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Bhawana Sharma
Assistant Professor, Genetics and Plant Breeding, College of Agriculture and Research station, Chhuikhadan, Rajnandgaon Indira Gandhi Krishi, Vishwavidyalaya, Raipur, Chhattisgarh, India

Priyanka Biswas
Research Scholar, Department of Genetics and Plant Breeding, Indira Gandhi Krishi Vishwavidyalaya, Raipur, Chhattisgarh, India

Mangla Parikh
Scientist, Department of Genetics and Plant Breeding, Indira Gandhi Krishi Vishwavidyalaya, Raipur, Chhattisgarh, India

Corresponding Author:
Bhawana Sharma
Assistant Professor, Genetics and Plant Breeding, College of Agriculture and Research station, Chhuikhadan, Rajnandgaon Indira Gandhi Krishi, Vishwavidyalaya, Raipur, Chhattisgarh, India

Multivariate analysis for yield and lodging resistant characteristics of different rice genotypes grown under the irrigated transplanted condition

Bhawana Sharma, Priyanka Biswas and Mangla Parikh

Abstract
Principal component analysis was utilized to examine the variation in 225 rice genotypes and to estimate the relative contribution of various yield and lodging resistant characters for total variability. The PC1 showed 22.155%, while, PC2, PC3, PC4, PC5, PC 6, PC 7 and PC 8 exhibited 11.941%, 10.012%, 7.590%, 7.125%, 6.190%, 5.038% and 4.782% variability. Principal component analysis highlights the characters with maximum variability. The results revealed that PC1 and PC2 yield and yield attributing traits while PC3, PC 4, PC 5, PC6 and PC 7 exhibited better performance in yield, low lodging incidence with good diameter of basal internodes. Bashabhog, IC 299800, Ganga Godavari, RAU 3061, Assamchudi (A179 II), Pratiksha, IC 300381, IC 125666 (Deshi safri) were identified for developing high yielding varieties. Kolijoha exhibited better performance in yield, low lodging incidence with good diameter of basal internodes. Likewise IC 125666 (Chhote dubraj) has relation with high yield and low lodging incidence traits.

Keywords: Principal component, multivariate analysis, yield, lodging resistance, rice

Introduction
Lodging is a serious problem that results in reduced grain crop yield. Lodging causes decreases in yield and quality by reducing photosynthesis in the canopy, increased respiration, reduced translocation of nutrients and carbon for grain filling, and increased susceptibility to pests [1] Lodging resistance is the complex trait, determined by plant height, root thickness, culm daimater, strength and elasticity, and the weight of the upper part of the plant [2, 3]. Many studies have shown that the culm characteristics contributing to lodging resistance include basal internode lengths and thickness, plant height, culm wall thickness, leaf sheath wrapping and thickness [4, 5, 6, 7]. Plant height, particularly the length of basal internodes, is an important component of plant architecture affecting lodging resistance and relating to crop yield [8]. The proportionality between the physical strength in basal internodes and the weight of the upper part determines the vulnerability of a given cultivar to lodging. Accordingly, lodging is occurred in the basal internodes owning to loss of balance between the weight of upper part and the sturdiness of the basal internodes [9, 10]. On the other hand, culm diameter, culm wall thickness and dry matter weight of basal internodes were significantly correlated with the physical strength of rice plant [7, 11].

Breeding lodging-resistant varieties have been highly attended to as a genetic improvement strategy to increase yield in rice, wheat, and other crops [12, 13]. Since the ‘‘green revolution’’ began in the 1960s, the introduction of lodging-resistant semi-dwarf varieties of rice and wheat has achieved great success in increasing the worldwide production of grain [14, 15, 16]. The recessive sd1 (dee-geo-woo-gen) was first introduced into rice for breeding of semi-dwarf varieties [17] and widely distributed across Asia to improve lodging resistance in rice[18, 19, 20]. However, despite the importance of breeding lodging-resistant semi-dwarf rice varieties, the sd1 allele is the only verified semidwarf gene suitable for use to engineer improvements in lodging resistance to date. Given that extensive use of one gene may disadvantage the diversification of rice varieties and hinder the genetic improvement process[21, 22] over time, the development of new genetic resources for breeding lodging-resistant varieties is highly desirable. The exploitation of narrow genetic base in breeding program has resulted in reduced gain in yield improvement. It is felt that local land races and wild species still have a good number of untapped genes. Considering the importance of tall rice, the present study was undertaken with the objective to access the genetic diversity of rice germplasm accessions and identification of better accessions for yield and lodging resistance traits.

Genetic variability studies are important in selection of parents for hybridization [23]. It ensures crop improvement through the use of appropriate selection methods. Characterization of germplasm is of great importance for current and future agronomic and genetic improvement of the crop. These accessions should be thoroughly screened for their resistance to lodging and their associated traits for identification of desirable donors.

Materials and Methods

Source material and experimental site: Plant material for the present investigations consisted of 225 accessions of rice (*Oryza sativa* L.) with seven popular standard checks *viz.*, IR 64, Jaldubi, Indira barani dhan 1, Pusa 1121, Safri17, Indira aerobic 1 and Dubraj selection 1 (Table 1). It includes varieties, red rice and land races. The material was grown in Augmented Completely Randomized Block Design during wet season, 2017 at IGKV, Raipur. The experimental material was planted in four blocks and each block comprised of 55 genotypes. Each entry was transplanted in a plot comprising two rows having one meter length at spacing of 20 cm between rows and 15 cm between plants. Check varieties were randomized within the block. The recommended agronomical practices were adopted to raise good crop in the season. Observations were recorded on five randomly chosen plants of each genotype for various agronomical and lodging related parameters.

Table 1: List of Two Hundred Twenty Five rice genotypes under study

S. No.	Accession Name
1	IC 459184
2	IC 459199
3	IC 459207
4	IC 459212
5	IC 459231
6	IC 459599
7	IC 459643
8	IC459644
9	IC 125044 – Baikoni
10	IC 125505 – Assamchudi
11	IC 125614 – Danigoda
12	IC 125622 - Dashehra matiya
13	IC 125666 - Deshi safri
14	IC 125746 – Bowebarangi
15	IC 125747 - Chhote dubraj
16	IC 125715 - Dubraj II
17	IC 125764 – Dudhmani
18	IC 125776 – Dhanwar
19	IC 125783 –Dhanwar
20	IC 133283
21	IC 133333
22	IC 99264
23	IC 114166
24	IC 299804 – Bhejari
25	IC 299821 – Bhejari
26	IC 299800
27	IC 299879 – Bhimsen
28	IC 300138
29	IC 300381
30	IC 300381 - Chinikapoor
31	IC 300532 – Jiktalu
32	IC 377373 – Kalikhujee
33	IC 377986 – Koha
34	IC 378045 – Kosa
35	IC 378093 – Laji
36	IC 378184 – Luchai
37	IC 378466 – Luchai
38	IC 378472 - Bade luchai
39	IC 378562 – Luchaipeela
40	IC 378547
41	Tulsimanjari
42	Shrikamal
43	Tulsikanthi
44	Acharamati
45	Dangurchudi
46	Ganjeikalli
47	IC 214465
48	IC 124822 – Ajawain
49	IC 124845 – Anjan
50	IC 124891 – Aoleshar
51	IC 124963 – Laxmibhog
52	IC 124964 – Laxmibhog
53	IC 125011 – Bagmuda
54	IC 125138 - Bangoli-1
55	IC 113990 – Baragi
56	Bargi
57	IC 114138 – Bhokala
58	IC 114194 – Bohata
59	Bohita
60	Bohita
61	IC 114196 – Bohita
62	IC 114200 – Bohita
63	IC 114201 – Bohita
64	IC 114202 – Bohita
65	IC 125383 – Chhatri
66	Assamchudi (A:376)
67	IC 125524 – Assamchudi
68	IC 125526 – Assamchudi
69	IC 125644 - Deshi dubraj
70	IC 125629 – Datphally
71	IC 125737 – Dubraj
72	IC 125739 – Dubraj
73	IC 125945 – Gedrel
74	IC 125946 – Gedrel
75	IC 126050 – Gurmatiya
76	IC 126260 – Hansli
77	IC 114273 – Jeeradhan
78	Janjle (J:383)
79	Jhal (J:173)
80	Jhal (J:356)
81	Kasawari (K:1672)
82	IC 300254 – Petabuchhi
83	IC 376532 – Gujiye
84	IC 376536 – Gumdi
85	IC 376537 – Gumdi
86	IC 376538 – Gumdi
87	Agyasal (A:726)
88	Barhasal (B:2919)
89	Dubraj (D:1438)
90	Dubraj (D:1439)
91	Ganga (G:1041)
92	Ganga (G:1042)
93	Ganga (G:1043)
94	Sarojni (S:1739)
95	Savni (S:1740)
96	Barhasal (B:2931)
97	Barhasal (B:2932)
98	Gangaprasad (G:1045)
99	Gangasafri (G:1046)
100	Gangachur (G:1047)
101	Gangaprasad (G:1048)
102	Gangtai (G:1049)
103	Gopal bhog (G:1051)
104	Jouphool (J:543)
105	Jawaphool (J:544)
106	Kalajira (K:2650)
107	Kalajira (K:2621)
108	Kapurbhog (K:2630)
109	Laxmibhog (L:1279)
110	Mohlainbanko (M:1188)
111	Sarsariya (S:1748)
112	Banspatri
113	Modak B
114	RAU 3061
115	RAU 3036
116	RAU 3044
117	Barikumja
118	Jala
119	Mahulakuchi
120	RAU 3073
121	Jalaka
122	Kalajuvam
123	Chhabiswa
124	IGSR 3-1-5
125	IGSR 2-1-6
126	NDRIRRI 67
127	Neelabati
128	Jaigundi
129	Shyamjira
130	Jasmine scented
131	NDR 8022
132	Tulasiful
133	Gopal bhog
134	Dudhkhasa
135	Kolijoha
136	Krishna kamod
137	MILFOR – 6
138	Dulhabhog
139	Hawmmali
140	Malagkit sung song
141	Kalia
142	Dudhsar
143	Lalgori
144	Muigai
145	IR 74728-134-1-3
146	IET 15832
147	IET 15835
148	IC 252242
149	IC 300131
150	IC 300202
151	IC 332998
152	IC 333018

153	IC 352794
154	IC 376393
155	IC 376567
156	IC 376653
157	IC 377051
158	IC 377173
159	IC 381834
160	IC 451788
161	IC 466813
162	IC 466877
163	IC 554801
164	IC 577033
165	IC 577109
166	AMAJHOPA (A:200)
167	Khaju Jhopa (K:1788)
168	Hathi Panjari (H:144)
169	Thakur Bhog (T:114)
170	BhainsaMundariya (B:1394)
171	Katina (K:1591)
172	Nagodar (N:806)
173	Soth (S:468)
174	KDML-105
175	IC22787 (RP45941-121-148-24-11)
176	Kanika bhog
177	Thaland/CBC

178	Co Acc167(T167)
179	Guinata
180	Tarunbhog
181	Hiaw Hawm mali
182	Hung-mi-hsiang-ma-Tsan
183	Luchai
184	Kherkakuchi
185	Pratiksha
186	Pataniyajhuli
187	Jheeli
188	Dubraj
189	Agyasaal
190	Maasuri
191	Barhasaal
192	Barhasaal-1
193	Barhasaal-2
194	Menjharidhan
195	Bhunduluchai
196	Barhasaal-3
197	Ganga-Godavari
198	Bashabhog
199	Nariyalful
200	Badshahbhog
201	Kanakgopala
202	ShreeRam

203	Anjagdhan
204	Matkodhan
205	Tulsigatti
206	Kakdodhan
207	Chinnore (C:395)
208	Assamchudi (A:179 II)
209	Lalmua (L:23)
210	Bade Luchai (B:2719)
211	Ludako (L:793 II)
212	Matko (M:417 II)
213	Nagpuri (N:761)
214	Parewadhan (P:469 IV)
215	Pihi kirwa (P:368)
216	Safri (S:790)
217	Deshi safri (D:1311)
218	Saraiya (S:258 II)
219	IR 64 (CH 1)
220	Jaldubi (CH 2)
221	Indira barani dhan1 (CH 3)
222	Pusa1121 (CH 4)
223	Safri17 (CH 5)
224	Indira aerobic1 (CH 6)
225	Dubraj selection 1 (CH 7)

Assessment of characteristics: All the agronomical traits studied *viz.*, days to 50 per cent flowering (DF), flag leaf length (FLL), flag leaf width (FLW), plant height (PH), panicle length (PL), number of productive tillers per plant (PTP), number of spikelets per plant (SP), number of filled spikelets per plant (FSP), spikelet fertility % (SF) , thousand grain weight (TGW), grain yield per plant (GYP), biological yield per plant (BYP), harvest index (HI), upper biological yield (dry weight of the plant above 40 cm) (UBY), lower biological yield (dry weight of the plant below 40 cm) (LBY), grain yield / upper biological yield ratio (GY/UBY), upper biological yield / lower biological yield ratio (UBY/LBY), culm length (CL), internode numbers (IN), diameter of basal internode I (DBI), diameter of basal internode II (DBII), basal internode length I (BIL I), basal internode length II (BIL II), lodging incidence (LI %) and transformed lodging incidence (TLI%). Lodging related traits were determined at 30 days after 50 per cent flowering. Five representative main stems were sampled to measure the characteristics related to lodging in each plot. Diameter of basal internode I (first from ground) and diameter of basal internode II (second from ground) was measured in mm at the mid portion of the main culm. Whereas, length of basal internode I (first from ground) and length of basal internode II (second from ground) was measured in cm. For upper biological yield, dry weight of the plant above 40 cm was taken in gm after harvesting likewise dry weight of the plant below 40 cm was taken in gm after harvesting for lower biological yield. The ratio of grain yield to the biological yield was calculated in percentage and expressed as harvest index. Lodging incidence was taken in percentage at the time of heading to maturity. It was calculated as: Number of lodged plants / Total number of plants × 100. To obtain transformed lodging incidence %, an arc sin transformation is used in lodging incidence %.

Statistical analysis: In order to identify the patterns of variation, Principal component Analysis (PCA) was conducted. The observations recorded were statistically analyzed using XLSTAT 2014 software. Those PCs with Eigen values greater than one were selected as proposed by Jeffers (1967) [24]. The principal component analysis was computed using the following equation:

PCA

$$PC1 = \sum_{1}^{p} a\, jXj$$

Where; PC = Principal component, a1j = Linear coefficient – Eigen vectors

Results and Discussion

Principal component analysis and Cluster analysis

Principal Component Analysis (PCA) is a powerful tool in modern data analysis because this is a well-known multivariate statistical technique which is used to identify the minimum number of components, which can explain maximum variability out of the total variability [25, 26] and also to rank genotypes on the basis of PC scores. Principal components are generally estimated either from correlation matrix or covariance matrix. When the variables are measured in different units, scale effects can influence the composition of derived components. In such situations it becomes desirable to standardize the variables. The results of the principal component analysis substantially confirms the pattern of character co-variation among the genotypes studied. It also identified the characters that contribute most to the variation within a group of entries [27]. The biological meaning of the principal components can be accessed from contribution of the different variables to each principal component according to the Eigen vectors [28]. The results of the principal component analysis show that different characters contributed differently to the total variation as indicated by their Eigen vectors as well as their weight and loading on the different principal axes. Each component score obtained is a linear combination of the traits similar to an index, such that the maximal amount of variance is shown on the first principal component, second maximal amount is shown on the second component, third maximal amount is shown on the third component and so on.

Principal component analysis was performed for all yield and its ancillary traits of rice genotypes to reveal the pattern of data matrix for determination and identification of selection criteria. The result of PCA explained the genetic diversity among the rice accessions. According to Brejda *et al*. (2000) [29], data were considered in each components with Eigen value >1 which determined at least 10% of the variation. The higher Eigen values were considered as best representative of system attributes in principal components. Statistically, first few principal components usually account for most of the variation in the original set of data. The total variance is simply the sum of variances of these variables [30]. The arithmetic sign of the coefficient is irrelevant since a common rule of thumb for determining the significance of a trait coefficient is to treat coefficient greater than 0.3 as having a large enough effect to be considered important [31]. Traits having less than 0.2 coefficient value were considered to be of no effect to the overall variation observed in the present study.

Out of 24, eight principal components exhibited more than one eigen value and showed about 74.832% variability among the traits studied for each genotypes. So, these eight principal components were given due importance for the further explanation. For each principal axis there are numbers of character contributing to the total variation. The PC1 had 22.155%, PC2 showed 11.941%, PC3 exhibited 10.012%, PC4 showed 7.590 %, PC5 showed 7.125 %, PC6 showed 6.190 %, PC7 showed 5.038 % and PC8 showed 4.782 % variability among the genotypes for the traits under study. Eigen value and variance associated with each principal, decreased gradually and stopped at 0.006 and 0.023%, respectively

Table 2: Eigen value, % variance and cumulative variances of rice germplasm

Principal Components	Eigen value	% Total Variance	Cumulative variance %
PC1	5.539	22.155	22.155
PC 2	2.985	11.941	34.096
PC 3	2.503	10.012	44.108
PC 4	1.898	7.590	51.698
PC 5	1.781	7.125	58.823
PC 6	1.548	6.190	65.013
PC 7	1.259	5.038	70.051
PC 8	1.195	4.782	74.832
PC 9	0.963	3.852	78.685
PC 10	0.880	3.521	82.205
PC 11	0.777	3.107	85.312
PC 12	0.734	2.937	88.249
PC 13	0.665	2.661	90.910
PC 14	0.557	2.227	93.138
PC 15	0.495	1.980	95.118
PC 16	0.429	1.718	96.835
PC 17	0.290	1.161	97.997
PC 18	0.242	0.970	98.967
PC 19	0.087	0.347	99.314
PC 20	0.086	0.345	99.658
PC 21	0.056	0.223	99.882
PC 22	0.016	0.064	99.946
PC 23	0.008	0.032	99.977
PC 24	0.006	0.023	100.000

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. Within each PC, only highly loaded traits were retained for further explanation (Table 3). The first PC was more related to BYP, UBY, PH and CL so it must be considered for direct selection. In second principal component GYP, HI, DWP and GY/UBY were the more related traits. The third principal component exhibited positive effects for TGW. It showed maximum variation for these characters. The fourth principal component was positively more related to LBY and negatively related to TLI. Likewise PC 5 was positively more related to DB I and DB II. The PC6 was positively more related with BIL I and BIL II, while PC7 was highly loaded with UBY/LBY. The PC8 was highly loaded with FLL and FLW. First three PCs were predominantly related to yield and yield contributing traits, although next three PCs were related with lodging related traits.

Table 3: Principal components for yield and lodging resistant characters of rice accessions

Characters	Principal Components							
	PC1	PC 2	PC 3	PC 4	PC 5	PC 6	PC 7	PC 8
DF	0.488	-0.300	-0.115	0.052	0.280	-0.395	0.135	-0.135
FLL	0.362	-0.086	0.157	-0.045	-0.027	-0.021	-0.385	0.502
FLW	0.380	0.142	0.438	-0.120	0.018	-0.061	-0.090	0.502
PH	0.761	-0.220	0.224	-0.019	-0.076	0.120	-0.334	-0.275
PL	0.307	-0.154	-0.153	-0.311	-0.100	-0.223	-0.291	-0.337
PTP	0.197	-0.112	-0.009	0.094	-0.315	-0.176	0.142	-0.280
SP	0.363	0.363	-0.692	-0.216	0.189	-0.060	-0.246	0.116
FSP	0.389	0.411	-0.732	-0.178	0.172	0.009	-0.177	0.080

SF%	0.263	0.323	-0.369	0.056	0.007	0.223	0.156	-0.076
TGW	0.094	0.278	0.757	-0.031	-0.050	0.115	0.140	0.069
GYP	0.204	0.867	0.140	0.091	-0.111	-0.035	0.062	-0.245
BYP	0.792	0.225	-0.082	0.383	-0.239	0.131	0.175	-0.019
HI	-0.470	0.715	0.272	-0.201	0.084	-0.153	-0.113	-0.235
UBY	0.774	0.254	-0.095	0.020	-0.354	0.034	0.322	0.010
DWP	0.382	0.628	0.051	-0.118	0.073	0.113	-0.043	0.265
LBY	0.528	0.102	-0.033	0.759	0.012	0.221	-0.098	-0.053
GY/UBY	-0.471	0.627	0.311	0.125	0.209	-0.044	-0.293	-0.264
UBY/LBY	0.209	0.130	-0.021	-0.706	-0.364	-0.200	0.400	-0.007
CL	0.756	-0.265	0.208	-0.019	-0.076	0.149	-0.271	-0.215
IN	0.400	0.043	0.188	-0.041	-0.435	-0.164	-0.012	0.131
DBI I	0.585	-0.031	0.193	0.057	0.541	-0.456	0.148	-0.032
DBI II	0.596	0.030	0.243	0.067	0.509	-0.455	0.141	0.012
BIL I	0.207	-0.119	0.037	-0.259	0.464	0.512	0.284	-0.118
BIL II	0.347	-0.082	0.199	-0.358	0.384	0.589	0.119	-0.076
TLI	0.422	-0.115	0.220	-0.431	-0.161	0.072	-0.337	-0.180

Scree Plot: Scree plot explained the percentage of variance associated with each principal component obtained by drawing a graph between eigen values and principal component numbers. PC1 showed 22.155 % variability with eigen value 5.539 which then declined gradually herewith Nachimuthu *et al.* 2014 [32] also got highest variability in PC1 with eigen value more than 1.0. Curve line is obtained after eight PC tended to become straight with little variance observed in each PC. From the graph, it is clear that the maximum variation was observed in PC1 in comparison to other 24 PCs. So, selection of lines from this PC will be useful **(**Fig. 1). Those principal components having more than one eigen value that showed more variation among the rice genotypes for the selection of the diverse parents

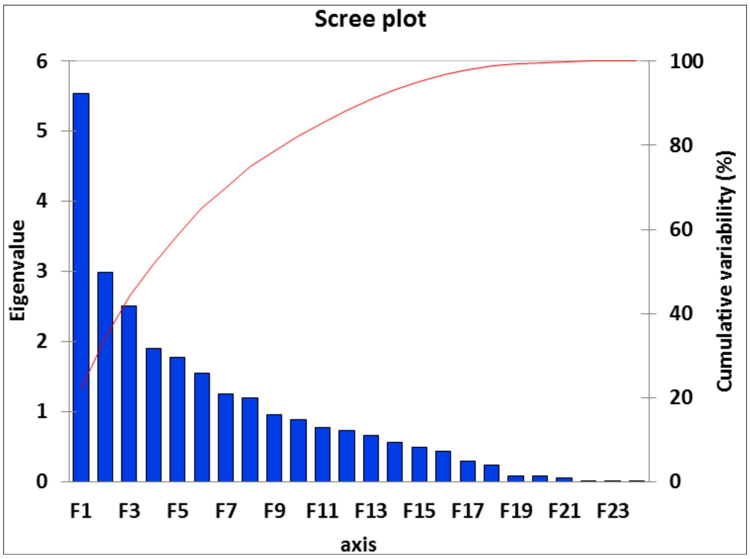

Fig 1: Scree plot of rice germplasm between Eigen value and Principal Components

The prominent characters coming together in different principal components and contributing towards explaining the variability have the tendency to remain together which may be kept into consideration during utilisation of these characters in breeding programme. Through PCA we could identify the number of plant characters which are responsible for the observed genotypic variation within a group. PCA also helps us to indentify the characters which have great impact of phenotype of different accessions of rice, and this is very much important to the selection procedure of breeding programme. This result is in agreement with the findings of Ashfaq *et al.* (2012); Kumar *et al.* (2013); Chakraborty *et al.* (2013); Sinha and Mishra, 2013 and Nachimuthu *et al.* (2014) [33, 34, 35, 32]. Chakravorty *et al.* (2013) [35] identified six principal components with eigen value greater than 1.0 and that explained 75.9% of the total cumulative variance within the axes could effectively be used for selection among them.

PC scores of the germplasm selected on the basis of >1.0 each PCs

Based on the PC scores of the each component (PC 1, PC 2, PC3, PC4, PC5, PC6, PC7 and PC8) having positive values & more than >1.0 in each PCs, few germplasm accessions are selected (Table 4).

Table 4: Top selected accessions on the basis of PC scores in each Principal components.

PC 1	PC 2	PC 3	PC 4	PC 5	PC 6	PC 7	PC 8
221 (Indira barani dhan 1, 3.465)	198 (Bashabhog 12.099)	27(IC 299879 – Bhimsen 5.003)	168 (Hathi Panjari (H:144) 5.294)	135 (Kolijoha 8.014)	135 (Kolijoha 8.482)	41 (Tulsimanjari 3.617)	2 (IC 459199 3.71)
31 (IC 300532 – Jiktalu,	26 (IC 299800	114 (RAU 3061	135 (Kolijoha	64 (IC 114202 –	40 (IC 378547	206 (Kakdodhan	6 (IC 459599

3.331)	4.424)	3.218)	3.47)	Bohita3.768)	3.227)	3.44)	3.402
172 (Nagodar (N:806) , 2.668)	197 (Ganga-Godavari 2.869)	158 (IC 377173 3.119)	15 (IC 125747 - Chhote dubraj 3.328)	216 (Safri (S:790) 3.713)	75 (IC 126050 - Gurmatiya 2.993)	173 (Soth (S:468) 3.358)	179 (Guinata 2.478)
222 (Pusa1121, 2.456)	114 (RAU 3061 2.732)	168 (Hathi Panjari (H:144) 2.73)	30 (IC 300381 - Chinikapoor 2.841)	26 (IC 299800 3.233)	26 (IC 299800 2.609)	135 (Kolijoha 3.345)	130 (Jasmine scented 2.213)
177 (Thaland/CBC, 2.269)	208 (Assamchudi (A:179 II) 2.25)	41 (Tulsimanjari 2.709)	77 (IC 114273 - Jeeradhan2.631)	102 (Gangtai (G:1049) 2.825)	178 (Co Acc167(T167) 2.584)	92(Ganga (G:1042) 2.951)	131 NDR 8022 2.192)
198 (Bashabhog, 2.213)	185 (Pratiksha 1.953)	115 (RAU 3036 2.675)	155 (IC 376567 1.855)	162 (IC 466877 2.419)	64 (IC 114202 – Bohita 2.325)	89(Dubraj (D:1438) 2.86)	42 (Shrikamal 2.005)
130 (Jasmine scented, 2.141)	29 (IC 300381 1.877)	43 (Tulsikanthi 2.655)	7 (IC 459643 1.759)	217 (Deshi safri(D:1311) 2.41)	122 (Kalajuvam 2.319)	125 (IGSR 2-1-6 2.532)	134 (Dudhkhasa 1.891)
69 (IC 125644 - Deshi dubraj,2.058)	13 (IC 125666- Deshi safri1.728)	25(IC 299821 – Bhejari 2.423)	178 (Co Acc167(T167) 1.753)	139 (Hawmmali 2.361)	109(Laxmibhog (L:1279) 2.25)	137 (MILFOR – 6 2.07)	66(Assamchu di (A:376) 1.887)
112 (Banspatri, 1.97)	156 (IC 376653 1.642)	181 (Hiaw Hawm mali2.344)	164 (IC 577033 1.661)	19 (IC 125783 – Dhanwar 2.194)	70 (IC 125629 - Datphally 1.895)	15 (IC 125747 - Chhote dubraj 1.82)	103 (Gopal bhog (G:1051) 1.801)
157 (IC 377051, 1.847)	15 (IC 125747 - Chhote dubraj1.624)	113 (Modak B 2.275)	214 Parewadhan (P:469 IV)1.605)	150 (IC 300202 1.723)	173 (Soth (S:468) 1.766)	193 (Barhasaal-2 1.639)	163 (IC 554801 1.763)
24 (IC 299804 – Bhejari,1.818)	124 (IGSR 3-1-5 1.548)	127 (Neelabati 2.06)	182 (Hung-mi-hsiang-ma-Tsan1.594)	215 (Pihi kirwa (P:368)1.613)	3 (IC 459207 1.723)	57 (IC 114138 – Bhokala 1.508)	122 (Kalajuvam 1.729)
100 (Gangachur (G:1047), 1.59)	175 (IC22787(RP45941-121-148-24-11) 1.503)	122 (Kalajuvam 2.032)	6 IC 459599 1.588)	46 (Ganjeikalli 1.539)	58 (IC 114194 – Bohata 1.638)	171 (Katina (K:1591) 1.498)	58 (IC 114194 – Bohata 1.673)
64 (IC 114202 – Bohita, 1.445)	34 (IC 378045 – Kosa 1.485)	152 (IC 333018 1.871)	76 (IC 126260 - Hansli 1.541)	205 (Tulsigatti 1.511))	105 (Jawaphool (J:544) 1.533)	107 (Kalajira (K:2621) 1.495)	166 (AMAJHOPA (A:200) 1.569)
179 (Guinata, 1.39)	135 (Kolijoha 1.469)	134 (Dudhkhasa 1.76)	57 (IC 114138 – Bhokala 1.511)	170 (BhainsaMundariya (B:1394) 1.452)	180 (Tarunbhog 1.504)	108 (Kapurbhog (K:2630) 1.398)	41 (Tulsimanjari 1.559)
125 (IGSR 2-1-6, 1.374)	176 (Kanika bhog 1.386)	13 (IC 125666- Deshi safri 1.745)	68 (IC 125526 - Assamchudi 1.44)	39 (IC 378562 – Luchaipeela 1.448)	159 (IC 381834 1.478)	120 (RAU 3073 1.373)	17 (IC 125764 – Dudhmani 1.538)
120 (RAU 3073, 1.357)	50 (IC 124891 – Aoleshar 1.344)	133 (Gopal bhog 1.681)	83 (IC 376532 - Gujiye 1.375)	24 (IC 299804 – Bhejari 1.438)	170 (Bhainsa Mundariya (B:1394) 1.471)	141 (Kalia 1.369)	89 (Dubraj (D:1438) 1.504)
102 (Gangtai (G:1049), 1.331)	92 (Ganga (G:1042) 1.325)	203 (Anjagdhan 1.59)	78 (Janjle (J:383) 1.331)	60 (Bohita 1.401)	138 (Dulhabhog 1.423)	65 (IC 125383 - Chhatri 1.362)	107 (Kalajira (K:2621) 1.487)
175 (IC22787(RP45941-121-148-24-11), 1.269)	157 (IC 377051 1.322)	202 (ShreeRam 1.419)	150 (IC 300202 1.323)	40 (IC 378547 1.249)	57 (IC 114138 – Bhokala 1.418)	111 (Sarsariya (S:1748) 1.343)	176 (Kanika bhog 1.476)
208 (Assamchudi (A:179 II),1.25)	201 (Kanakgopala 1.223)	169 (Thakur Bhog (T:114)1.252)	165 (IC 577109 1.322)	57 (IC 114138 – Bhokala 1.188)	216 (Safri (S:790) 1.333)	138 (Dulhabhog 1.313)	51(IC 124963 – Laxmibhog 1.418)
54(IC 125138 - Bangoli-1, 1.191)	7 (IC 459643 1.029)	102(Gangtai (G:1049) 1.243)	67 (IC 125524 - Assamchudi 1.265)	16 (IC 125715 - Dubraj II 1.111)	175 (IC22787(RP45941-121-148-24-11) 1.31)	42 (Shrikamal 1.246)	37(IC 378466 – Luchai 1.302)
137 (MILFOR – 6,	153 (IC 352794	69 (IC 125644 -	189 (Agyasaal	38 (IC 378472 -	78 (Janjle (J:383)	105 (Jawaphool	223 (Safri17

1.107)	1.012)	Deshi dubraj 1.141)	1.256)	Bade luchai 1.103)	1.306)	(J:544) 1.244)	1.256)
119 (Mahulakuchi, 1.073)	3 (IC 459207 1.003)	97 (Barhasal (B:2932) 1.135)	216 (Safri (S:790) 1.223)	190 (Maasuri 1.036)	42 (Shrikamal 1.256)	32 (IC 377373 – Kalikhujee 1.229)	148 (IC 252242 1.177)
37 IC 378466 – Luchai, 1.045)	136 (Krishna kamod 1.002)	131 (NDR 8022 1.119)	132 (Tulasiful 1.159)	142 (Dudhsar 1.015)	2 (IC 459199 1.237)	50(IC 124891 – Aoleshar 1.186)	35 (IC 378093 – Laji1.174)
58 (IC 114194 – Bohata,1.04)		173 (Soth (S:468) 1.103)	194 (Menjharidhan 1.09)		28 (IC 300138 1.22)	69(IC 125644 - Deshi dubraj 1.177)	192 (Barhasaal-1 1.173)
197 (Ganga-Godavari, 1.016)		150 (IC 300202 1.081)	128 (Jaigundi 1.075)		62 (IC 114200 – Bohita 1.208)	61 (IC 114196 – Bohita 1.146)	20 (IC 133283 1.151)
		206 (Kakdodhan 1.013)	190 (Maasuri 1.072)		53 (IC 125011 – Bagmuda 1.204)	3 (IC 459207 1.084)	65(IC 125383 - Chhatri 1.137)
		209(Lalmua (L:23) 1.007)	160 (IC 451788 1.071)		22 (IC 99264 1.194)	196 (Barhasaal-3 1.037)	43 (Tulsikanthi 1.136)
			63(IC 114201 – Bohita 1.025)		174 (KDML-105 1.162)	220 (Jaldubi 1.021)	139 (Hawmmali 1.101)
			192 (Barhasaal-1 1.023)		192 (Barhasaal-1 1.151)	132 (Tulasiful 1.016)	155 (IC 376567 1.101)
					86 (IC 376538 - Gumdi 1.083)		208 (Assamchudi (A:179 II) 1.086)
							48 (IC 124822 – Ajawain 1.078)
							28 (IC 300138 1.063)
							56 (Bargi 1.033)

It can be observed that germplasm Bashabhog comes in PC1 and PC2 both which has relation with yield and yield attributing trait both. Kolijoha comes in PC3, PC4, PC5, PC 6 and PC 7 which exhibited better performance in yield, low lodging incidence with good diameter of basal internodes. IC 125666 (Chhote dubraj) comes in PC2, PC4 and PC7 has relation with yield and low lodging incidence traits. So such germplasm were the best for both yield and lodging resistance traits can be recommended directly for cultivation programme. Bashabhog, IC 299800, Ganga Godavari, RAU 3061, Assamchudi (A179 II), Pratiksha, IC 300381, IC 125666 (Deshi safri) exhibited high score in PC2 (Table 6). So, selection of germplasms with high score in PC2 will be desirable for developing high yielding varieties.

A further understanding was obtained by plotting the PC scores for individual observations in relation to the axes of PC1 and PC2 (Fig. 2). Two dimensional scaling of the genotypes by the first two PCs showed two distinct groups of genotypes. Genotype 198 (Bashabhog) was the most distinct from the others.

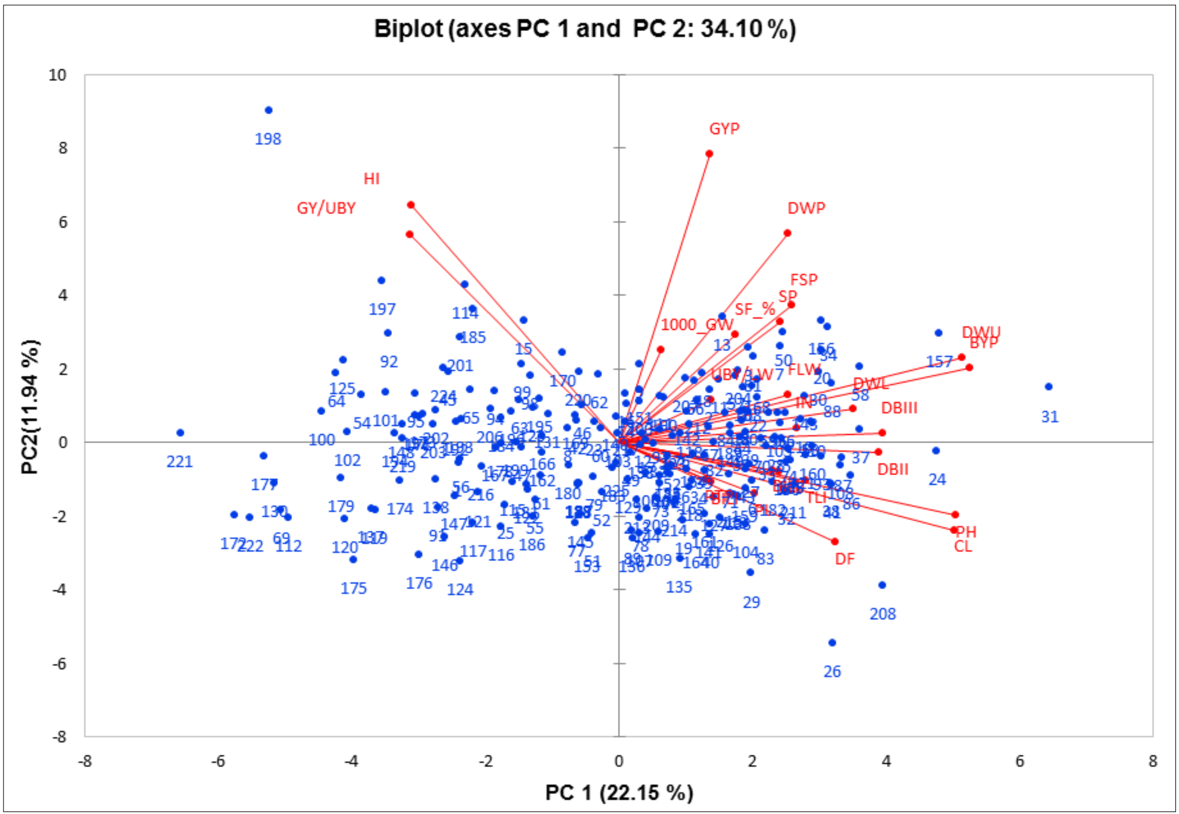

Fig 2: Distribution and grouping of 225 rice accessions across first two components based on PCA

Conclusions

This study, which used multivariate techniques to assess the extent of genetic variation for yield and lodging resistant traits in two hundred twenty five rice accessions, was a first step in gaining an insight into the germplasm divergence, which is an important step towards an efficient exploitation of genetic resources of rice genotypes. Principal component analysis was utilized to examine the variation and to estimate the relative contribution of various yield and lodging resistant characters for total variability. The PC1 showed 22.155%, while, PC2, PC3, PC4, PC5, PC 6, PC 7 and PC 8 exhibited 11.941%, 10.012%, 7.590%, 7.125%, 6.190%, 5.038% and 4.782% variability. It can be concluded that principal component analysis highlights the characters with maximum variability.

The results revealed that PC1 and PC2 yield and yield attributing traits while PC3, PC 4, PC 5, PC6 and PC 7 exhibited better performance in yield, low lodging incidence with good diameter of basal internodes.So, intensive selection procedures can be designed to bring about rapid improvement of yield and lodging resistant characters.

Bashabhog, IC 299800, Ganga Godavari, RAU 3061, Assamchudi (A179 II), Pratiksha, IC 300381, IC 125666 (Deshi safri) will be desirable for developing high yielding varieties. It can be observed that germplasm Kolijoha exhibited better performance in yield, low lodging incidence with good diameter of basal internodes. IC 125666 (Chhote dubraj) has relation with yield and low lodging incidence traits. So such germplasm were the best for both yield and lodging resistance traits can be recommended directly for cultivation programme.

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