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Review Article

Selection of Core Collection from *Jesso-Balam* Rice (*Oryza sativa* L.) Accessions Using Quantitative, Qualitative and Molecular Characters-A Review

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Abstract
Genetic improvement of rice (*Oryza sativa* L.) for yield is important for increasing demand of the growing population and the changing climate of the world. Recent studies showed that backcrossing twice using modern varieties as receptor and mini core collection as doner, most of the undesirable traits could be improved remarkably and in other words its maximum allele diversity could be brought back into rice fields. Core collection is defined as a subset chosen to represent the most genetic diversity of an initial collection with a minimum of redundancies. The objective of the present study was to review the selection of core collection of *Jesso-Balam* group of rice genotypes through quantitative, qualitative and molecular characters. Earlier, the same germplasms were characterized for agro-morphological, physico-chemical and molecular characters and grouped into different clusters by different methods at Bangladesh Rice Research Institute during 2009-12. Finally, the core collection was selected by reviewing the above characterized data and using the hierarchical cluster analysis. Moreover, the selection processes of core collection were improved by applying composite evaluation methods; such as agro-morphological traits, biochemical characters and so on, through sampling strategies based on genotypic values, predicted genotypic value, comparing different genetic distances, cluster methods and sampling strategies methods, molecular characterization or SSR marker base data. As a result, the selected core germplasm of *Jesso-Balam* rice accessions were JBPL1, JBPL8, JBPL9, JBPL10, JBPL13, JBPL15, JBPL16, JBPL17, JBPL19, JBPL20, JBPL21, JBPL23, JBPL25 and JBPL26. In conclusion, the core collection need to be considered as the 'working collection' of *Jesso-Balam* rice genotypes for their easy and safe conservation and effective utilization in Gene bank.

Keywords: Rice, *Jesso-Balam*, characterization, core collection.

1. Introduction

1.1 Utilization of rice germplasm

Rice (*Oryza sativa* L.) is one of the most important components of human diet in Asia, Africa and Latin America. Consequently, rice is also considered as the major crop in Bangladesh. Therefore, the genetic improvement of rice for yield is important to meet the food demand of the growing population.

1.2 Concept of core collection of germplasm

Frankel (1984) first termed a collection to 'core collection'. It is a subset chosen from an initial whole collection. The core collection forms the 'active collection', while the remainders are considered as 'reserve collection'. The representativeness evaluation is a significant step in the procedure of core collection construction. A series of evaluating parameters are required in

representativeness evaluation for core accessions (Wang *et al.*, 2007). Li *et al.* (2004a) developed rice core collections based on the predicted genotypic values from 992 rice varieties with 13 quantitative traits. But limited work has been done on the core collection of rice in Bangladesh.

1.3 Definition of core collection of germplasm

'Core' means the central or innermost and the most important part. A core collection is a limited set of accessions, with a minimum of repetitiveness, representing the genetic diversity of a crop species and its wild relatives (Frankel, 1984).

1.4 Advantages of core collection of germplasm

A large number of germplasm have been collected in Gene banks all over the world, but managing and utilizing it efficiently remain challenging task. The main drawback of germplasm collections is its high management cost (Liang *et al.*, 2015). Frankel (1984) proposed the concept of core collection to utilize and manage the germplasm more easy and effectively. It provides a new way of management and utilization of plant germplasm resources (Guo *et al.*, 2014) and has some utility for plant improvement (Jansky *et al.*, 2015).The advantages of selecting core collection are the improvement of Gene bank operations.

Core collections increase the efficiency of characterization and utilization of collections stored in the Gene banks (Brown, 1989). It is convenient to study and utilize germplasm resources (Zhang *et al*., 2010), characterization could be more efficient (El Bakkali *et al.*, 2013) and facilitate the study of its genetic diversity (Mario Paredes *et al.*, 2010).It is considered as a helpful mean to better evaluate and use of plant germplasm and Mini core approach is an effective methodology to enrich and enhance crop improvement programmes (Upadhyaya *et al.*, 2010). Recent studies showed that backcrossing twice using modern varieties as receptor and mini core collection as doner, most of the undesirable traits could be improved remarkably (Yan *et al*., 2012) which need to be utilized for bringing back the allele diversity into rice fields.

Finally, core collections may be useful tools as a first step in genetic association studies (Aranzana *et al.*, 2010). Association mapping based on it would help to capture as much phenotypic variation as possible (Zhang *et al*., 2014) and provide users with more flexibility for choosing varieties (El Bakkali *et al.*, 2013). It is extremely useful for sequencing mining polymorphism to associate polymorphisms with phenotypic traits (Xu *et al*., 2016). Further, the bulk core collections might provide a way of increasing the amount of genetic diversity (Van Hintum *et al.*, 2000). With this in mind, the objective of the present study aims to review the selection of core collection of *Jesso-Balam* group of rice accessions through quantitative, qualitative and molecular characters**.**

2. Methods for selecting core collection

2.1 Core collections in germplasm

Brown (1989) suggested that core collection with 10% sampling percentage could represent 70% genetic diversity of the initial population, when the number of the initial accessions was over 3000. Zhang *et al*. (2010) used 10 morphological traits to select the primary core collection of 64 accessions from 435 apple cultivars, which could well represent the genetic diversities of the entire collection. Xu *et al.* (2004) constructed a cotton core collection from 168 initial accessions with 30% sampling percentage. Zhang *et al.* (2011) established a rice core collection consisting of 150 entries from 2260 varieties by using 274 SSR markers.

2.2 Methods for selecting core collection of germplasm

One common approach for constructing a core collection is grouping the entire collection according to the growing regions or ecotypes, then selecting representative core accessions from each of the groups to form core subsets, and the entire core collection is constructed by

combining all core subsets (Wang *et al.*, 2007). The core accessions need to be analyzed for its genetic diversity to ensure their representativeness (Cui *et al.*, 2004).

3. Selection of core collection from *Jesso-balam* rice

3.1 Characterization, clustering and ranking of Jesso-balam rice accessions

Ahmed *et al.* (2015) studied 27 *Jesso-Balam* rice accessions (Table 1) and grouped the genotypes into seven clusters for 18 quantitative morpho-physicochemical characters (Table 2) based on Mahalanobis' D^2 statistics. Ahmed *et al.* (2016a) also studied the same genotypes for 19 qualitative agro-morphological characters and grouped the genotypes into three major clusters (Fig. 1) using UPGMA clustering based on Dice coefficient. Earlier, Ahmed *et al.* (2014) also studied the same genotypes for 45 microsatellite or SSR markers (Table 3) and grouped the genotypes into three major clusters (Fig. 2) using UPGMA clustering based on Nei's genetic distance. Besides, the cumulative ranking (CR) based on D^2genetic distance 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 were calculated on the basis of the superiority of 27 *Jesso-Balam* rice accessions. For this, all the genotypes were primarily arranged in ascending order for each character or distances and were ranked as higher the rank with higher value of morpho-physicochemical character or higher genetic distance values (Ahmed, 2015)(Table 4). However, the morpho-physicochemical features of the core collection for *Jesso-Balam* rice accessions as reported by Ahmed *et al.* (2016b) are also presented in Table 5.

3.2 Method of selecting core collection from Jesso-balam rice accessions

In the present study, the core collection was selected using the hierarchical cluster analysis according to Zewdie *et al.* (2004), where accessions were sorted into different clusters, sub-clusters, groups and sub-groups from which a representative sample was drawn as suggested by Brown (1989). For this, the core sub-set was selected from each cluster for their representativeness (Cui *et al.*, 2004) from the seven clusters as grouped by Ahmed *et al.* (2015). Accessions were also selected according to their origins, geographical stratification, sampling strategy, cluster and random sampling to constitute the core collection (Zhang *et al.*, 2010). Moreover, the core selection process was improved by applying composite evaluation methods; such as sampling strategies based on genotypic values (Hu *et al.*, 2000), predicted genotypic value (Li *et al.*, 2004a), comparing different genetic distances, cluster methods and sampling strategies methods (Xu *et al.*, 2004), molecular characterization or SSR marker base data (Wang *et al.*, 2007; Zhang *et al.*, 2011), geographic distribution and characterization data (Li *et al.*, 2004b) and evaluating combined parameters along with scientific selection within groups (Wang *et al.*, 2007). The suitable sampling size of the core accession was usually about 10 to 30% of the entire collections (Zhang *et al.*, 2010).

The genotypes in the core collection should be superior, potential and representative as well as diverse. Considering this, genotype from each group/cluster having superior traits and criterion were selected. More or less similar strategies were also practiced earlier by Hu *et al.* (2000), Cui *et al.* (2004), Li *et al.* (2004b) and Upadhyaya *et al.* (2006). Wang *et al.* (2007) also identified different evaluating parameters for rice core collection based on genotypic values and molecular marker information.

3.3 Selection of core collection from Jesso-balam rice accessions

JBPL1, JBPL3, JBPL5, JBPL10, JBPL20 and JBPL26 genotypes were constellated into cluster I by Mahalanobis' D^2 clustering (Table 2). Again, the most diversed genotype was JBPL10, followed by JBPL5, JBPL1, JBPL20, JBPL26 and JBPL3 in D^2 genetic distance ranking (Table 4).

Table 1. Alphabetical list of 27 *Jesso-Balam* Transplant Aman Pure Line (TAPL) rice germplasm with BRRI Gene bank accession number (Ahmed *et al.*, 2015)

Sr. No.	Name	Code	Acc. no.	Sr. No.	Name	Code	Acc. no.
1	*Jesso-Balam* TAPL	JBPL1	2470	15	*Jesso-Balam* TAPL	JBPL15	2480
2	,,	JBPL2	2468	16	,,	JBPL16	2474
3	,,	JBPL3	2461	17	,,	JBPL17	2455
4	,,	JBPL4	2457	18	,,	JBPL18	2463
5	,,	JBPL5	2460	19	,,	JBPL19	2453
6	,,	JBPL6	2467	20	,,	JBPL20	2476
7	,,	JBPL7	2465	21	,,	JBPL21	2472
8	,,	JBPL8	2458	22	,,	JBPL22	2477
9	,,	JBPL9	2475	23	,,	JBPL23	2473
10	,,	JBPL10	2469	24	,,	JBPL24	2466
11	,,	JBPL11	2462	25	,,	JBPL25	2454
12	,,	JBPL12	2471	26	,,	JBPL26	2459
13	,,	JBPL13	2479	27	,,	JBPL27	2478
14	,,	JBPL14	2464	--	--	--	--

Table 2. Distribution of 27 *Jesso-Balam* rice accessions into seven clusters For 18 morpho-physicochemical characters based on Mahalanobis D^2 statistics (Ahmed *et al.*, 2015)

Cluster	No. of genotypes	Name of genotypes
I	6	JBPL1, JBPL3, JBPL5, JBPL10, JBPL20, JBPL26
II	3	JBPL8, JBPL13, JBPL17
III	6	JBPL2, JBPL6, JBPL7, JBPL19, JBPL24, JBPL25
IV	3	JBPL15, JBPL16, JBPL23
V	2	JBPL18, JBPL21
VI	5	JBPL4, JBPL9, JBPL11, JBPL12, JBPL14
VII	2	JBPL22, JBPL27

Legend: JBPL=*Jesso-Balam* Transplant Aman Pure Line.

On the other hand, JBPL1, JBPL3 and JBPL5 were the most diversed genotypes in Nei's genetic distance and cumulative ranking. However, all the genotypes except JBPL5 grouped in the same cluster according to the qualitative characters (Fig. 1), where as JBPL1, JBPL3, JBPL5 constellated into a same cluster, but JBPL10, JBPL20 with JBPL26 into a different cluster according to the UPGMA clustering based on Nei's genetic distance (Fig. 2). Again, JBPL26, JBPL10, JBPL1, JBPL20 and JBPL5 morphologically ranked as 2, 5, 7, 8 and 10, respectively (Table 4) and showed the highest and higher mean values for several important morpho-physicochemical characters (Table 5). Therefore, Ahmed (2015) selected the first sub-set of core collection for *Jesso-Balam* group of rice as JBPL26, JBPL10, JBPL1 and JBPL20. Zewdie *et al.* (2004) also emphasized on the use of cluster analysis with enlightened selection of accessions. Again, Zhang *et al.* (2010) reported that when to construct the core collection, the morphologic data usually applied extensively because of those data were recorded comprehensively.

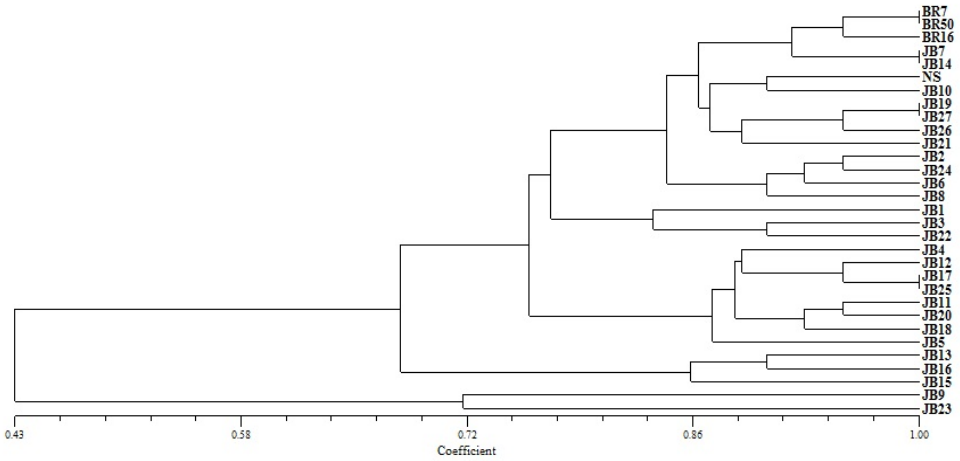

Figure 1. Dendrogram of 27*Jesso-Balam* rice accessions for 19 qualitative agro-morphological traits (Ahmed *et al.*, 2016a)

Table 3. List of 45 SSR markers used for molecular characterization of 27 *Jesso-Balam* rice accessions (Ahmed *et al.*, 2014)

Chrom. number	Primer Name	Position (cM)	Chrom. number	Primer Name	Position (cM)	Chrom. number	Primer Name	Position (cM)
1	RM283	31.4	5	RM413	26.7	9	RM296	0.0
	RM259	54.2		RM267	28.6		RM242	73.3
	RM237	115.2		RM161	96.9		RM215	99.4
	RM302	147.8		--	--		--	--
2	RM154	4.8	6	RM133	0.0	10	RM311	25.2
	RM279	17.3		RM584	26.2		RM271	59.4
	RM324	66.0		RM541	75.5		RM258	70.8
	RM250	170.1		RM162	108.3		RM171	92.8
3	RM60	0.0	7	RM125	24.8	11	RM21	85.7
	RM218	67.8		RM214	34.7		RM229	77.8
	RM55	168.2		RM18	90.4		RM206	102.9
	RM227	214.7		--	--		RM224	120.1
4	RM307	0.0	8	RM337	1.1	12	RM286	0.0
	RM273	94.4		RM223	80.5		RM19	20.9
	RM241	106.2		RM256	101.5		RM247	32.3
	RM127	150.1		RM433	116		RM260	61.7

Ref: http://www.gramene.org.

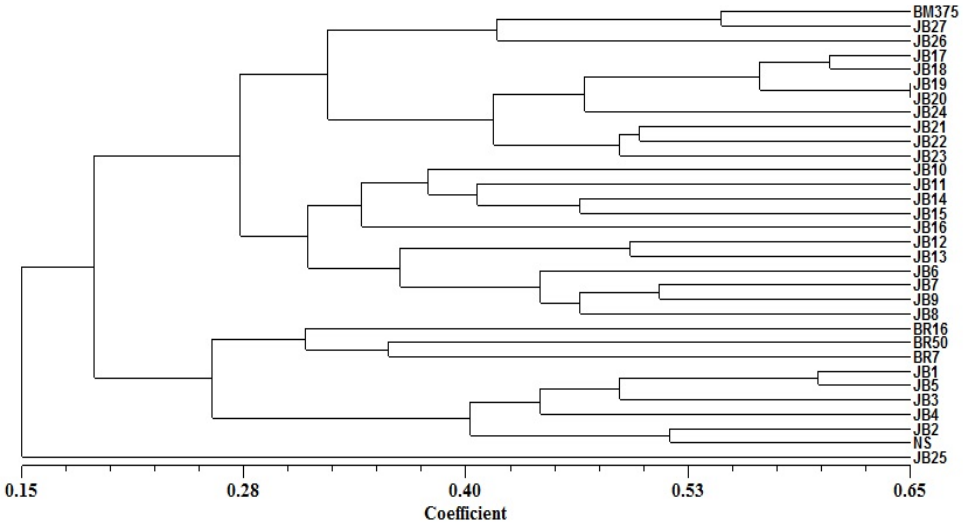

Figure 2. Dendrogram of 27 *Jesso-Balam* rice derived from UPGMA cluster analysis using Nei's genetic distance across 45 SSR markers (Ahmed *et al.*, 2014)

Similarly, JBPL8, JBPL13 and JBPL17 constellated into cluster II based on Mahalanobis' D^2 statistics (Table 2), where JBPL13 and JBPL21 were the most diversed genotypes, but JBPL17 and JBPL8 were the most diversed genotypes for Nei's genetic distance ranking and JBPL13 and JBPL17 for cumulative ranking (Table 4). Again, JBPL13, JBPL8 and JBPL17 morphologically ranked as 3, 4 and 16, respectively (Table 4) and showed the highest and higher mean values for several important morpho-physicochemical characters (Table 5). But, all these genotypes grouped into the same sub-cluster according to the UPGMA clustering method based on Nei's genetic distance (Fig. 2), whereas JBPL13 clubbed into a different cluster than from JBPL8 and JBPL17 according to the qualitative characters (Fig. 1). Therefore, Ahmed (2015) selected the second sub-set of core collection for *Jesso-Balam* group as JBPL13, JBPL8 and JBPL17. Wang *et al.* (2007) also mentioned that the key to improve the representativeness of a core collection is the scientific selection within groups.

Again, JBPL2, JBPL6, JBPL7, JBPL19 and JBPL24 and JBPL25 constellated into cluster III based on Mahalanobis D^2 statistics (Table 2), where the most diversed genotype was JBPL25 for D^2 genetic distance ranking, followed by JBPL19, JBPL6 and JBPL2, but JBPL25, JBPL2 and JBPL19 were the most diversed genotypes according to Nei's genetic distance and cumulative rankings (Table 4). Again, JBPL24, JBPL6, JBPL2, JBPL7, JBPL25 and JBPL19 morphologically ranked as 13, 19, 20, 23, 26 and 27, respectively (Table 4).

As a result, JBPL24 also showed higher means for seedling height (like JBPL13), effective tiller number, panicle length, milling outturn and lower mean for cooking time like JBPL25 (Table 5), whereas JBPL19 had the lowest mean for culm and plant height and higher mean for milling outturn and LB ratio along with lower mean for growth duration, while JBPL7 gave the highest mean for grain length and higher mean for LB and elongation ratio. Again, JBPL13 was already selected for similar characters.

Table 4. Different types of ranking based on morpho-physicochemical characters and inter-genotype distances (D^2, Dice coefficient and Nei's genetic distances) of 27 *Jesso-Balam* rice accessions (Shows only the *Jesso-Balam* rice) (Ahmed, 2015)

Genotype code	Morphological ranking (MR)	D^2Genetic distance ranking (DGDR)	Qualitative ranking (QR)	Nei's genetic distance ranking (NGDR)	Cumulative ranking (CR)
JB01	7	13	8	5	6
JB02	20	22	16	8	11
JB03	25	23	10	9	14
JB04	21	16	13	7	8
JB05	10	8	18	16	13
JB06	19	11	5	27	22
JB07	23	24	6	25	26
JB08	4	9	15	12	12
JB09	15	15	26	26	23
JB10	5	7	3	23	16
JB11	24	18	24	6	10
JB12	11	17	20	18	20
JB13	3	1	1	14	4
JB14	22	20	7	2	7
JB15	6	2	17	10	3
JB16	9	3	2	3	2
JB17	16	6	11	4	5
JB18	18	21	21	11	17
JB19	27	10	22	15	15
JB20	8	14	25	17	18
JB21	12	5	4	13	9
JB22	14	26	14	24	27
JB23	1	12	27	20	19
JB24	13	25	9	22	24
JB25	26	4	12	1	1
JB26	2	19	19	19	21
JB27	17	27	23	21	25

Note: For unfilled grain number, unfilled grain weight, awn length and cooking time, higher was 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 was the rank with higher superiority or diversity or genetic distance.

Table 5. Morpho-physicochemical features of selected core collection of *Jesso-Balam* rice accessions (Ahmed *et al*., 2016b)

Genotype	SH	PLL	PLW	PLA	FLL	FLW	FLA	CH	CD	PH	ETN	DM	PL	GYP	GYH	SYH	HI	BY	PBN	PBL	PBFGN	PBFGW	SBN	SBL	SBFGN	SBFGW	GL	LBR	TGW	MOT	HROT	CT	ER	IR	AC	PC
JBPL1	72.3	55.6	11.3	47.2	36.0	13.4	36.4	119	5.5	147	14	157	27.5	2.6	25.2	42.4	23.6	55.6	10	12.9	4.7	1.1	32	26.5	2.3	1.5	8.3	3.1	19.7	73	96	16	1.5	2.9	23.7	7.9
JBPL8	71.8	62.3	11.2	52.3	38.2	14.0	40.2	127	5.5	153	11	151	26.1	2.9	20.1	31.5	32.2	46.3	12	12.7	5.1	1.3	44	28.1	2.0	1.6	8.3	3.3	19.6	73	96	16	1.4	2.3	24.3	9.3
JBPL9	65.7	56.0	10.9	45.6	35.4	13.5	35.8	106	4.7	135	14	152	28.6	2.9	25.9	32.3	34.9	49.6	12	13.5	5.0	1.2	49	27.6	2.1	1.7	7.5	3.2	18.3	74	68	15	1.7	3.1	22.9	9.3
JBPL10	72.6	58.2	11.3	49.2	34.0	13.6	34.6	125	5.8	152	15	157	27.4	3.2	21.6	41.6	24.4	55.2	13	13.6	4.4	1.2	45	27.0	2.0	2.1	8.2	3.2	19.7	69	93	14	1.5	2.9	24.3	6.0
JBPL13	73.7	65.4	10.6	52.0	39.5	13.9	41.1	115	5.4	144	11	150	28.6	3.0	26.0	34.0	37.3	53.6	11	11.7	4.7	1.5	30	27.0	2.2	1.5	9.2	3.2	25.9	69	90	18	1.5	2.8	25.2	6.3
JBPL15	66.4	65.2	12.4	60.5	38.1	14.6	41.9	125	5.7	153	8	139	27.8	3.1	20.3	26.1	33.2	39.1	12	12.4	4.1	0.9	49	28.1	2.6	2.2	8.5	3.4	20.3	70	90	17	1.4	3.1	24.1	7.1
JBPL16	73.6	69.2	13.0	67.3	35.0	16.0	42.2	114	5.9	140	10	154	25.3	3.1	19.9	36.0	34.5	54.9	12	11.6	4.9	1.3	40	24.7	2.3	1.8	8.8	3.2	24.0	72	88	18	1.3	2.6	22.6	7.0
JBPL17	56.1	66.6	11.8	58.9	38.1	13.9	39.8	113.9	5.3	140	12	36.7	147	2.1	26.5	23.6	32.4	53.7	12	12.1	4.5	0.1	53	27.7	2.2	2.0	8.3	3.3	19.2	72	86	16	1.3	2.9	25.3	7
JBPL19	55.5	52.3	10.2	40.1	33.1	13.1	32.5	100	4.4	123	13	140	23.5	1.8	19.4	23.1	34.7	35.1	10	9.9	4.0	1.0	20	23.1	2.3	0.8	8.5	3.5	21.1	74	93	18	1.2	2.9	24.6	6.0
JBPL20	66.6	56.2	11.2	47.1	34.3	13.7	35.3	122	5.5	150	12	150	27.9	3.4	21.3	32.6	33.0	48.6	13	12.4	4.6	1.4	41	24.8	2.7	2.0	7.7	2.9	18.8	73	95	17	1.3	2.9	25.6	7.0
JBPL21	64.3	59.3	11.7	52.0	33.5	14.0	35.3	139	5.6	168	14	160	29.9	2.4	22.7	47.0	21.2	59.7	12	11.7	4.5	1.1	39	26.3	2.0	1.4	8.1	3.2	17.8	73	85	15	1.3	3.1	23.5	7.9
JBPL23	68.5	59.3	13.1	58.2	40.2	15.9	47.8	117	5.8	143	13	156	26.3	2.9	26.1	36.2	35.7	56.3	12	10.4	4.6	1.2	37	20.1	2.5	1.6	8.6	3.3	21.1	72	95	16	1.4	2.9	26.5	7.0
JBPL25	50.6	55.0	9.2	37.8	33.7	11.0	27.9	113	4.7	143	15	145	29.4	2.6	16.7	21.0	33.3	31.6	11	11.0	5.6	0.7	49	23.0	2.3	1.9	5.9	2.8	11.0	75	95	14	1.2	3.1	25.1	9.9
JBPL26	65.0	60.1	10.7	48.1	34.8	14.0	36.6	122	5.3	149	14	146	26.8	3.3	26.2	33.7	31.7	49.5	12	12.2	4.7	1.4	41	26.9	2.4	1.9	8.5	3.3	21.9	71	79	17	1.3	2.9	25.8	7.2
Range	50.6-73.7	46.6-69.2	9.2-13.1	36.9-67.3	28-40.2	11-16.0	28.5-47.8	100-139	4.4-6	123-168	7-15	139-160	23.5-29.9	1.7-3.4	16.7-26.5	21-47	21.2-43.2	31.6-59.7	9.7-13.7	9.7-13.6	4-5.6	0.1-1.6	19.7-53	20-28.1	1.6-2.7	0.8-2.2	5.9-9.4	2.8-3.6	11-25.9	69-75	48-96	12-19	1.2-1.7	2.3-3.1	22.6-26.5	5.9-9.9

Legend:
SH=Seedling height (cm), PLL=Penultimate leaf length (cm), PLW=Penultimate leaf width (mm), PLA=Penultimate leaf area (cm^2), FLL=Flag leaf length (cm), FLW=Flag leaf width (mm), FLA=Flag leaf area (cm^2), CH=Culm height (cm), CD=Culm diameter (mm), PH=Plant height (cm), ETN=Effective tiller number per hill, DM=Days to maturity, PL=Panicle length (cm), GYP=Grain yield per panicle (g), GYH=Grain yield per hill (g), SYH=Straw yield per hill (g), HI=Harvest index, BY=Biological yield, PBN=Primary branch number, PBL=Primary branch length (cm), PBFGN=Primary branch filled grain number, PBFGW=Primary branch filled grain weight (g), SBN=Secondary branch number, SBL=Secondary branch length (mm), SBFGN= Secondary branch filled grain number, SBFGW= Secondary branch filled grain weight (g), GL=Grain length (mm), LBR=Length-breath ratio, TGW=1000-grain weight (g), MOT= Milling outturn (%), HROT= Head rice outturn (%), CT=Cooking time (min), ER=Elongation ratio, IR=Imbibition ratio, AC=Amylose content (%) and PC=Protein content (%).

However, JBPL25 gave the highest mean for effective tiller number and higher means for panicle length like JBPL24 and secondary branch number, while JBPL6 gave the highest imbibitions ration like JBPL25 and higher grain yields per panicle and hill like JBPL13. Again, all these genotypes grouped into the same cluster according to the qualitative characters (Fig. 1). But JBPL24 grouped with JBPL6, JBPL7 and JBPL19, while JBPL2 clubbed into a different sub-cluster under the same cluster and JBPL25 clubbed into a different single cluster in UPGMA clustering method based on Nei's genetic distance (Fig. 2). Moreover, JBPL6 clubbed into the same sub-cluster with JBPL8, while JBPL19 was duplicated with JBPL20 for the same molecular characters and both JBPL8 and JBPL20 were already selected. But, JBPL19 was different from JBPL20 for plant height, days to maturity, grain yield per panicle, primary branch length and secondary branch filled grain weight characters (Table 5). Therefore, Ahmed (2015) selected the third sub-set of core collection for *Jesso-Balam* germplasm as JBPL19 and JBPL25. Wang *et al*. (2007) also identified different evaluating parameters for rice core collection based on genotypic values and molecular marker information.

Next, JBPL15, JBPL16 and JBPL23 constellated into cluster IV (Table 2), where the most diversed genotype was JBPL15 for D^2 genetic distance ranking, followed by JBPL16 and JBPL23 (Table 4). On the other hand, JBPL16, JBPL15 and JBPL23 were the most diversed genotypes for Nei's genetic distance and cumulative ranking. But, JBPL23, JBPL15 and JBPL16 morphologically ranked as 1, 6 and 9, respectively (Table 4). As a result, JBPL23 also showed the highest means for penultimate leaf width, flag leaf length and area, grain yield per hill, biological yield and amylose percent and higher mean for flag leaf width, while JBPL16 gave the highest means for seedling height, penultimate leaf length and area and flag leaf width and higher means for flag leaf area and grain length, whereas JBPL15 had the highest secondary branch length and filled grain weight per secondary branch and higher means for penultimate and flag leaf lengths and areas, plant height, grain yield per panicle, primary branch number and length and secondary branch number and the lowest mean for days to maturity (Table 5). Besides, JBPL15 and JBPL16 constellated into the different cluster from JBPL23 for qualitative characters (Fig. 1) and all the genotypes constellated into the same cluster based on Nei's genetic distance (Fig. 2). Therefore, Ahmed (2015) selected the forth sub-set of core collection for *Jesso-Balam* rice as JBPL23, JBPL16 and JBPL15.

Again, JBPL18 and JBPL21 constellated into cluster V (Table 2), where JBPL21 was more diversed according to D^2 genetic distance, qualitative and cumulative rankings, but JBPL18 was more diversed in case of Nei's genetic distance ranking (Table 4). But, JBPL21 and JBPL18 morphologically ranked as 12 and 18. As a result, JBPL21 also showed the highest means for culm and plant heights, panicle length, days to maturity, straw and biological yields and higher means for culm diameter and effective tiller number (Table 5). On the other hand, both the genotypes constellated into the same cluster for both qualitative characters (Fig. 1) as well as for Nei's genetic distance (Fig. 2). Therefore, Ahmed (2015) selected the fifth sub-set of core genotype for *Jesso-Balam* group as JBPL21. Upadhyaya *et al.* (2006) also developed core subset by using the data based on quantitative traits.

Again, JBPL4, JBPL9, JBPL11, JBPL12 and JBPL14 constellated into cluster VI (Table 2), where JBPL14, JBPL4 and JBPL11 were the most diversed for Nei's genetic distance and cumulative rankings (Table 4). However, all the genotypes except JBPL9 constellated into the same cluster for qualitative characters (Fig. 1), as well as for molecular characters, where only JBPL4 grouped in different sub-cluster (Fig. 2). But, JBPL12 and JBPL9 morphologically ranked as 11 and 15 (Table 4), where JBPL9 gave the highest means for elongation and imbibitions ratio and higher means for effective tiller

number, panicle length, primary branch number and length, secondary branches number, grain yield per hill, milling outturn and protein content, but lower mean value for culm and plant height (Table 5). But, JBPL9 was the only genotype that formed a single major cluster for the qualitative characters (Fig. 1). Therefore, Ahmed (2015) selected the sixth sub-set of core genotype for *Jesso-Balam* rice as JBPL9.

Finally, JBPL22 and JBPL27 were grouped together in cluster VII by D^2 clustering (Table 2) and morphologically ranked as 14 and 17, respectively (Table 4). As a result, JBPL22 also gave the highest means for harvest index, LB and imbibitions ratios, whereas JBPL27 gave the higher means for flag leaf length, effective tiller number, grain yield per hill, harvest index, primary branch number and LB ratio and lower mean values for culm and plant heights (Table 5). But JBPL10, JBPL13, JBPL15, JBPL19, JBPL23 and JBPL25 were already nominated for core collection for similar characters. Moreover, JBPL22 clubbed into the same cluster with JBPL1, whereas JBPL27 was duplicated with JBPL19 according to the qualitative characters (Fig. 1). Again, JBPL22 grouped in the same sub-cluster with JBPL21 and JBPL23, while JBPL27 with JBPL26 according to the molecular characters (Fig. 2). Therefore, Ahmed (2015) selected no genotype for core collection of *Jesso-Balam* group of rice from this cluster. 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.

4. Conclusions

Genotypes JBPL1, JBPL8, JBPL9, JBPL10, JBPL13, JBPL15, JBPL16, JBPL17, JBPL19, JBPL20, JBPL21, JBPL23, JBPL25 and JBPL26 were selected as the core collection of *Jesso-Balam* rice having all the possible superior morpho-physicochemical traits of the group. Moreover, the identified genotypes may be considered as the 'working collection' of *Jesso-Balam* group of rice for their safe conservation and effective utilization in Gene bank.

References

Ahmed, M. S. 2015. Agro-morphological, physico-chemical and molecular characterization for developing core collections from similar named rice (*Oryza sativa* L.) groups of Bangladesh. *Ph. D. Thesis*, Department of Genetics and Plant Breeding, BAU, Mymensingh, Bangladesh, 41-179 pp.

Ahmed, M. S., Bashar, M. K., Wazuddin, M. and Shamsuddin, A. K. M. 2015. Genetic divergence of *Jesso-Balam* rice (*Oryza sativa* L.) of Bangladesh. *International Journal of Agricultural Research, Innovation and Technology*, 5(1): 22-27.

Ahmed, M. S., Bashar, M. K., Wazuddin, M. and Shamsuddin, A. K. M. 2016a. Agro-morphological qualitative characterization of *Jesso-Balam* rice (*Oryza sativa* L.) accessions in Bangladesh. *International Journal of Agronomy and Agricultural Research*, 8(1): 50-58.

Ahmed, M. S., Bashar, M. K., Wazuddin, M. and Shamsuddin, A. K. M. 2016b. Morpho-physicochemical study of *Jesso-Balam* rice (*Oryza sativa* L.) accessions of Bangladesh. *Asian Journal of Crop Science*, 8(1):1-13. DOI: 10.3923/ajcs.2016.13.23.

Ahmed, M. S., Khalequzzaman, M., Bashar, M. K., and Shamsuddin, A. K. M. 2014.Genetic diversity of *Balam* and *Jesso-Balam* rice (*Oryza sativa*L.) germplasm of Bangladesh revealed by SSR markers. *Bangladesh Journal of Plant Breeding and Genetics*, 27(2): 17-24.DOI:http://dx.doi.org/10.3329/bjpbg.v27i2.27847.

Aranzana, M. J., Abbassi, E. K., Howad, W. and Arus, P. 2010. Genetic variation, population structure and linkage disequilibrium in peach commercial varieties. *BioMed Central Genetics*, 11:69.

Brown, A. H. D. 1989. Core collections: a practical approach to genetic resources management. *Genome*, 31: 818-824.

Brown, A. H. D. 1995. The core collection at the crossroads. In: *Core Collections of Plant Genetic Resources*, (eds.). T. Hodgkin, A. H. D. Brown, T. J. L. van Hintum and E. A. V. Morales, Chichester, John Wiley and Sons, UK, 3-19 pp.

Cui, Y. H., Qiu, L. J., Chang, R. Z. and Lu, W. H. 2004. Representative test for primary core collection of summer sowing soybeans in Huanghuai Region of China. *Acta Agronomica Sinica*, 30: 284-288.

El Bakkali, A., Haouane, H., Moukhli, A., Costes, E., Van Damme, P. and Khadari, B. 2013. Construction of core collections suitable for association mapping to optimize use of Mediterranean Olive (*Olea europaea* L.) genetic resources. *PLoS ONE*, 8(5): e61265. doi:10.1371/journal.pone.0061265.

Frankel, O. H. 1984. Genetic perspectives of germplasm conservation, In: *Genetic manipulation: impact on man and society*, (eds.). W. Arber, K. Llimensee, W. J. Peacock, and P. Starlinger, Cambridge, Cambridge University Press, 161-70 pp.

Guo, Y., Li, Y., Hong, H. and Qiu, L. J. 2014. Establishment of the integrated applied core collection and its comparison with mini core collection in soybean (*Glycine max*). *The Crop Journal*, 2: 38-45.

Hu, J., Zhu, J. and Xu, H. M. 2000. Methods of constructing core collections by stepwise clustering with three sampling strategies based on the genotypic values of crops. *Theoretical and Applied Genetics*, 101: 264-68.

Jansky, S. H., Dawson, J. and Spooner, D. M. 2015. How do we address the disconnect between genetic and morphological diversity in germplasm collections? *American Journal of Botany*, 102(8): 1213-1215.

Li, C. T., Shi, C. H., Wu, J. G., Xu, H. M., Zhang, H. Z. and Ren, Y. L. 2004a. Methods of developing core collections based on the predicted genotypic value of rice (*Oryza sativa* L.). *Theoretical and Applied Genetics*, 108: 1172-76.

Li, Y., Shi, Y. S., Cao, Y. S. and Wang, T. Y. 2004b. Establishment of a core collection for maize germplasm preserved in Chinese National Gene bank using geographic distribution and characterization data. *Genetic Resources and Crop Evolution*, 51: 845-852.

Liang, W., Dondini, L., De Franceschi, P., Paris, R., Sansavini, S. and Tartarini, S. 2015. Genetic diversity, population structure and construction of a core collection of apple cultivars from Italian germplasm. *Plant Molecular Biology Reporter*, 33:458-473. DOI: 10.1007/s11105-014-0754-9.

Mario Paredes, C., Viviana Becerra, V., Juan Tay, U., Matthew W., B. and Gabriel Bascur, B. 2010. Selection of a representative core collection from the Chilean common bean germplasm. *Chilean Journal of Agricultural Research*, 70(1):3-15.

Upadhyaya, H. D., Gowda, C. L. L., Pundir, R. P. S., Reddy, V. G. and Singh, S. 2006. Development of core subset of finger millet germplasm using geographical origin and data on 14 quantitative traits. *Genetic Resources and Crop Evolution*, 53(4): 679-685.

Upadhyaya, H. D., Yadav, D., Dronavalli, N., Gowda, C. L. L. and Singh, S. 2010. Mini core germplasm collections for infusing genetic diversity in plant breeding programs. *Electronic Journal of Plant Breeding*, 1(4): 1294-1309.

Van Hintum, Th. J.L., Brown, A.H.D., Spillane, C. and Hodgkin, T. 2000. Core collections of plant genetic resources. IPGRI Technical Bulletin No. 3. International Plant Genetic Resources Institute, Rome, Italy.

Wang, J. C., Hu, J., Zhang, C. F. and Zhang, S. 2007. Assessment on evaluating parameters of rice core collections constructed by genotypic values and molecular marker information. *Rice Science*, 14(2): 101-110.

Xu, C., Gao, J., Du, Z., Li, D., Wang, Z., Li, Y. and Pang, X. 2016. Identifying the genetic diversity, genetic structure and a core collection of *Ziziphus jujuba* Mill. var. jujuba accessions using microsatellite markers. *Scientific Reports*, 6:31503. DOI: 10.1038/srep31503.

Xu, H. M., Qiu, Y. X., Hu, J. and Wang, J.C. 2004. Methods of constructing core collection of crop germplasm by comparing different genetic distances, cluster methods and sampling strategies. *Acta Agronomica Sinica*, 30: 932-36.

Yan, L., Feng, Y., Yang, C. Y., Shi, X. L. and Zhang, M. C. 2012. The character of protein and oil content distribution among introgression lines using Jidou12 as recipient parent. *Acta Agriculturae Boreali Sinica*, 27:87-92.

Zewdie, Y., Tong, N. K. and Bosland, P. 2004. Establishing a core collection of Capsicum using a cluster analysis with enlightened selection of accessions. *Genetic Resources and Crop Evolution*, 51: 147-151.

Zhang, J., Wang, Y., Zhang, X. Z., Li, T. H., Wang, K., Xu, X. F. and Han, Z. H. 2010. Sampling strategy to develop a primary core collection of apple cultivars based on fruit traits. *African Journal of Biotechnology*, 9:123-127.

Zhang, P., Jinquan, L., Xiaoling, L., Xiangdong, L., Xingjuan, Z. and Yonggen, L. 2011. Population structure and genetic diversity in a rice core collection (*Oryza sativa* L.) investigated with SSR Markers. *PLoS ONE*, 6(12): 1-13.

Zhang, P., Liu, X., Tong, H., Lu, Y. and Li, J. 2014. Association mapping for important agronomic traits in core collection of Rice (*Oryza sativa* L.) with SSR Markers. *PLoS ONE*,9(10):e111508.doi:10.1371/journal.pone.0111508.