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Diversity of Similar Named Jirasail Group of Rice Germplasm of Bangladesh

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ABSTRACT

Fifteen duplicate and similar named Jirasail group of rice germplasms were studied for 14 yield and yield contributing characters at Bangladesh Rice Research Institute during Boro 2019-20 season. The objective of the present study was to evaluate the diversity among the studied genotypes.The first five components in principal component analysis, contributed 81.41% of the total variation among the 15 Jirasail rice germplasm. The genotypes were grouped into five clusters on the basis of cluster analysis. Maximum four germplasms were clubbed into the cluster II and cluster V and cluster III contained the lowest (1). The intra-cluster distance ranged from 1.34 to 0.0 and inter-cluster distance from 6.33 to 33.51 which indicate wide range of diversity where the highest inter-cluster distance was observed between clusters II and III.Cluster V showed the highest seedling height (11.4 cm), grain length (8.7 mm), grain LB ratio (3.16), 1000-grain weight (17.4 g) and grain yield per hill (23.5 g) and the lowest plant height (88.5 cm) and days to maturity (147). Whereas, cluster III showed the highest leaf length (43.2 cm), panicle length (27.2 cm), plant height (124.8 cm), filled grains per panicle (251), unfilled grains per panicle (18) and the lowest leaf width (0.8 cm), grain length (5.5 mm), dehull grain LB ratio (2.3), 1000-grain weight (8.9 g). As a result, the germplasm under clusters V may be selected for crossing with the germplasm from cluster III for developing high yielding Jirasail rice variety with long leaf length, long panicle, high effective tiller numbers per hill, tall plant, short growth duration, higher grains per panicle and long-slender type grain. Moreover, the plant heights, filled grain per panicle and grain yield were positive for both the vectors (I and II) and contributed maximum towards divergence. Finally, Jirasail group of germplasm show a valuable gene pool, which need to conserve in Genebank and utilize in suitable breeding programs.

Key word: Agronomic traits, Bangladesh, D^2-statistics, Jirasail, rice, similar named

1. INTRODUCTION

Rice based livelihood is the way of the people's life in Bangladesh. Currently, Bangladesh is self-sufficient of rice production from three-forth of its total cropped area to provide maximum rural employment, calorie supply and some extent of protein intakes of the population. Moreover, rice sector contributes one-half of the agricultural GDP and one-sixth of the national income in Bangladesh. Almost all of the 13 million farm families of the country grow riceon about 10.5 million hectares which has remained almost stable over the past three decades(1).

Besides, the demand for rice is rising up steadily with steep increase of population along with the shrinking of available rice land. AEZ (Agro Ecological Zone) based new rice varieties that combine yield potential with respective zone along with or without resistance to both biotic and abiotic stress, good grain quality and traditional and medicinal values are needed to meet the future demands. Because, lack of adaptable varieties, stress, climate change, and poor agronomic practices are the major limiting factors of rice yield (2).

Exploring the genetic aspects of germplasm using genotypic and phenotypic analysis is more reliable for the development of rice varieties that could lead to the attainment of food security. This is because genetic variations provide a space for recombinants, which is an important factor in new varietal development (3).Genetic variability is the backbone for any successful breeding programme. Hence, assessing the level of genetic variation among germplasm is of great interest to plant breedersfor the development of climate smart high yielding varieties. Therefore, knowledge of the genetic diversity of the conserved germplasm is an important foundation for crop improvement.

Rice diversity play the major role for achieving heterotic transgressive segregant and as well as choosing parents for variety development programmes. Because, inclusion of more diverse parents (within a limit) is believed to increase the chances for obtaining stronger heterosis and give broad spectrum of variability in segregating generations (4).Moreover, the amount of genetic enrichment is reliant on the extent of genetic diversity inherent in a population (5).However, in conventional plant breeding, genetic diversity is based on morphological variation of quantitative traits, which is easy to study and cost-effective.But, the success of selection of superior breeds from segregating population is entirely dependent on the presence of genetic variation, heritability, genetic advance, and selection skill of breeders (6).Therefore, the genetic divergence study, after incorporating selected genotypes in respective breeding programmes, can help to develop climate smart superior recombinants in any crop improvement program.

However, it was identified that duplicate(s) named rice germplasm were cultivated all over Bangladesh (7). As a result, a particular cultivar got many slightly deviated names or even different cultivars got the same name given by different farmers. Hence, similar and duplicate named rice germplasm need to be studied. The genetic diversity among 87 rice accessions of which 68 genotypes from six African countries along with 19 genotypes from IRRI, Philippines were studied on 17 quantitative traits (8). Finally,the genetic variability and diversity of 32 coloured rice accessions were evaluated using 13 agro-morphological characteristics (3).

Lack ofphenotypic information is still seen as an obstacle for the utilization of conserved germplasm in variety development.However,more detailed studies on similar named groups of rice germplasm of Bangladesh need to be done for its more effective utilization.Therefore, the present study was conducted to evaluate the diversity among the duplicate and similar named Jirasail group of rice germplasm of Bangladesh through quantitative traits for selecting genotypes in variety development programme. This study will open the knowledge of the genetic diversity of Jirasail rice germplasm to facilitate its use in future.

2. MATERIALS AND METHODS

A total of 15 genotypes including 11accessions and four new collections (NC) of duplicate and similar named Jirasail group of rice germplasms received from Bangladesh Rice Research Institute (BRRI) Genebank (Table 1) were grown during Boro 2019-20 season for studying their quantitative and qualitative Agro-morphological diversity. The unit plot comprised with three rows of each 5.4 m long. The thirty-days-old single seedling was transplanted with a spacing of 20 × 20 cm between rows and plants, respectively. Fertilizers were applied @ 80:20:40:12 kg N, P, K and S per hectare respectively. Crop management such as weeding, irrigation etc. were done in time. Appropriate control measures were taken for insect pests, diseases and weeds when necessary.

The germplasms were characterized through 14 quantitative characters.The observed quantitativecharacters were seedling height (cm), leaf length (cm), leaf width (cm), culm diameter (mm), effective tiller number, panicle length (cm), plant height (cm), days to maturity, filled grains per panicle, un-filled grains per panicle, grain length (mm), decorticated grain length breadth ratio, 1000-grain weight (g) and grain yield per hill (g). However, multivariate analyses were performed in computer using GENSTAT 5.5 programme.

3. RESULTS AND DISCUSSION

3.1.1Principal component analysis

The first five components in principal component analysis with eigen values >1, contributed 81.41% of the total variation among the 15 similar and duplicate named Jirasail group of rice germplasm for 14 morphological characters (Table 2). The first five components contributed 81.04% of the total variation in 19 rice varieties for 15 morphological characters (9).

3.1.2 Cluster analysis

The similar and duplicate named Jirasail rice germplasms were grouped into five clusters on the basis of cluster analysis (Table 3). Maximum 4 germplasms were grouped into the cluster II and cluster V followed by 3 in cluster I and cluster IV. The cluster III contained the lowest (1) number of landraces. But no duplicate was existed among the germplasms for the studied characters. Five clusters were found by studying 19 rice varieties for 15 quantitative traits (9). No association was found between the geographical distribution of genotypes and genetic divergence (10). Considering this, parents should be selected on the basis of genetic diversity rather than geographic diversity (11).

Table 4 indicates the variations among the intra and inters cluster distances. All the inter-cluster distances were larger than the intra-cluster distance indicating the homogeneous nature of the germplasm within the cluster. The highest intra-cluster

Table 1-List of similar and duplicate named Jirasail group of rice germplasms.

Sl. No.	Code	Acc. no.*	Name	Upazila	District	Collection year	Season
1	JS1	7591	Jira Sail	Sadar	Dinajpur	-	B. Amon
2	JS2	5061	Jira Shail	--	Dinajpur	2001	Aman
3	JS3	6694	Jirasail	Fulbari	Dinajpur	-	T. Aman
4	JS4	6718	Jirasail	Mahadevpur	Naogaon	-	T. Aman
5	JS5	8056	Jirasail (Indian)	Mohadevpur	Naogaon	2014	Boro
6	JS6	4828	Jira Bhog (Bolder)	Chirrbanoar	Dinajpur	1997	T. Amon

7	JS7	4831	Jira Bhog (Finer)	Chirrbanoar	Dinajpur	1997	T. Amon
8	JS8	1984	Jira Buti	Sribordi	Mymensingh	1977	T. Amon
9	JS9	5313	Jira Dhan	Dumuria	Khulna	2004	T. Aman
10	JS10	5045	Jira Katari	--	Dinajpur	2001	Aman
11	JS11	5975	Gira Katari	Dinajpur	Dinajpur	2005	T. Aman
12	JS12	NC**	Jira	--	Bogura	2018	T. Aman
13	JS13	NC	Jirasail	--	Jashore	2018	T. Aman
14	JS14	NC	Jirasail	--	Rajshahi	2018	T. Aman
15	JS15	NC	Jirasail	Modhupur (BADC)	Tangail	2018	T. Aman

*BRRI Genebank accession number, **New collection.

Table 2-Latent roots (eigen value) and their variation for 14 morphological characters of 15 similar and duplicate named Jirasail group of rice germplasm.

Principal	Latent	Variation	Cumulative
I	4.638	33.13	33.13
II	2.222	15.87	49.00
III	1.943	13.88	62.88
IV	1.435	10.25	73.13
V	1.159	8.28	81.41
VI	0.888	6.34	87.75
VII	0.689	4.92	92.67
VIII	0.520	3.72	96.39
IX	0.200	1.43	97.82
X	0.174	1.24	99.06
XI	0.103	0.73	99.79
XII	0.019	0.14	99.93
XIII	0.009	0.06	99.99
XIV	0.001	0.01	100.00

Table 3-Distribution of 15 similar and duplicate named Jirasail group of rice germplasm into five clusters for 14 morphological characters.

Cluster	Genotypes		Class contribution	Genotypes with BRRI accession no.
	Number	%		
I	3	20	527.7	Jirasail (JS3)(6694), Jira Bhog (Bolder)(JS6)(4828), Jira Buti (JS8)(1984)
II	4	26.66	1359.7	Jirasail (JS4)(6718), Jira Bhog (Finer)(JS7)(4831), Jira Katari (JS10)(5045), Jirasail (JS13)(NC)
III	1	6.66	0.0	Jira Dhan (JS9) (5313)
IV	3	20	750.7	Jira Shail (JS2) (5061), Gira Katari (JS11) (5975), Jirasail (JS14) (NC)
V	4	26.66	850.4	Jira Sail (JS1) (7591), Jirasail (Indian)(JS5) (8056), Jira (JS12) (NC), Jirasail (JS15) (NC)

Table 4-Average intra-(bold) and inter-cluster distances (D^2) for 14 morphological characters of 15 similar and duplicate named Jirasail group of rice germplasm.

Cluster	I	II	III	IV	V
I	**1.01**				
II	8.86	**1.10**			
III	33.51	25.41	**0.0**		
IV	23.11	14.75	10.71	**1.34**	
V	15.17	6.33	19.70	9.02	**0.97**

distance was recorded for cluster IV (1.34), followed by cluster II (1.10) and cluster I (1.01) indicated the high genetic diversity among the germplasm belonging to the respective clusters, where cluster IVhad the most heterogeneousgermplasm. Again, there were marked variations in intra-cluster distances indicating the presence of wider diversity among the germplasm of different clusters. However, the lowest intra-cluster distance was observed in cluster III (0.0) due to the presence of a single genotype in the clusters (Jira Dhan, code JS9 and accession no. 5313).The inter-cluster D^2 values ranged from 6.33 to 33.51 which indicate wide range of diversity. The highest inter-cluster distance was observed between clusters II and III (33.51) suggested wide diversity between these clusters followed by cluster II and III (25.41), cluster I and IV (23.11), cluster III and V (19.70), cluster I and V (15.17) and cluster II and IV (14.75). The lowest inter-cluster distance was observed between clusters II and V (6.33), followed by clusters I and II (8.86) and cluster IV and V (9.02) indicated the close relationship between the germplasm of these clusters and hence, may not beemphasized upon to be crossed each other in hybridization programmes. Intra-cluster distance ranged from 0.0 to 1.02 was reported for aromatic and fine grain landraces (12) and inter-cluster distance ranged from 7.70 to 24.16 was reported for BRRI rice varieties (9).However, germplasm belonging to higher cluster distances may be used in hybridization programme for the improvement of Jirasail rice. Because, crosses involving parents belonging to the most divergent clusters would be expected to manifest maximum heterosis and wide variability of genetic architecture (13).

Table 5 indicates the cluster means of studied genotypes. Cluster V showed the highest seedling height (11.4 cm), grain length (8.70 mm), grain LB ratio (3.16), 1000-grain weight (17.4 g) and grain yield per hill (23.5 g)and the lowest plant height (88.5 cm) and days to maturity (147).Cluster I showed the highest leaf length (43.2 cm), number of effective tillers per hill (10), days to maturity (149) and the lowest filled grains per panicle (83), unfilled grains per panicle (10) and dehull grain LB ratio (2.3). Cluster II showed the highest leaf width (1.1 cm), culm diameter (4.3 mm) and number of effective tillers per hill (10). Cluster III showed the highest leaf length (43.2 cm), panicle length (27.2 cm), plant height (124.8 cm), filled grains per panicle (251), unfilled grains per panicle (18) and the lowest leaf width (0.8 cm), grain length (5.5 mm), dehull grain LB ratio (2.3), 1000-grain weight (8.9 g). Cluster IVshowed the higher grain yield per hill (15.9 g). As a result, the germplasm under clusters Vmay be selected for crossing with the germplasm from cluster III, I, II and IVCluster V showed the highest seedling height (11.4 cm), grain length (8.7 mm), grain LB ratio (3.16), 1000-grain weight (17.4 g) and grain yield per hill (23.5 g) and the lowest plant height (88.5 cm) and days to maturity (147). Whereas, cluster III showed the highest leaf length (43.2 cm), panicle length (27.2 cm), plant height (124.8 cm), filled grains per panicle (251), unfilled grains per panicle (18) and the lowest leaf width (0.8 cm), grain length (5.5 mm), dehull grain LB ratio (2.3), 1000-grain weight (8.9 g). As a result, the germplasm under clusters V may be selected for crossing with the germplasm from cluster III for developing high yielding Jirasail rice variety with long leaf length, long panicle, high effective tiller

Table 5-Cluster means of 15 similar and duplicate named Jirasail group of rice germplasm for 14 morphological and yield contributing characters.

Cluster	**SH (cm)**	**LL (cm)**	**LW (cm)**	**CD (mm)**	**ETN**	**PL (cm)**	**PH (cm)**	**DM (Days)**	**FGPP**	**UFGPP**	**GL (mm)**	**DG LBR**	**TGW (g)**	**GY (g/hill)**
I	10.8	43.2	1.0	3.8	10	26.8	114.5	149	83	10	6.97	2.31	15.8	12.5
II	11.1	38.8	1.1	4.3	10	25.3	105.6	148	126	17	7.02	2.48	12.3	12.8
III	11.6	43.2	0.8	3.7	8	27.2	124.8	148	251	18	5.50	2.30	8.9	10.0
IV	9.8	42.8	1.0	3.8	8	25.3	100.9	147	194	12	6.83	2.44	13.1	15.9
V	11.4	32.6	1.0	4.1	9	23.0	88.5	147	147	15	8.70	3.16	17.4	23.5
Range	9.8-11.6	32.6-43.2	0.8-1.1	3.7-4.3	8.0-10.0	23-27.2	88.5-124.8	147-149	83-251	10.0-18.0	5.5-8.7	2.3-3.16	8.9-17.4	10-23.5
Mean ± SE	10.94±0.18	40.12±1.19	0.98±0.03	3.94±0.06	9±0.26	25.52±0.43	106.86±3.55	147.8±0.22	160.2±16.68	14.4±0.87	7±0.29	2.54±0.09	13.5±0.85	14.94±1.35

CV%	6.5	11.5	11.2	6.4	11.1	6.5	12.9	0.6	40.3	23.3	16.2	14.0	24.4	35.0
LSD (5%)	0.62	4.03	0.10	0.22	0.88	1.45	12.04	0.73	56.62	2.95	1.00	0.31	2.88	4.58

numbers per hill, tall plant, short growth duration, higher grains per panicle and long-slender type grain. The similar trend of conclusions was earlier also reported using Mahalanobis' D^2 statistic for rice (14).

3.1.3 Canonical variate analysis

It appeared from the canonical analysis that 45.28% of the total variation was accounted for canonical root 1 and 23.87% by canonical root 2 and the first four canonical roots with value>1, accounted 91% of the total variation (Table 6).

3.1.4 Contribution of characters towards divergence

Table 7 presents the coefficients pertaining to the different characters in the first two canonical roots. The canonical variate analysis revealed that the plant height, filled grain per panicle and grain yield were positive for both the vectors (I and II) and were the most responsible for both the primary and secondary differentiations and contributed maximum towards genetic divergence. Such results indicated that these characters will offer a good scope for selection of parents. But, unfilled grains per panicle, grain length and brown rice length-breadth ratio(9) and yield, grain breadth, days to flowering, days to maturity, culm diameter, ligule length (15) were found positive for both the canonical vectors.

4. CONCLUSION

Morphological characterization is an important prerequisite for preliminary evaluation because it is fast, simple, effective for germplasm conservation management and can be used as a general approach for assessing genetic diversity among cultivarsto ensure its effective utilization. Considerable ranges of genetic variations were observed among the studied Jirasail germplasm for the studied agro-morphological characters though have the similar or duplicate named.The identified traits could be used as selection criteria for indirect selections of genotypes for yield improvement. The germplasm under clusters V may be selected for crossing with the germplasm from cluster III, I, II and IV for developing high yielding varieties with long leaf length, long panicle, high effective tiller numbers per hill, short growth duration, high grains per panicle and long-slender type grain.Finally, it can be said that studied Jirasail group of germplasm show a valuable gene pool, which need to conserve in Genebank and utilize in suitable breeding programs.

Table 6-Values of latent roots (canonical roots) of 14 morphologicaland yield contributing characters of 15 similar and duplicate named Jirasail group of rice germplasm.

Canonical root	**Values of the canonical root**	**Percentage of variation absorbed by the canonical root**	**Cumulative % of variation**
1	4.74	45.28	45
2	2.50	23.87	69
3	1.23	11.74	81
4	1.08	10.30	91
5	0.30	2.86	94
6	0.18	2.86	97
7	0.17	1.61	99
8	0.12	1.16	100
9	0.08	0.81	100
10	0.04	0.40	101
11	0.02	0.19	101
12	0.00	0.19	101
13	0.00	0.01	101
14	0.00	0.00	101
Total			101

Table 7-Latent vectors for 14 morphologicaland yield contributing characters of 15 similar and duplicate named Jirasail group of rice germplasm.

Character	Vector I	Vector II	Combined ranking*
SH	-0.1788	-0.0271	12
LL	-0.1612	0.1274	7
LW	-2.8747	1.1738	14
CD	-0.5025	-1.0263	13
ETN	0.1082	-0.2867	9
PL	-0.1124	0.1615	5
PH	0.033	0.0953	2
DM (Days)	-0.3931	0.3469	8
FGPP	0.2045	0.0034	1
UFGPP	-0.1697	-0.0115	10
GL (mm)	0.1955	-0.1965	6
DG LBR	-0.5542	0.37	11
TGW (g)	-0.0154	0.1252	4
GY (g/hill)	0.083	0.0365	3

*Combined ranking is estimated by summing the values of vector I and II, then higher (1) is the rank with higher positive value.

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