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Selection of core collections from *Kartiksail* and *Dhaliboro* rice landraces of Bangladesh

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Key words: Rice, *Kartiksail*, *Dhaliboro*, Landraces, Core collection.

Abstract

Rice is one of the most important cereals in the world for being as the staple food. Rice has widespread popularity across Bangladesh, where it uniquely suited to wet environments. Presently, a large number of germplasm have been collected in gene banks all over the world, but methods for the effective management and utilization of such huge collections remain a challenging task. On the other hand, the concept of core collection provides a new way of management and utilization of plant germplasm resources. Frankel first termed a collection to a core collection which would represent the genetic diversity of a crop species with a minimum of repetitiveness. But systematic study has yet been done on core collection of rice in Bangladesh. The objective of the present review study was, therefore, to select the core collections from previously agro-morphologically, physico-chemically and molecularly characterized *Kartiksail* and *Dhaliboro* rice. In the present study, the core collections were selected using the hierarchical cluster analysis, where a representative sample with high phenotypic values was drawn from each group. Moreover, the selection processes were improved by combining several evaluation methods. However, special emphasis was given on the genotypic values of the germplasm. In the conclusion, the core collections for *Kartiksail* landraces were KS1, KS5, KS6, KS7, KS9, KS11, KS13, KS16, KS19, KS20 and KS21, whereas that of *Dhaliboro* were DB3, DB4, DB7, DB8 and DB10. The selected landraces may be utilized in different hybridization programmes for developing new variety.

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Introduction

Rice (*Oryza sativa* L.) is one of the most important cereals in the world for being as the staple food. Rice has widespread popularity across Bangladesh, where it uniquely suited to wet environments. In spite of many constraints, Bangladesh has already met the MDG (Millennium Development Goal) hunger target and towards its sustainable food security.

Mining elite genes within rice landraces is of importance for the improvement of cultivated rice (Zhang *et al.*, 2014). Rice genetic resource is the primary material for rice breeding (Zhang *et al.*, 2011). It is a rich reservoir of valuable genes that plant breeders can harness for crop improvement (Yadav *et al.*, 2013).

Continuous collection of germplasm resources makes the sizes of the collected germplasm larger and larger, which hindered its safe preservation, evaluation and effective use. Frankel (1984) first termed a collection to a core collection which would represent the genetic diversity of a crop species with a minimum of repetitiveness. Core collections access the users to a sample of small sizes with keeping the most of the genetic variability contained within the gene pool of that crop (Brown, 1995).The representativeness is the most important property and selecting a series of evaluating parameters is the most important aspect of a core collection. Therefore, if a more reliable core collection is required, evaluating parameters should be combined for evaluation (Wang *et al.*, 2007).Recent studies showed that backcrossing twice using modern varieties as receptor crossing with accessions from mini core collection, most of the undesirable traits could be improved remarkably (Zhang *et al.*, 2011a; Yan *et al.*, 2012). But systematic study has yet been done on selection of core collection of rice in Bangladesh. Therefore, the objective of the present review study was to select the core collections from previously agro-morphologically, physico-chemically and molecularly characterized *Kartiksail* and *Dhaliboro* rice landraces of Bangladesh.

Core collection of germplasm

The core means the central part. Frankel (1984) first termed a collection to a core collection which represents the genetic diversity of a crop species and its relatives with a minimum of repetitiveness. Core collection can also be defined as the collections seek to increase the balance between the different types of material in a relatively small selection of accessions from the total collection. The main purpose of the core collection is to provide an efficient access to the whole collection by setting up a hierarchical structure. It also facilitates the selection of parents for hybridization programs. Therefore, the core collection forms the active collection for germplasm conservation, evaluation and exchange, while the remaining parts of the whole collection are kept as a reserve collection in the genebank. However, a core collection of germplasm accessions serve several purposes: (1) for duplicate conservation, (2) to promote use of the IRGC, (3) to study diversity *per se,* and (4) to exploit synteny among grass genomes (Jackson, 1999). Marita *et al.* (2000) suggested the two general purposes for creating the core collections as: (1) maximising the total genetic diversity in a core and (2) maximising the representativeness of the genetic diversity of the whole collection.

Importance of core collection of germplasm

Presently, a large number of germplasm have been collected in gene banks all over the world, but methods for the effective management and utilization of such huge collections remain a challenging task. On the other hand, the concept of core collection provides a new way of management and utilization of plant germplasm resources (Guo *et al.*, 2014).Thus, the establishment of core collections is a helpful means to make better use of plant germplasm and to assist in the management of the entire collection.

Characterized and grouped Kartiksail and Dhaliboro rice landraces

Ahmed (2015a) grouped the similar or duplicate named *Kartiksail* and *Dhaliboro* rice germplasm through agro-morphological, physicochemical and molecular characters. The genetic diversity analysis

based on Mahalanobis' D^2 statistics grouped the *Kartiksail* and *Dhaliboro* genotypes into seven clusters (Table 1). The UPGMA clustering based on Dice coefficient grouped the *Kartiksail* genotypes into four clusters (Fig. 1) and the *Dhaliboro* genotypes into three clusters (Fig. 2). Again, the UPGMA clustering based on Nei's genetic distance across the 45 microsatellite markers grouped the genotypes into ten clusters (Fig. 3).

Table 1. Distribution of 31 duplicate and similar named rice germplasm into seven clusters for 18 morpho-physicochemical characters.

Cluster	No. of genoty	Name of genotypes
I	6	KS1, KS2, KS3, KS12, KS15, KS16
II	2	KS5, BR23
III	6	KS4, KS7, KS10, KS13, KS20, KS21
IV	2	DB5, DB10
V	8	KS6, KS8, KS9, KS11, KS14, KS17, KS18, KS19
VI	4	DB2, DB3, DB7, DB8,
VII	4	DB1, DB4, DB6, DB9

(Sources: Ahmed *et al.*, 2016).

Existing procedure of selecting core collection

The first major issue for developing core collection is size. For this, two approaches were reported. The first one is to decide upon an almost arbitrary proportion, as five to 10 per cent would be appropriate. The second approach is to nominate an upper limit for a category of accessions (e.g. 3,000 per species). Brown (1989a) estimated that with the 10% level of sampling, the core will generally contain over 70% of the alleles present in the whole collection. Once the size is decided, to identify the degrees of genetic similarity among the accessions is essentially a hierarchical cluster analysis, where every accession is sorted into a related subgroup from which a representative sample can be drawn. To identify these groups, passport, characterization and evaluation data can also be used (Brown, 1989b). However, there is no fixed method for selecting core collection of germplasm. It depends on the specific objections for which the core collection is selected or developed.

Methods applied to select the core collection

In the present study, the hierarchical cluster analysis was used to select the core collections as suggested by Zewdie *et al.* (2004), where a representative sample was drawn from each group (Brown, 1989a).For this, the genetic diversity analysis based on Mahalanobis' D^2 statistics that grouped the *Kartiksail* and *Dhaliboro* rice genotypes into ten clusters by Ahmed *et al.*(2016) were applied for their high and effective representativeness (Cui *et al.*, 2004) to select the core collections. However, the quality of selection method of core selection was also improved through applying sampling strategies based on the genotypic values of the genotypes as suggested by Hu *et al.*(2000), using predicted genotypic value as suggested by Li *et al.* (2004a), comparing different genetic distances, cluster methods and sampling strategies methods as suggested by Xu *et al.*(2004), using SSR marker base data as suggested by Zhang *et al.*(2011),using geographic distribution data as suggested by Li *et al.* (2004b) and composite method of evaluation as suggested by Singh *et al.* (1991).

Finally, the genotypes in the core collection should be potential, superior, representative as well as diverse. Considering this view, selection of one genotype having better traits along with additional criterion from each group/cluster was done. Similar strategies were also practiced earlier by Singh *et al.*(1991), Hu *et al.* (2000), Cui *et al.* (2004), Li *et al.* (2004b) and Upadhyaya *et al.*(2006). However, Wang *et al.* (2007) also identified different evaluating parameters for rice core collection based on genotypic values and molecular marker information.

Selecting core collection from Kartiksail group of rice accessions

In the present study, the cumulative ranking (CR) based on inter-genotype distance ($D=\sqrt{D^2}$) ranking (DGDR) and Nei's genetic distance ranking (NGDR), morphological ranking (MR) based on morpho-physicochemical characters and qualitative ranking (QR) based on Dice coefficient of 31 similar named rice germplasm were done on the basis of their

genetic distances. The Table 2 shows the ranks of 31 germplasm according to their diversity.

An attempt was made in the present study to select the core collections from 31 landraces of similar or duplicate named rice germplasm of which 21 were *Kartiksail* and 10 were *Dhaliboro* groups (Table 3).

In Mahalanobis' D^2 clustering, the KS1, KS2, KS3, KS12, KS15 and KS16 landraces of *Kartiksail* group rice genotypes were constellated in cluster I (Table 1). Again, on the basis of inter-genotype distance ($D=\sqrt{D^2}$) ranking (IGDR) based on Mahalanobis' D^2 statistics, the most diverse genotypes were KS15 and KS3, while medium diverse genotypes were KS1, KS12 and KS16 (Table 2). On the other hand, on the basis of Nei's genetic distance ranking (NGDR) estimated from Nei's distances for molecular characters using SSR markers, the most diverse genotypes were KS12 and KS16, while rest were less diverse. Moreover, KS1 was more diverse genotype than KS2, and KS3 in cumulative ranking. However, the medium diverse genotypes were KS12 and KS16. On the other hand, genotype KS1 had the highest seedling height and higher panicle grain yield values among the 98 landraces, but higher straw yield and biological yield within the *Kartiksail* group, while KS16 showed higher means for secondary branches filled grain number, milling outturn and elongation ratio among the 98 genotypes, along with highest/higher mean for effective tiller number, secondary branch length and filled grain number, but lower mean values for culm and plant height as well as growth duration (Ahmed, 2015a). But, on the basis of UPGMA clustering method based on Dice coefficient on qualitative characters, all the genotypes were constellated into the same sub-cluster (Fig. 1). Finally, on the basis of UPGMA clustering method based on Nei's genetic distance for molecular characters using SSR markers, the genotypes KS15 and KS16 were separately constellated in a sub-cluster with KS12, whereas genotype KS1 grouped with KS2 and KS3 in different sub-cluster (Fig. 3).Last but not the least, both KS1 and KS16 were collected from Sylhet district (Table 3). Therefore, it can be concluded that the first sub-set of core genotypes for *Kartiksail* group are KS1 and KS16. Upadhyaya *et al.* (2006) developed core subset of finger millet germplasm by using the geographical origin and the data based on quantitative traits.

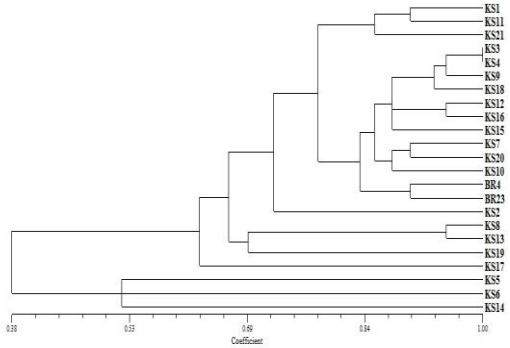

Fig.1. Dendrogram of 21 *Kartiksail* rice germplasm for 19 qualitative agro-morphological characters. (Sources: Ahmed *et al.*, 2015b).

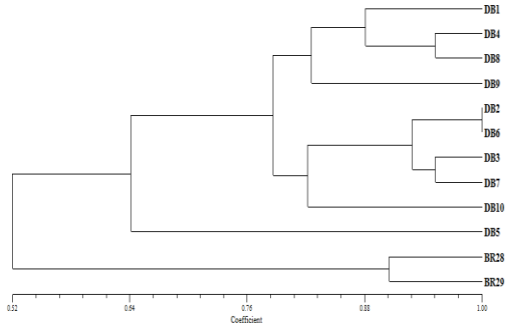

Fig. 2. Dendrogram of 10 duplicate named *Dhaliboro* rice for 19 qualitative agro-morphological characters. (Sources: Ahmed *et al.*, 2015c).

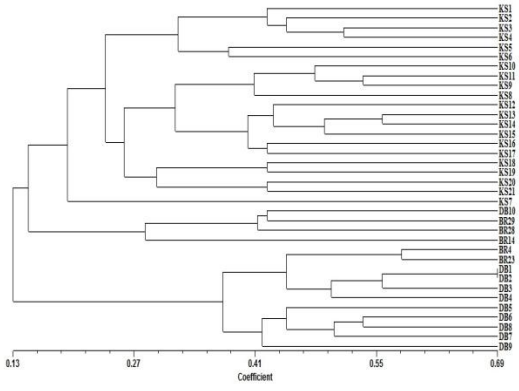

Fig. 3. Dendrogram of 31 duplicate and similar named rice germplasm derived from UPGMA cluster analysis based on Nei genetic distance across 45 SSR markers.
(Sources: Ahmed *et al.*, 2016).

Similarly, KS4, KS7, KS10, KS13, KS20 and KS21 landraces of *Kartiksail* group rice genotypes were constellated in cluster III (Table 1). Again, the most diverse genotypes were KS13 and KS3, while the medium diverse was KS20 on the basis of inter-genotype distance ($D=\sqrt{D^2}$) ranking (IGDR) (Table 2). On the other hand, on the basis of Nei's genetic distance ranking (NGDR), the most diverse genotypes was KS7, the medium diverse was KS21 and rest were less diverse. Moreover, on the basis of cumulative ranking, the most diverse genotypes was KS7 and the medium diverse were KS13 and KS21. Again, KS21, KS7 and KS10 morphologically ranked as 49, 65 and 75, respectively. As a result, KS21 had higher mean values for harvest index and amylose percent among the 98 genotypes and higher values for panicle length, panicle grain yield, LB ratio, primary branch length, primary and secondary branch number but lower mean value for culm and plant height within the *Kartiksail* group (Ahmed, 2015a), while genotype KS7 showed higher mean for panicle length, primary and secondary branch number and hill grain yield among the 98 genotypes, whereas genotype KS10 gave average performance for all the characters studied. On the other hand, KS13 gave the highest mean for amylose percent and higher mean for grain length and thousand grain weight among the 98 genotypes, but the highest seedling height and lower mean values for culm and plant height as well as growth duration within the group. Moreover, genotype KS20 showed higher mean for elongation ratio and amylose percent among the 98 genotypes and the highest mean for protein percent and higher mean for hill grain yield and lower mean values for culm and plant height as well as growth duration within the group. But, on the basis of UPGMA clustering method based on Dice coefficient on qualitative characters, all the genotypes were constellated into the same sub-cluster except KS13 (Fig. 1). Finally, on the basis of UPGMA clustering method based on Nei's genetic distance for molecular characters using SSR markers, the genotype KS7 was separately grouped, while rest of all were constellated into the same sub-cluster (Fig. 3). Again, KS7 was collected from Sherpur, KS13 from Dhaka, KS20 from Khulna and KS21 from Sylhet regions (Table 3). Therefore, it can be concluded that the second sub-set of core genotypes for *Kartiksail* group are KS21, KS7, KS13 and KS20. Wang *et al.* (2007) also mentioned that the key to improve the representativeness of a core collection is the scientific selection within groups.

Again, KS6, KS8, KS9, KS11, KS14, KS17, KS18 and KS19 genotypes were constellated in cluster V (Table 1). Again, on the basis of inter-genotype distance ($D=\sqrt{D^2}$) ranking (IGDR) estimated from principal coordinate analysis (PCoA) also based on Mahalanobis' D^2 statistics, the most diverse genotypes were KS8, KS6, KS19, while medium were KS11 and KS9 and the least diverse was KS17, respectively (Table 2). Besides, on the basis of UPGMA clustering method based on Dice coefficient on qualitative characters, the genotypes KS6 and KS14 were constellated in the cluster I, where as the rest of the genotypes were grouped in different cluster and groups (Fig. 1). On the other hand, on the basis of Nei's genetic distance ranking (NGDR) estimated from Nei's distances for molecular characters using SSR markers, the most diverse genotype was KS17, medium diverse genotypes were KS19 and KS11 and the least diverse were KS9 and KS6, respectively. Again, KS8, KS19 and KS6 were the most diverse genotypes, where as KS9 and KS11 were the least diverse genotypes on the basis of cumulative ranking (Table 2). Besides, genotypes KS19, KS9 and KS11 morphologically ranked as 39, 52 and 58, respectively. As a result, KS19 had higher mean values for primary branch filled grain weight, grain length, LB ratio, harvest index and elongation ratio among the 98 genotypes and the highest mean for hill grain yield, LB ratio and elongation ratio among the 98 landraces and gave the highest mean for effective tiller number, hill grain yield and LB ratio and higher values for panicle grain yield within the *Kartiksail* group, while genotype KS9 showed the highest mean for harvest index and higher mean for secondary branch filled grain weight and amylose percent among the 98 genotypes and the highest mean for penultimate and flag leaf area and harvest index and higher mean for panicle and hill grain yield and

secondary branch number within the group, where as genotype KS11 gave higher mean for harvest index, amylose percent and thousand grain weight among 98 genotypes, whereas gave the highest mean for panicle grain yield and higher mean for culm diameter, hill grain yield and secondary branch filled grain weight, but the lowest mean value for growth duration within the group. Moreover, genotype KS6 showed the highest mean values for culm and plant height and higher mean for seedling height, primary branches filled grain number and protein percent within the *Kartiksail* group (Ahmed, 2015a).

Table 2. List of different types of ranking based on morphological and inter-genotype distances (D^2, Dice coefficientand Nei's genetic distances) for 98 similar or duplicate named rice germplasm.

GTC	Morphological ranking (MR)	D^2 Genetic distance ranking (DGDR)	Qualitative ranking (QR)	Nei's genetic distance ranking (NGDR)	Cumulative ranking (CR)
KS01	23	18	14	25	24
KS02	22	28	9	28	30
KS03	27	16	6	29	27
KS04	18	22	7	27	29
KS05	3	24	28	20	23
KS06	13	12	25	30	20
KS07	7	26	5	3	11
KS08	10	9	22	22	16
KS09	4	27	12	31	31
KS10	15	21	2	21	21
KS11	6	25	13	26	28
KS12	24	19	3	12	13
KS13	17	10	29	18	12
KS14	5	30	21	16	25
KS15	31	15	1	24	18
KS16	29	20	11	14	14
KS17	8	31	31	15	22
KS18	12	29	4	17	26
KS19	1	14	17	19	17
KS20	19	17	8	23	19
KS21	2	23	10	13	15
DB01	14	4	19	11	9
DB02	20	3	26	10	7
DB03	9	7	20	9	8
DB04	30	13	15	5	6
DB05	26	5	23	7	5
DB06	25	8	27	2	3
DB07	11	1	24	4	1
DB08	16	11	16	8	10
DB09	21	2	30	6	4
DB10	28	6	18	1	2

Note: For unfilled grain number, unfilled grain weight, awn length and cooking time, higher is the rank with lower values and cumulative ranking (CR) was done based on D^2 genotype distance rank (DGDR) and Nei's genetic distance rank (NGDR), where (including QR) higher is the rank with higher diversity.

Zewdie *et al.* (2004) also emphasized on the use of cluster analysis with enlightened selection of accessions. Finally, on the basis of UPGMA clustering method, based on Nei's genetic distance for molecular characters using SSR markers, where genotype KS8 was clustered with KS9 and KS11, while genotype KS14 with KS17, as well as genotype KS18 with KS19, where as the genotype KS6 was grouped differently in sub-cluster (Fig. 3). Similarly, Li *et al.* (2004a) also reported the deviation sampling strategy in combination with the un-weighted pair-group average method of hierarchical clustering retained the greatest degree of genetic diversities of the initial collection. Wang *et al.* (2007) also identified different evaluating parameters for rice core collection based on genotypic values and molecular marker informations. Moreover, KS6 was collected from Tangail as the only B. Aman variety, whereas KS9,

KS11 and KS19 collected from Sylhet, Dhaka and Sylhet regions, respectively (Table 3). Therefore, it can be concluded that the third sub-set of core genotypes for *Kartiksail* group are KS19, KS9, KS11 and KS6. Hintum (1995) also used hierarchical cluster analysis to develop core collection in rice.

However, KS5 was the only genotype of *Kartiksail* group in cluster II (Table 1). So, it should be included as the forth sub-set of core collection for *Kartiksail* group.

Finally, it can be concluded that the core collection for *Kartiksail* group of landraces of rice germplasm are KS1, KS5, KS6, KS7, KS9, KS11, KS13, KS16, KS19, KS20 and KS21. Moreover, the genotypes KS19 and KS9 may be used as parents in breeding programs.

Selecting core collection from Dhaliboro group of rice accessions

In Mahalanobis' D^2 clustering, the DB5 and DB10 genotypes were constellated into cluster IV (Table 1) and the genotype DB10 was more diverse in Nei's genetic distance ranking (NGDR) and in cumulative ranking than DB5 (Table 2). Besides, genotype DB5 formed a single cluster, while DB10 constellated into a separate sub-cluster according to the qualitative characters (Fig. 2). But the genotype DB10 grouped separately with BR14, BRRI dhan28 and BRRI dhan29, whereas DB5 constellated into a separate cluster with other group members in UPGMA clustering method based on Nei's genetic distance (Table 3). Therefore, it can be concluded that the first sub-set of core genotype for *Dhaliboro* group is DB10. Previously, Zewdie *et al.* (2004), Li *et al.* (2004a) and Hintum (1995) also used hierarchical cluster analysis to develop core collection.

Similarly, DB2, DB3, DB7 and DB8 landraces of *Dhaliboro* group rice genotypes were constellated in cluster VI (Table 1). Again, on the basis of inter-genotype distance ($D=\sqrt{D^2}$) ranking (IGDR) estimated from principal coordinate analysis (PCoA) also based on Mahalanobis' D^2 statistics, the most diverse genotypes were DB7, medium diverse was DB2 and the least diverse was DB8 (Table 2).

Table 3. Alphabetical list of the *Kartiksail* and *Dhaliboro* genotypes with BRRI accession number.

Local name	Code name	Accession number	Place of collection		Date of collection	Growing season
			Thana	District		
Kartik Sail	KS1	3243	Balaganj	Sylhet	18/03/86	T. Aman
Kartik Sail	KS2	776	Raojan	Chittagong	14/01/74	T. Aman
Katih Shail	KS3	438	Natore	Rajshahi	12.01.74	T. Aman
Kartik Sail	KS4	539	Panchabibe	Rangpur	18.04.74	T. Aman
Kartik Sail	KS5	77	Lohajanj	Dhaka	18/07/74	T. Aman
Kati Shail	KS6	170	Kotowali	Tangail	08.02.74	B. Aman
Kartik Sail	KS7	3662	Sherpur	Sherpur	27/10/86	T. Aman
Kati Shail	KS8	3631	Siagra	Rajshahi	25.10.86	T. Aman
Kartika	KS9	4053	Jaimlapur	Sylhet	Nov.,1988	T. Aman
Kartik Sail	KS10	4881	Haluaghat	Tangail	Nov.,1997	T. Aman
Kartik Sail	KS11	76	Manik Gonj	Dhaka	18/07/74	T. Aman
Kati Shail	KS12	437	Natore	Rajshahi	10.01.74	T. Aman
Kartik Sail	KS13	78	Lohajanj	Dhaka	02.02.74	T. Aman
Kartik Sail	KS14	1882	Hossainpur	Kishorganj	21.01.76	T. Aman
Kartik Sail(2)	KS15	689	B.Baria	Comilla	21/03/73	T. Aman
Kartik Sail(2)	KS16	846	Kawaighat	Sylhet	17/12/73	T. Aman
Kartik Sail	KS17	664	Faridganj	Comilla	24/11/74	T. Aman

Local name	Code name	Accession number	Place of collection		Date of collection	Growing season
			Thana	District		
Kartik Sail	KS18	1887	Nandail	Kishorganj	05/02/76	T. Aman
Kartik Sail	KS19	844	Ch. Ghat	Sylhet	15/12/73	T. Aman
Katih Shail	KS20	994	Phultala	Khulna	13.12.73	T. Aman
Kartik Sail	KS21	845	Biswanalh	Sylhet	02/12/73	T. Aman
Dhali Boro	DB1	2250	Sylhet sadar	Sylhet	22/05/81	Boro
Dhali Boro	DB2	2247	,,	,,	,,	,,
Dhali Boro	DB3	2249	,,	,,	,,	,,
Dholi Boro	DB4	180	Kali kati	Tangail	29-04-74	,,
Dhali Boro	DB5	2245	Sylhet sadar	Sylhet	22/05/81	,,
Dholi Boro	DB6	4396	,,	,,	April, 94	,,
Dhali Boro	DB7	2246	,,	,,	22/05/81	,,
Dhali Boro	DB8	2244	,,	,,	,,	,,
Dhali Boro	DB9	2248	,,	,,	,,	,,
Dhali Boro	DB10	2243	,,	,,	,,	,,

(Source: Ahmed, 2015).

But, genotype DB7 showed higher mean values for days to maturity, secondary branch length and filled grain number, LB ratio, milling outturn percent among the 98 genotypes and the highest values for grain length, thousand grain weight and harvest index within the *Dhaliboro* group, while genotype DB8 had the highest mean for secondary branch length and filled grain number and the longest growth duration among the 98 genotypes and higher mean for effective tiller number, panicle length, secondary branch number and the lowest mean cooking time within the *Dhaliboro* group (Ahmed, 2015a). As a result, the genotypes DB3, DB7 and DB8 morphologically ranked as 9, 11and 16, respectively (Table 2). Besides, on the basis of UPGMA clustering method based on Dice coefficient on qualitative characters, the genotypes DB2 and DB3 were grouped with DB7, while DB8 constellated into a separate sub-cluster (Fig. 2). On the other hand, on the basis of inter-genotype and genetic distance as well as cumulative ranking, the most diverse genotype was DB7 (Table 2). Again, on the basis of UPGMA clustering method based on Nei's genetic distance for molecular characters using SSR markers, the genotypes DB7 was constellated with DB8, whereas DB2 was grouped with DB3 (Fig. 3). Finally, DB2 was collected from Chittagong, while DB3 and DB8 from Rajshahi and DB7 from Sherpur districts. Therefore, it can be concluded that the second sub-set of core genotypes for *Dhaliboro* group are DB3, DB7 and DB8. Upadhyaya *et al.* (2006) also developed core collection based on quantitative traits.

Similarly, DB1, DB4, DB6 and DB9 landraces of *Dhaliboro* group rice genotypes were constellated in cluster VII (Table 1). Again, on the basis of inter-genotype distance ($D=\sqrt{D^2}$) ranking (IGDR) estimated from principal coordinate analysis (PCoA) also based on Mahalanobis' D^2 statistics, the most diverse genotypes were DB9, medium diverse was DB6 and the least diverse was DB4 (Table 2). But, genotype DB4 had higher mean for LB ratio, straw yield, biological yield and shorter values for growth duration with the highest mean for head rice outturn, protein percent and the shortest grain length and the lowest mean for thousand grain yield and lower growth duration within the group, while DB9 gave higher values for secondary branch length and filled grain number, LB ratio among the 98 genotypes and higher mean for thousand grain weight within the group (Ahmed, 2015a). As a result, the genotypes DB4 morphologically ranked as 30 (Table 2). Besides,

on the basis of UPGMA clustering method based on Dice coefficient on qualitative characters, the genotypes DB1, DB4 and DB9 were grouped into the same sub-cluster, while DB6 constellated into a different sub-cluster (Fig. 2). Again, on the basis of UPGMA clustering method based on Nei's genetic distance for molecular characters using SSR markers, the genotypes DB4 constellated with DB1, while DB6 with DB9 (Fig. 3). Finally, DB4 was the only genotype collected from Tangail and rest from Sylhet districts. Therefore, it can be concluded that the third sub-set of core genotypes for *Dhaliboro* group are DB7, DB8 and DB4. Wang *et al.* (2007) also used different evaluating parameters for developing rice core collection.

Finally, it can be concluded that the core collection for *Dhaliboro* group of landraces of rice germplasm are DB3, DB4, DB7, DB8 and DB10. Moreover, the genotype DB7 may be used as parent in breeding programs.

Conclusion

The selected landraces with diverse genes need to be utilized in different hybridization programmes for broadening the genetic base of modern rice, because they indicate unique and potential yield contributing characters for improvement of *Balam* rice in Bangladesh. Secondly, the selected core collections may be utilized as working samples in Genebank for their effective conservation and their QTL mapping for potential characters need to be done.

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