fig. 3. Biplot diagram of principal components

(Lokesh Gour *et al.,* 2017). The percentage of variance for the five factors was 22.46, 15.75, 13.11, 11.63 and 11.23 per cent. Together they accounted for 74.19 % of the variability of the genotypes used for the diversity analysis. The contributions of the quality characters for the principal component are presented in **Table 5**. Based on factor loadings, an exact picture of the component traits that are contributing to maximum variability is obtained. Grain width, L/B ratio and grain length were a major contributor to the PC1 component while grain width and zinc content to the PC2. Likewise, traits such as GC and amylose to PC3, ASV and amylose to PC4, ASV and GC to PC5 were identified as major contributing traits to their respective PCs. Selection based on these traits would improve the accessions. These traits have the largest participation in the divergence and carry the largest portion of its variability. Similar studies were done by (Nachimuthu *et al*., 2014, Vishnu Varthini *et al.,* 2014, Lokesh Gour *et al.,* 2017, Umadevi *et al.,* 2020 and Sheela *et al*., 2020). The biplot diagrams of principal components were presented in **Fig.3**. The biplot diagram between PC 1 and PC2, PC1 and PC3, PC2 and PC3 explained the distribution and the nature of diversity for both variables and the genotypes. The loading plot depicted that almost all the genotypes and variables showed a high degree of variation. Similar reports were observed by (Ravi *et al.,* 2018).

The rice germplasm studied showed considerable variability for all the traits studied. Cluster analysis based on grain quality grouped the genotypes into two clusters. Considering the nine main components, the first five components explained 74% of total variations in data. Results showed that cluster analysis based on PCA is a more precise indicator and can be a useful tool for the selection of the most efficient genotype. Traits such as grain width, L/b ratio, amylose and Zinc content exhibited higher contributions towards total divergence as selection based on these traits would be given top priority. Above all, the data generated will shorten the time it takes for the plant breeders to screen large populations for potential breeding stock.

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