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## Phenotypic divergence and variability analysis for yield and lodging resistant characteristics of different rice genotypes grown under the irrigated transplanted condition

Priyanka Biswas, Bhawana Sharma and Mangla Parikh

### Abstract

Two Hundred twenty five rice (*Oryza sativa* L.) genotypes including seven standard checks were evaluated during *khariif* 2015 for phenotypic characterization and assessment of variability parameters for yield and lodging resistance under irrigated transplanted condition. The result of ANOVA showed that there were considerable inherent genetic differences among check varieties for different characters. Among quantitative traits, the coefficient of variation was more than 10% for all the characters with the exception of days to 50 per cent flowering and panicle length. Highest coefficient of variation was recorded for grain yield per plant (34.19%) followed by harvest index (33.15%). Similarly, wide range of genetic variability was observed for almost all the lodging resistance traits. Highest coefficient of variation was recorded for lodging incidence percentage (65.94%). Based on the results of the adjusted means values, Hathi Panjari (H:144) identified superior for highest 1000-grain weight (47.01); IC 299800 for productive tillers per plant (12.53); whereas the accession Bashabhog was found superior for grain yield per plant (37.74) and harvest index (84.53). Minimum (0%) lodging incidence showed by IC 459207, IC 459643, IC125622 (Dashehra matiya), IC 125666 (Deshi safri) and Ganjeikalli.

**Keywords:** phenotypic divergence, variability, yield, lodging resistance, rice.

### Introduction

Food scarcity is becoming a serious global problem because of the constantly increasing world population and the effects of global climate change on food production. In the 1960s, remarkable success was attained in increasing grain production through the development and widespread adoption of high-yielding, semi-dwarf varieties of rice. Extensive cultivation of these varieties led to a major increase in grain production, consequently averting a predicted large-scale famine. This phenomenal achievement was referred to as the Green Revolution. A major factor in the Green Revolution was the widespread use of fertilizers in the cultivation of high-yielding, semi-dwarf varieties. A recent trend in rice breeding has been the development of semi-dwarf rice cultivars, which are suitable for high-density cultivation with intensive use of fertilizers [13]. These cultivars typically feature a short sturdy culm, multiple tillers and upright leaves, and their high productivity has been reported in numerous studies [24]. However, over-reliance on semi-dwarf rice cultivars developed using the single semidwarf gene *sd1* [6,7] is not without its own intrinsic limitations. The attendant risks are especially clear in view of rapidly growing pressure for food supply to support an ever expanding world population in the 21<sup>st</sup> century.

In an effort to avert another looming food crisis, rice breeders are developing new varieties with increased plant biomass and harvest index to further increase the grain yield. However, the yield potential of inbred and hybrid rice cultivars has apparently reached a plateau in the improvement of biomass and harvest indices [14]. Several approaches have been proposed to breach the yield ceiling of rice cultivars. One approach is to find a new plant type with the ideal morphology, large panicles, photosynthetic efficiency, and lodging resistance [25]. Long culm rices have particular characteristics that favour high biomass production. Notably, long culm rices have lower leaf area density than short culm rices because of their greater height. A lower leaf area density is associated with high gas diffusion efficiency inside stands, which provide a strong CO<sub>2</sub> supply for photosynthesizing leaves [20]. If the disadvantage of lodging in

long culm rices could be overcome, their potential for increasing the biomass yield could be realized.

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 [9]. Lodging resistance is the complex trait, determined by plant height, root thickness, culm diameter, strength and elasticity, and the weight of the upper part of the plant [11,12]. 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 [1,10,19]. In general, the basal internodes of the rice plant support the heavier upper part, including leaves, panicles and upper stem. 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 owing to loss of balance between the weight of upper part and the sturdiness of the basal internodes [16, 22]. 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 [17, 18].

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 morphological 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 [2]. 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

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 morphological, agronomical and lodging related parameters.

**Table1:** List of 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	Jaijundi
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	Kanagopala
202	ShreeRam
203	Anjagadhan
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)
CH 1	IR 64
CH 2	Jaldubi
CH 3	Indira barani dhan1
CH 4	Pusa1121
CH 5	Safri17
CH 6	Indira aerobic1
CH 7	Dubraj selection 1

All the agro-morphological traits studied *viz.*, basal leaf sheath colour, leaf blade colour, auricle colour, ligule colour, collar colour, stigma colour, anthocyanin coloration of internode, panicle type, panicle exertion, awning, days to 50 per cent flowering (DTF), flag leaf length (FLL), flag leaf width (FLW), plant height (PH), panicle length (PL), number of effective tillers per plant (ETP), 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%).

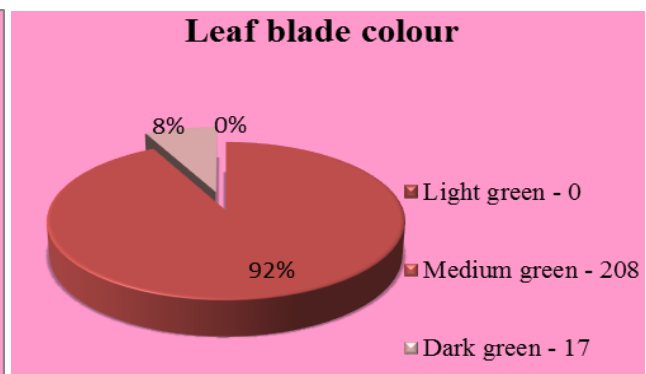
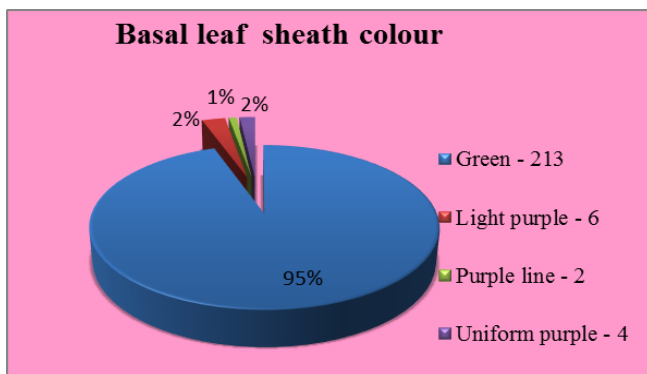
Lodging related traits were determined at 30 days after 50 per cent flowering. Five representative main stems were sampled to measure the characteristics related to lodging in each plot. Diameter of basal internode I (first from ground) and diameter of basal internode II (second from ground) was measured 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

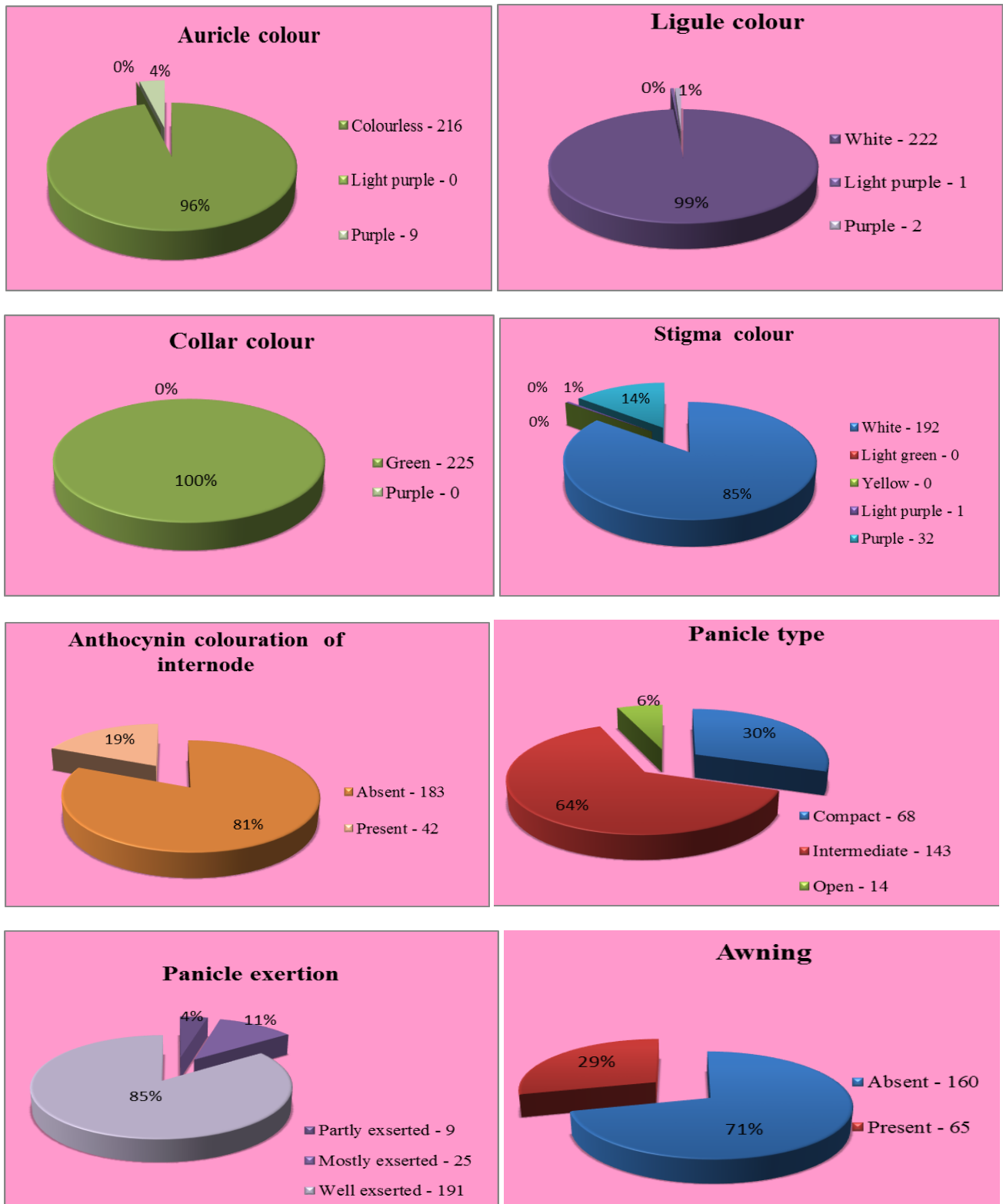
lodged plants / Total number of plants  $\times$  100. To obtain transformed lodging incidence%, an arc sin transformation is used in lodging incidence%.

Frequency distribution was computed to categorize the genotypes into different classes. Analysis of variance using descriptive statistics such as mean, standard deviation, and coefficient of variation for each agronomical studied trait were calculated. ANOVA is calculated using online statistical package for augmented block design analyses in the IASRI website (<http://www.iasri.res.in/spadweb/default.aspx>). Statistical analysis was done according to the standard statistical procedures [4, 5].

## Results and Discussion

**Morphological characterization:** Any variety can be identified through its distinguished stable morphological traits. The stable morphological traits can be used as reliable morphological markers for identification of a variety. Each variety must have certain novel diagnostic features which will distinguish a variety from others. Such diagnostic characters should uniformly present in the population and should be inherited in next generation then only the character is supposed to be stable and can be used as morphological marker traits to distinguish that variety. To establish distinctness among rice germplasm accessions, a total of eighteen qualitative traits were used. Qualitative traits are considered as morphological markers in the identification of rice, because they are less influenced by environmental changes. Qualitative characters are important for plant description [15] and mainly influenced by the consumers preference, socio-economic scenario and natural selection [8]. Frequency distribution for ten qualitative traits is presented in Fig. 1. Frequency distribution for the traits showed a lot of variability among the accessions evaluated. The variable expressions of most of the morphological characters were recorded for different accessions except collar colour. A majority of genotypes were found to be possessed green basal leaf sheath colour (95.0%), green leaf blade colour (92.0%), colourless auricle (96.0%), white ligule (99.0%), white stigma (85.0%), intermediate panicle type (64.0%), well exerted panicle (85.0%) and no awning (71.0%). On the basis of morphological characterization the phenotypic diversity was present in all the genotypes under study for their respective traits. These results are in agreement with some earlier findings reported by Chouhan *et al.* and Sarawgi *et al.* [3, 23].





**Fig 1:** Frequency distribution for ten morphological characters in 225 genotypes of rice.

**Variability parameters:** The basic requirement in any breeding programme is the availability of genetic variability (presence of differences among the individuals of a plant population), without which neither the improvement of existing lines nor development of new lines is feasible. The analysis of variance of mean square values of all the

morphological traits are presented in the Table 2. ANOVA (Analysis of variance) indicated significant ( $P < 0.01$  &  $0.05$ ) effects of genotypes in almost all the traits studied. A wide range of genetic variability was observed for most of the quantitative traits base on the descriptive statistics for yield and lodging related traits (Table 3).

**Table 2:** Analysis of variance for different quantitative and lodging characters in 225 rice genotypes

S.No.	Sources of Variation	Mean Sum of Squares		
		Check	Block	Error
	Characters	6 df	3 df	18 df
1.	DTF (days)	310.833**	7.476	22.865
2.	FLL (cm)	263.652**	9.107	6.074
3.	FLW (cm)	0.321**	0.018	0.079
4.	PH (cm)	2514.112**	63.452	141.826
5.	PL (cm)	14.066*	10.071	3.921
6.	ETP	0.836	0.390	0.723
7.	SF%	298.621**	10.724	62.932
8.	TGW (g)	30.198*	8.742	8.405
9.	GYP (g)	32.658*	10.515	10.343
10.	BYP (g)	425.199*	46.472	136.314
11.	HI (%)	161.953	58.580	61.279
12.	UBY (g)	246.592	45.696	99.421
13.	LBY (g)	49.978*	7.337	16.456
14.	GY/UBY	0.028	0.055	0.050
15.	UBY/LBY	0.541	0.244	0.252
16.	CL (cm)	2210.210**	89.670	114.220
17.	IN	1.470**	0.011	0.082
18.	DB I (mm)	6.471**	0.332	0.264
19.	DB II(mm)	6.831**	0.250	0.300
20.	BILI (mm)	5.273**	0.454	0.319
21.	BILII (mm)	51.925**	0.225	4.306
22.	LI (%)	4030.952**	308.333	283.333
23.	TLI (%)	3059.975**	209.076	174.542

**Note :-** \*\*Significant at 1% level of probability, \* Significant at 5% level of probability, df = degree of freedom

DTF= Days to 50% flowering, FLL = Flag leaf length, FLW = Flag leaf width, PH = Plant height, PL = Panicle length, ETP = Effective tillers per plant, SF% = Spikelet fertility%, TGW = 1000 grain weight, GYP = Grain yield per plant, BYP = Biological yield per plant, HI = Harvest index, UBY = Upper biological yield ( Dry of plant above 40 cm), LBY= Lower Biological yield (Dry weight of plant below 40 cm), GY/UBY = Grain yield/Upper biological yield Ratio, UBY/LBY = Upper biological yield/ Lower Biological Yield, CL = Culm length (cm), IN = Internode number, DB I = Diameter of basal internode I, DB II = Diameter of basal internode II, BIL I = Basal internode length I, BIL II = Basal internode length II, LI% = Lodging incidence%, TLI% =

Transformed lodging incidence% (an arc sin transformation is used in lodging incidence%).

The coefficient of variation (CV) is useful tool for obtaining comparisons of variability in different characters. A reasonable amount of genetic variation was displayed for the traits evaluated. Fifty per cent flowering and panicle length were the only characters with less than 10% coefficient of variation. However, most traits have CV values above 10% and as high as 65.94% for the lodging incidence indicating that selection based on these characters is expected to be effective [26]. High CV% for lodging incidence% was similar with the findings of Pal and Sabesan [21].

**Table 3:** Estimates of variability parameters for 23 Quantitative (yield and lodging) characters in 225 accessions of rice

S. No.	Characters	Mean	Range		Standard deviation	Standard Error	Coefficient of variation%
			Minimum	Maximum			
1	DTF (days)	106.69	77.79	123.5	7.93	0.53	7.44
2	FLL (cm)	34.91	18.79	57.69	7.94	0.53	22.74
3	FLW (cm)	1.56	0.68	2.28	0.25	0.02	15.83
4	PH (cm)	141.38	78.23	194.77	21.53	1.44	15.23
5	PL (cm)	25.28	19.27	33.98	2.21	0.15	8.74
6	ETP	7.29	4.81	12.53	0.94	0.06	12.86
7	SF%	83.58	35.57	97.36	8.67	0.58	10.37
8	TGW (g)	23.77	3.18	47.01	6.55	0.44	27.55
9	GYP (g)	13.5	3.36	37.74	4.61	0.31	34.19
10	BYP (g)	50.89	17.04	83.42	13.85	0.92	27.22
11	HI (%)	27.66	4.89	84.53	9.17	0.61	33.15
12	UBY (g)	31.8	9.45	58.94	9.57	0.64	30.1
13	LBY (g)	19.09	4.63	42.17	6.74	0.45	35.33
14	GY/UBY	0.45	0.1	1.31	0.16	0.01	36.66
15	UBY/LBY	1.69	0.48	3.28	0.51	0.03	30.31
16	CL (cm)	118.85	46.39	163.46	20.46	1.36	17.21
17	IN	5.94	4	7.38	0.61	0.04	10.34
18	DB I (mm)	5.68	1.52	10.53	1.78	0.12	31.27
19	DB II(mm)	5.77	1.95	10.38	1.75	0.12	30.37
20	BILI (mm)	4.08	1.33	24.3	2.34	0.16	57.52
21	BILII (mm)	10.38	2.83	31.21	4.06	0.27	39.1

22	LI (%)	59.77	0.00	100	39.41	2.63	65.94
23	TLI (%)	53.07	0.72	89.25	33.47	2.23	63.06

The number of genotypes showed better performance for different quantitative traits are depicted in Table 4. It was seen that genotypes Hathi panjari, IC 377173, IC 299879, IC 330018 and Hiaw Hawmmali are top entries for 1000 GW. Bashabhog, Ganga-Godavari, RAU 3061, IC 377051 and IC124891 are the best performing entries for grain yield per

plant. Best genotypes for harvest index are Bashabhog, Ganga (G:1042), Ganga-Godavari, Safri (S:790) and IC 125044 (Baikoni). Genotypes IC 459207, IC 459643, IC125622 (Dashehra matiya), IC 125666 (Deshi safri) and Ganjeikalli showed minimum (0%) lodging incidence.

**Table 4:** List of top five genotypes for each quantitative (yield and lodging resistance) traits

S. No.	Traits	Top Ranking Genotypes				
		Genotype I	Genotype II	Genotype III	Genotype IV	Genotype V
1.	DTF (days)	Dangurchudi (77.79)	Ganjeikalli (77.79)	IC 125644 (Deshi dubraj) (84.50)	IR 64 (85.50)	Sarojini (S:1739) (85.50)
2.	FLL (cm)	Dubraj (D:1438) (57.69)	IC 300138 (55.52)	IC 37737 (Kalikhujee) (55.35)	Jouphool (J:543) (54.26)	IC 299879 (Bhimsen) (52.59)
3.	FLW (cm)	IR 64 (2.28)	Jaldubi (2.21)	Indira barani dhan1 (2.19)	Pusal 121 (2.18)	Safri17 (2.1)
4.	PH (cm)	IC 125747 (Chhote dubraj) (78.23)	IGSR 2-1-6 (90.14)	Banspatri (92.54)	Ganga Godavari (92.87)	Indira barani dhan1 (92.96)
5.	PL (cm)	Tulsimanjari (33.98)	Kalajira (K:2621) (33.04)	IC 124963 (Laxmibhog) (32.52)	IC 125747 (Chhotedubraj) (31.94)	Shrikamal (31.74)
6.	ETP	IC 299800 (12.53)	IC 299804 (Bhejari) (10.53)	IC 459231 (10.33)	IC 381834 (9.84)	IC 459199 (9.53)
7.	SF%	IC 125666 (Deshi safri) (97.36)	IGSR 2-1-6 (96.67)	IC 114201 (Bohita) (96.00)	IC 459644 (95.77)	Tulasiful (95.7)
8.	TGW (g)	Hathi Panjari (H:144) (47.01)	IC 377173 (43.29)	IC 299879 (Bhimsen) (39.83)	IC 333018 (39.12)	Hiaw Hawm mali (38.68)
9.	GYP (g)	Bashabhog (37.74)	Ganga-Godavari (25.16)	RAU 3061 (24.35)	IC 377051 (22.76)	IC 124891 (Aoleshar) (22.74)
10.	BYP (g)	Nagodar (N:806) (17.04)	Safri (S:790) (18.14)	IC 125644 (Deshi dubraj) (20.5)	Mahulakuchi (21.95)	IC22787 (22.44)
11.	HI (%)	Bashabhog (84.53)	Ganga (G:1042) (53.13)	Ganga-Godavari (48.27)	Safri (S:790) (47.7)	IC 125044 (Baikoni) (46.76)
12.	UBY (g)	IC 376538 (Gumdi) (58.94)	IC 114194 (Bohata) (56.96)	IC 299804 (Bhejari) (55.59)	IC 378045 (Kosa) (52.98)	IC 378472 (Bade luchai) (51.99)
13.	LBY (g)	Hathi Panjari (H:144) (42.17)	Agyasaal (36.88)	IC 376567 (34.86)	CoAcc167 (T167) (34.33)	IC 114138 (Bhokala) (33.69)
14.	GY/UBY	Hathi Panjari (H:144) (42.17)	Agyasaal (36.88)	IC 376567 (34.86)	CoAcc167 (T167) (34.33)	IC 114138 (Bhokala) (33.69)
15.	UBY/LBY	Gangtai (G:1049) (0.48)	IC 114202 (Bohita) (0.59)	IC 114273 (Jeeradhan) (0.59)	IC 114200 (Bohita) (0.61)	IC 125383 (Chhatrri) (0.73)
16.	CL (cm)	IC 125747 (Chhote dubraj) (46.39)	Ganga-Godavari (69.77)	Indira barani dhan1 (71.88)	IC 125138 (Bangoli-1) (72.43)	Bashabhog (72.81)
17.	IN	IC 299804 (Bhejari) (7.38)	IC 300532 (Jiktalu) (7.38)	IC 124891 (Aoleshar) (7.38)	Pataniyajhuli (7.33)	Jhal (J:173) (7.29)
18.	DB I (mm)	IC 300532 (Jiktalu) (10.53)	IC 459207 (9.19)	Agyasal (A:726) (9.16)	Hathi Panjari (H:144) (9.02)	Deshi safri (D:1311) (9.01)
19.	DB II(mm)	IC 300532 (Jiktalu) (10.38)	IC 99264 (10.24)	IC 125011 (Bagmuda) (10.1)	Hathi Panjari (H:144) (9.45)	Bhainsa Mundariya (B:1394) (9.28)
20.	BILI (mm)	Kherkakuchi (1.33)	Neelabati (1.44)	IGSR 3-1-5 (1.5)	Tulasiful (1.64)	IC 466877 (1.64)
21.	BILII (mm)	IC 378045 (Kosa) (2.83)	KDML-105 (2.98)	Banspatri (3.41)	IC 126260 (Hansli) (3.62)	Gangaprasad (G:1045) (3.92)

22.	LI (%)	IC 459207 (0)	IC 459643 (0)	IC 125622 (Dashehra matiya) (0)	IC 125666 (Deshti safri) (0)	Ganjeikalli (0)
23.	TLI (%)	IC 459207 (0.72)	IC 459643 (0.72)	IC 125622 (Dashehra matiya) (0.72)	IC 125666 (Deshti safri) (0.72)	Ganjeikalli (0.72)

### Conclusions

The phenotypic characterization showed significant differences among the 225 accessions, indicating the presence of wide genetic variation. The results also revealed that no duplicate genotypes were existed. Thus, it can be concluded that phenotypic variation of these rice genotypes could be a performance basis for selection of potential genotypes for better use in rice breeding.

After the evaluation of these accessions for ten morphological, eleven agronomical and twelve lodging related parameters, on the basis of adjusted mean values, top ranking genotypes were identified. Hathi panjari had the highest 1000GW followed by IC 377173, IC 299879, IC 330018 and Hiaw Hawmmali. Bashabhog, Ganga-Godavari, RAU 3061, IC 377051 and IC124891 (Aoleshar) are top ranking genotypes for grain yield per plant. Best performing genotypes for harvest index are Bashabhog, Ganga (G: 1042), Ganga-Godavari, Safri (S:790) and IC 125044 (Baikoni). Minimum (0%) lodging incidence showed by IC 459207, IC 459643, IC125622 (Dashehra matiya), IC 125666 (Deshti safri) and Ganjeikalli. Similarly other accessions could be select for different agronomical characters.

Thus, identifying rice genotypes for different yield and lodging related parameters in phenotypically divergent sources would help in pre breeding and can be used to broaden the genetic base of breeding programme.

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