



Agro-Morphological, Physico-Chemical and Molecular Characterization of Rice Germplasm with Similar Names of Bangladesh

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Abstract: Thirty-one duplicate and similar named rice germplasms of Bangladesh were studied to assess the genetic variation for the agro-morphological and physico-chemical traits and simple sequence repeat banding patterns during 2009–2012 at Bangladesh Rice Research Institute. The range of variations within the cultivar groups showed higher degree. The principal component analysis showed that the first five components with vector values > 1 contributed 82.90% of the total variations. The cluster analysis grouped the genotypes into four clusters, where no duplicate germplasm was found. The highest number (11) of genotypes was constellated in cluster I and the lowest (3) in cluster II. The intra- and inter-cluster distances were the maximum in cluster I (0.93) and between clusters I and IV (24.61), respectively, and the minimum in cluster IV (0.62) and between clusters I and III (5.07), respectively. The cluster mean revealed that the crosses between the genotypes of cluster I with those of clusters II and IV would exhibit high heterosis for maximum good characters. A total of 350 alleles varied from 3 (RM277) to 14 (RM21) with an average of 7.8 per locus were detected at 45 microsatellite loci across the 31 rice accessions. The gene diversity ranged from 0.48 to 0.90 with an average of 0.77, and the polymorphism information content values from 0.44 (RM133) to 0.89 (RM206) with an average of 0.74. RM206, RM21, RM55, RM258 and RM433 were considered as the best markers on the basis of their higher polymorphism information content values. The dendrogram from unweighted pair-group method with arithmetic average clustering also classified the genotypes into four groups, where group IV comprised of 20 genotypes and group III of one genotype, but no duplicate was found. Finally, similar and duplicate named rice germplasms need to be conserved in gene bank as are distinct from each other.

Key words: diversity; simple sequence repeat; similar name; landrace rice; agro-morphological and physico-chemical trait

Bangladesh has abundant diversified rice landraces from time immemorial, since rice plays an important role in the livelihood, cultures and socio-economic aspects of the people, and is also the main cereal food in Bangladesh. International Rice Research Institute (IRRI) gene bank contains more than 8 000 traditional

rice varieties collected from Bangladesh (Hossain et al, 2013). However, now rice diversity in Bangladesh is threatened due to extensive cultivation of modern varieties all over the country along with various intervention of rice habitat (Ahmed et al, 2010).

Exploring diversity in the landrace collection is

Received: 8 June 2015; **Accepted:** 14 December 2015

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Peer review under responsibility of China National Rice Research Institute

<http://dx.doi.org/10.1016/j.rsci.2016.06.004>

very important for identifying new genes and further improvement of the germplasm (Thomson et al, 2007). However, it was identified that duplicate(s) named rice germplasms were cultivated all over Bangladesh (Hamid et al, 1982). 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 germplasms need to be studied whether they are same or different.

Molecular characterized data are the legal evidence for the DUS (distinctness, uniformity and stability) test and is being practiced worldwide. Among PCR based markers, microsatellite marker (simple sequence repeat, SSR) is highly polymorphic, more reproducible, co-dominant and well distributed throughout the rice genome (Chen et al, 2002). Their map positions on the rice genome are well known. SSRs have been used to identify duplicates on germplasm banks and populations of different species (Irish et al, 2010) and to study individuals with close relations (Song et al, 2003). They are user friendly, suitable for purity control (Nandakumar et al, 2004) and elimination of duplicates (Lund et al, 2003). The present study was, therefore, undertaken to assess the genetic variation in 31 duplicate and similar named rice germplasms of Bangladesh by studying the agro-morphological and physico-chemical traits and SSR banding patterns.

MATERIALS AND METHODS

Agro-morphological and physico-chemical characterizations

Thirty-one genotypes in which 21 from Kartiksail and 10 from Dhali boro groups of Bangladesh along with BR23 as standard check were used (Table 1). To study 14 agro-morphological characters, the 35-day-old single seedlings were transplanted per hill for each accession with the space of 20 cm × 25 cm, at Gazipur, Bangladesh Rice Research Institute (BRRI). The chemical fertilizer (N-P-K-S) dose of 60-50-40-10 kg/hm² was applied. Nine plants from each entry were randomly selected for recording data on seedling height, plant height, culm diameter, panicle exertion, effective tillering number per hill, days to maturity, average primary and secondary branch number per panicle, grain yield per panicle, grain length, awn length, 1000-grain weight, grain yield per hill and biological yield. Besides for physico-chemical study, milling rate (Adair, 1952), cooking time (Juliano et al,

1969), amylose content (Juliano, 1971) and protein content (AOAC, 1995) were measured at Grain Quality and Nutrition Division, BRRI during 2011. Genetic diversity was worked out for the principal component analysis (Rao, 1964) and Mahalanobis' generalized distance (D²) analysis (Rao, 1952). All multivariate analyses were performed using the GENSTAT 5.5 program.

Molecular characterization

Plant materials and genomic DNA extraction

The 31 duplicate and similar named rice germplasms along with five popular BRRI varieties viz. BR4, BR14, BR23, BRRI dhan 28 and BRRI dhan 29 were studied in the Molecular Laboratory of Genetic Resources and Seed Division of BRRI during 2011–2012. Total genomic DNA was extracted from leaves of 10–12 day-old seedlings (Collard et al, 2007).

SSR markers and PCR amplification

Forty-five well distributed SSRs were selected from

Table 1. List of 31 duplicate and similar named rice germplasms of Bangladesh.

Serial No.	Accession name	Accession No. ^a	Origin
KS1	Kartik Sail	3243	Sylhet
KS2	Kartik Sail	776	Chittagong
KS3	Katih Shail	438	Rajshahi
KS4	Kartik Sail	539	Rangpur
KS5	Kartik Sail	77	Dhaka
KS6	Kati Shail	170	Tangail
KS7	Kartik Sail	3662	Sherpur
KS8	Kati Shail	3631	Rajshahi
KS9	Kartika	4053	Sylhet
KS10	Kartik Sail	4881	Tangail
KS11	Kartik Sail	76	Dhaka
KS12	Kati Shail	437	Rajshahi
KS13	Kartik Sail	78	Dhaka
KS14	Kartik Sail	1882	Kishorganj
KS15	Kartik sail (2)	689	Comilla
KS16	Kartik sail (2)	846	Sylhet
KS17	Kartik Sail	664	Comilla
KS18	Kartik Sail	1887	Kishorganj
KS19	Kartik Sail	844	Sylhet
KS20	Katih Shail	994	Khulna
KS21	Kartik Sail	845	Sylhet
DB1	Dhali Boro	2250	Sylhet
DB2	Dhali Boro	2247	Sylhet
DB3	Dhali Boro	2249	Sylhet
DB4	Dholi Boro	180	Tangail
DB5	Dhali Boro	2245	Sylhet
DB6	Dholi Boro	4396	Sylhet
DB7	Dhali Boro	2246	Sylhet
DB8	Dhali Boro	2244	Sylhet
DB9	Dhali Boro	2248	Sylhet
DB10	Dhali Boro	2243	Sylhet

^a, BRRI gene bank accession number.

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