



## Agro-morphological qualitative characterization of *Jesso-Balam* rice (*Oryza sativa* L.) accessions in Bangladesh

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### Abstract

Twenty-seven *Jesso-Balam* rice accessions of Bangladesh were studied for 21 qualitative agro-morphological characters at BRRI during T. Aman 2009 and T. Aman 2011 seasons. The presence and shape of penultimate leaf ligule showed no variations among the genotypes. Out of 19 characters, majority of the genotypes showed no anthocyanin color in leaf sheath (93%), medium intensity of anthocyanin color in basal leaf sheath (7%), green leaf blade (74%), strong surface pubescence of penultimate leaf blade (48%), no anthocyanin color in auricles and collar (93%), colorless ligule (93%), white color of stigma (93%), erect blade of flag leaf (52%), erect curvature of lateral tiller (100%), no anthocyanin color in nodes (93%), weak intensity of anthocyanin color in nodes (7%), weak intensity of anthocyanin color in internodes (67%), yellowish to straw anthocyanin color of lemma and palea (48%), medium intensity of anthocyanin color in lemma and palea (41%), yellowish/straw color of apiculus (93%), awnless (89%), awns at tip only (11%), yellowish white to straw color awns (100%) and intermediate type of leaf senescence (74%). On the other hand, the *Jesso-Balam* germplasm along with BR7, BR16, BRRI dhan50 and *Nizersail* were grouped into three major clusters according to the UPGMA clustering method based on Dice coefficient. Cluster III was the major group with maximum genotypes (26), while clusters I had two (JBPL9 and JBPL23) and cluster II had three genotypes (JBPL13, JBPL15 and JBPL16), respectively. The genetic distance ranged from 0.000 to 9.969. Three pairs of accessions (2465 and 2464), (2455 and 2454) and (2453 and 2478) in cluster III were found duplicates. Finally, the *Jesso-Balam* pure lines possessed exclusive variability and unique features which need safe conservation and sustainable use in future rice breeding programmes for issues like intellectual property rights.

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## Introduction

Rice (*Oryza sativa* L.) is the world's most important cereal crop and serves as the primary source of staple food for more than half of the global population (Emani *et al.*, 2008). Agriculture as the single largest economic sector and rice as the main cereal crop of the country, Bangladesh is one of the largest producers and consumers of rice in the world and self-sufficient for own demand. However, its national average productivity is still low and future demands need to adjust in the context of shrinking rice land and water resources of the country. Besides, global climate change now negatively affects rice production. As a result, diverse genes governing different biotic and abiotic factors as well as different quality traits like nutritional, medicinal and indigenous or traditional values, may be considered for future rice variety development.

Historically, abundant diversified rice landraces were cultivated in Bangladesh from time immemorial. Again, Ahmed *et al.* (2010) stated that rice diversity is now threatened due to extensive cultivation of Modern Varieties (MVs) all over the country and various interventions of rice habitat like cyclone, flood, soil salinity etc. Consequently, more rice germplasm need to be utilized in new rice varieties for maintaining rice gene diversity in farmer's field.

Harlan (1975) mentioned that crop landraces display genetic variation for useful quantitative and qualitative characters. Sarma *et al.* (2003) reported that rice germplasm is not only endowed with genetic diversity but also represents a wealth of valuable genes. Similarly, Yadav *et al.* (2013) observed that the rice germplasm is a rich reservoir of valuable genes that plant breeders can harness for crop improvement. Different agro-morphological traits (passport data) play very important roles for their characterization and varietal identification which ultimately helps rice breeder for its improvement (Laxuman *et al.*, 2011). Caldo *et al.* (1996) reported that rice genetic resources including landraces and traditional varieties is a good source of important alleles to develop new rice varieties. These germplasm

serve as the foundation of any rice breeding program because they are the source of important traits necessary for improving and developing new breeds of rice varieties.

Characterization of rice germplasm increases its utility in any breeding program. The use of agro-morphological traits is the most common approach utilized to estimate relationships between genotypes (Bajracharya *et al.*, 2006). On the other hand, knowledge of existing genetic diversity and its distribution in crop species is useful for germplasm conservation and selection of parents with diverse genetic background, thereby rendering crop improvement more efficient (Teklu *et al.*, 2006). The conservation and characterization of these genetic resources is a necessity not only for posterity, but also for utilization in different improvement programs such as breeding for improved yield and tolerance to various stresses. It is important to assess the diversity of these germplasm materials to provide insights in the diversity of these germplasm (Rabara *et al.*, 2014).

Ford-Lloyd *et al.* (1997) mentioned that the identification of duplicate accessions was done exclusively on the documentation of the accessions on morphological characters. However, the characterization of landraces will be useful for breeders, researchers and farmers to identify and choose the restoration and conservation of beneficial genes for crop improvement and also to seek protection under Protection of Plant Varieties and Farmer's Rights Act (Rao *et al.*, 2013). But, limited work has been done on characterization of rice accessions of Bangladesh. Therefore, systematic attempts have to be made to make a total inventory of this valuable gene pool for quantifying the availability of new useful genes of this source. Besides, it is very important to protect bio-piracy and geographical indications and issues related to intellectual property rights (IPRs). The present experiment was, therefore, undertaken to study the qualitative agro-morphological characters of 27 *Jesso-Balam* pure line rice accessions of Bangladesh for identification and better conservation and use of germplasm.

**Material and methods**

*Materials of the experiment*

In total 27 *Jesso-Balam* pure lines (PL) rice accessions of Bangladesh along with BR7, BR16, BRRI dhan50 and *Nizersail* were characterized for 21 qualitative agro-morphological traits (Table 1). Thirty days old single seedling for each accession was transplanted using spacing within and between rows of 20 and 25 cm, respectively during T. Aman 2009

and T. Aman 2011 seasons at BRRI Gazipur. The lands were medium high and homogenous with respect to soil fertility. The experimental plot was prepared thoroughly by 4-5 times deep ploughing and cross ploughing followed by laddering to attain a good puddle situation. The unit plot size was 4 rows of each 2.7 m long. The fertilizers were applied at the rate of 60-50-40-10 kg NPKS hectare<sup>-1</sup>.

**Table 1.** List of the 27 *Jesso Balam* TAPL\* accessions.

Code name	Accession <sup>1</sup> number	Code name	Accession <sup>1</sup> number	Code name	Accession <sup>1</sup> number	Code name	Accession <sup>1</sup> number
JBPL1	2470	JBPL8	2458	JBPL15	2480	JBPL22	2477
JBPL2	2468	JBPL9	2475	JBPL16	2474	JBPL23	2473
JBPL3	2461	JBPL10	2469	JBPL17	2455	JBPL24	2466
JBPL4	2457	JBPL11	2462	JBPL18	2463	JBPL25	2454
JBPL5	2460	JBPL12	2471	JBPL19	2453	JBPL26	2459
JBPL6	2467	JBPL13	2479	JBPL20	2476	JBPL27	2478
JBPL7	2465	JBPL14	2464	JBPL21	2472		

\* = Transplant Aman Pure Line <sup>1</sup> = BRRI Rice Genebank accession number.

*Method of the experiment*

The qualitative characters were studied and recorded using “Procedure of DUS tests for inbreed and hybrid Rice” (as approved by National Seed Broad, Ministry of Agriculture in Bangladesh, 2001) and “UPOV Rice Test Guidelines” (sources: TG/16/8; project 3). The states of the characteristics in numerical forms (1 to 9) were given against the state/codes of each characteristic in descriptor. However, the data were also studied by using the Bioversity International, IRRI, WARDA (2006).

*Analysis of the experiment*

For analysis, all recorded data were first transformed to binary form (Sneath and Sokal, 1973). The presence and absence of the different variants scored as 1 and 0, were determined using Power Marker version 3.25 software (Liu and Muse, 2005). Then the cluster analysis was performed with the NTSYS-pc version 2.2 software as described by Rohlf (2002). For this, a similarity matrix was determined with the Simqual subprogram using the Dice coefficient, followed by cluster analysis with the SAHN subprogram using the

un-weighted pair group method on arithmetic mean (UPGMA) clustering method. Finally, the DCenter of NTSYS-pc was performed for principal coordinate analysis (PCoA) of the similarity matrix data.

**Result and discussion**

*Features of the qualitative characters*

The 27 *Jesso-Balam* pure lines showed wide degree of differences for studied 19 qualitative agro-morphological characters. On the other hand, all the genotypes produced split or two-cleft type shape penultimate leaf ligule. Hossain (2008) reported similar result for green leaf color, presence of penultimate leaf ligule and two-cleft ligule shape. Nascimento *et al.* (2011) observed no variation for light green inter node color and intermediate panicle type. Mahalingam *et al.* (2012) found presence of leaf auricle, absence of anthocyanin coloration of nodes and well exerted panicle traits in rice.

The studied qualitative agro-morphological characters showed wide degree of variations among the pure lines (Fig. 1). Each of the studied characters

showed different types of variations. Out of 27 germplasm, anthocyanin coloration in leaf sheath was present on only JBPL9 and JBPL23 (7% germplasm). The rest of the 25 genotypes (93%) had no anthocyanin coloration in leaf sheath (Fig. 2). The

intensity of anthocyanin color in basal leaf sheath was absent or very weak in 93% germplasm and the rest of the two genotypes (JBPL9 and JBPL23) had medium intensity of anthocyanin color in basal leaf sheath (Table 2).

**Table 2.** Unique identified *Jesso-Balam* accessions.

Qualitative characteristics	Index value/score*	Unique pure lines
Leaf sheath: anthocyanin color	9 = present	JBPL9 and JBPL23
Penultimate Leaf: anthocyanin color of auricles and collar	9 = present	JBPL9 and JBPL23
Penultimate Leaf: color of ligule	4 = light purple	JBPL9 and JBPL23
Stigma: color of stigma	5 = purple	JBPL9 and JBPL23
Stem: anthocyanin color of nodes	9 = present	JBPL9 and JBPL23
Spikelet: anthocyanin color of lemma and palea	3 = brown spots/furrows on straw 6 = light purple on straw	JBPL1, JBPL3, JBPL13, JBPL21 and JBPL22 JBPL9
Spikelet: apiculus color.	8 = purple apex	JBPL9 and JBPL23

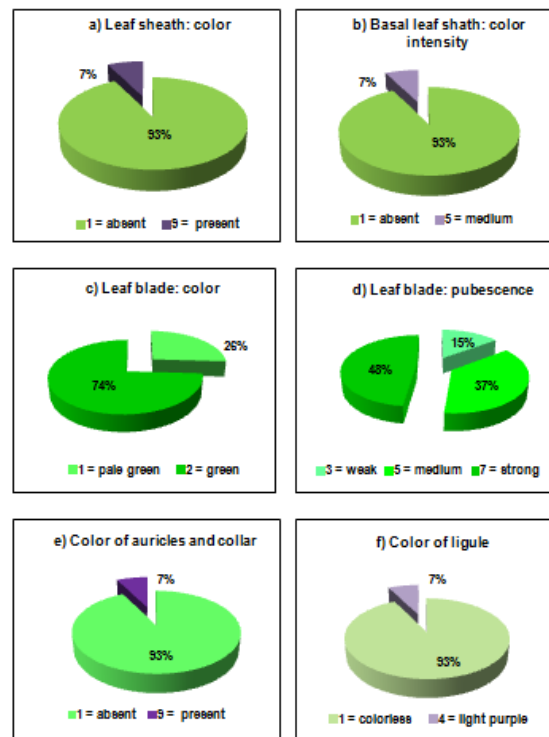
\* Procedure of DUS tests for inbred and hybrid Rice of Bangladesh



Legend: 1<sup>st</sup> row contains JB1 to JB9, 2<sup>nd</sup> row contains JB10 to JB18 and 3<sup>rd</sup> row contains JB19 to JB27 (all from left to right).

**Fig. 1.** Variation in grains among the 27 *Jesso-Balam* pure lines.

Maximum number of germplasm (74%) showed green color leaf blade, while 26% of the germplasm had pale green leaf blade. Maximum number of germplasm (48%) had strong surface pubescence on the penultimate leaf blade. On the other hand, 37% of the germplasm had medium and 15% had weak surface pubescence.

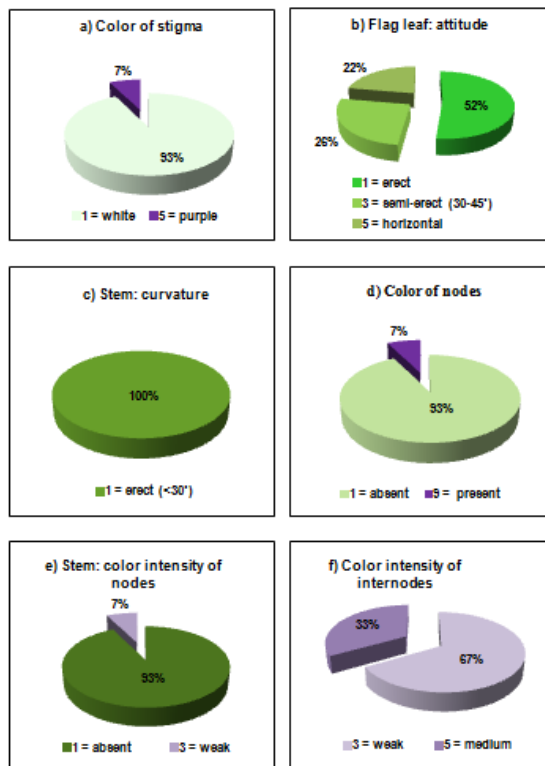


**Fig. 2.** Variation of leaf sheath color and its intensity, leaf blade color and its pubescence and auricles, collar and ligule color for *Jesso-Balam* rice.

Anthocyanin coloration of auricles and collar was present in only JBPL9 and JBPL23 (7%), while rest of the germplasm (93%) had no anthocyanin coloration.

Around, 93% of the germplasm had colorless ligule in penultimate leaf and only JBPL9 and JBPL23 (7%) had light purple color ligule.

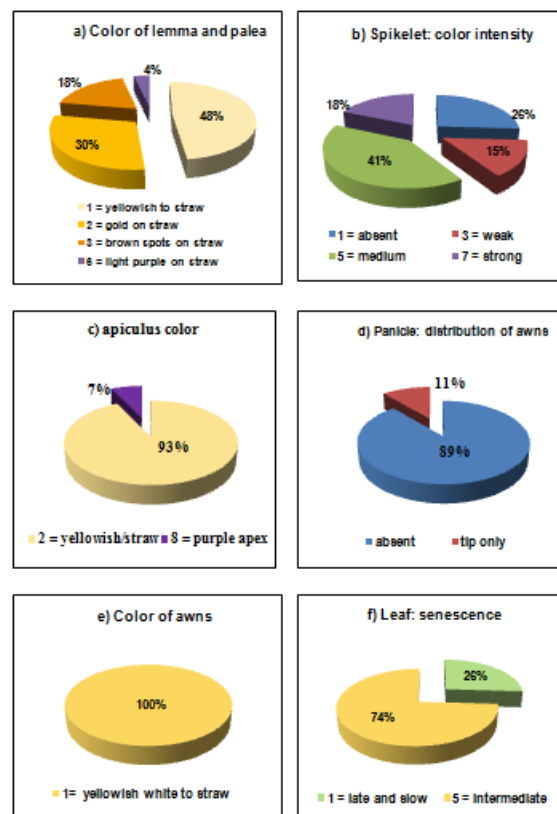
The color of the stigma of 93% germplasm was found as white, while only 7% of the germplasm *viz.* JBPL9 and JBPL23 had purple color of stigma (Fig. 3). Maximum number of germplasm (52%) had erect attitude of blade of the flag leaf. Whereas 26% of the germplasm had semi-erect and 22% of the germplasm had horizontal type of leaf blade. The main axes of the lateral tiller of stem of all the germplasm (100%) had erect curvature. Only JBPL9 and JBPL23 (7%) had weak intensity of anthocyanin coloration in nodes, while rest of the germplasm (93%) had no anthocyanin coloration. The anthocyanin coloration of internodes of 66% of the germplasm had weak and 33% germplasm had medium intensity.



**Fig. 3.** Variation of stigma color, flag leaf attitude, stem curvature, color of nodes and internodes and its intensity for *Jesso-Balam* rice.

The anthocyanin coloration of lemma and pale showed wide range of variability among the *Jesso-Balam* rice germplasm (Fig. 1). Out of the 27

germplasm, 48% of the germplasm had yellowish to straw color lemma and palea (Fig. 4), while 30% had gold and or gold furrows on straw, 18% had brown spots/furrows on straw and only 4% had light purple on straw color lemma and palea. Only JBPL9 germplasm had light purple on straw color lemma and pale, while JBPL1, JBPL3, JBPL13, JBPL21 and JBPL22 had brown spots/furrows on straw color. Around 41% of the germplasm had medium, 26% had absent or very weak, 15% had weak and 18% had strong intensity of anthocyanin coloration on lemma and palea. Around 93% of the germplasm showed yellowish/straw color and 7% of the germplasm (JBPL9 and JBPL23) showed purple apex color of apiculus.



**Fig. 4.** Variation of lemma and pale color and its intensity, apiculus color, awn distribution and its color and leaf senescence for *Jesso-Balam* rice.

Out of the 27 germplasm, awns were present only in 11% of the germplasm but rest of the genotypes (89%) was awnless. All the germplasm (11%) having awn showed awns at tip only of which all showed yellowish white to straw color awns. A maximum number of

germplasm (54%) had intermediate type of leaf senescence at the time of maturity, while rest of the germplasm showed late and slow type senescence.

#### *Distribution of the qualitative characters*

In the study, the majority of the genotypes showed no anthocyanin color in leaf sheath (93%) (Fig. 2), medium intensity of anthocyanin color in basal leaf sheath (7%), green leaf blade color (74%), strong surface pubescence of penultimate leaf blade (48%), no anthocyanin color in auricles and collar of penultimate leaf (93%), colorless ligule of penultimate leaf (93%), white color of stigma (93%) (Fig. 3), erect blade of flag leaf (52%), erect curvature of lateral tiller (100%), no anthocyanin color in nodes (93%), weak intensity of anthocyanin color in nodes (7%), weak intensity of anthocyanin color in internodes (67%), yellowish to straw anthocyanin color of lemma and palea (below apex area) (48%) (Fig. 4), medium intensity of anthocyanin color in lemma and palea (41%), yellowish/straw color of apiculus (93%), awnless (89%), awns at tip only (11%), yellowish white to straw color awns (100%) and intermediate type of leaf senescence (74%) for the 27 pure lines of *Jesso-Balam* rice germplasm.

Adair *et al.* (1966) reported that grain size and shape are the first criteria of quality that Breeders consider in developing new varieties for commercial production. Nascimento *et al.* (2011) observed white color of stigma and presence of the glumella pubescence as dominant types on upland rice of 146 accessions. Parikh *et al.* (2012) found majority of the genotypes to possess green basal leaf sheath color (84.5%), green leaf blade color (86.8%), green tip color (57.8%), green leaf margin color (57.8%), green collar color (97.3%), white ligule color (94.7%), light green auricle color (97.3%), semi erect plant habit (44.7%), white apiculus color (53.9%), white stigma color (94.7%), awnless (72.3%) and white sterile glume color (59.2%) in 71 aromatic rice.

#### *Dendrogram of the qualitative characters*

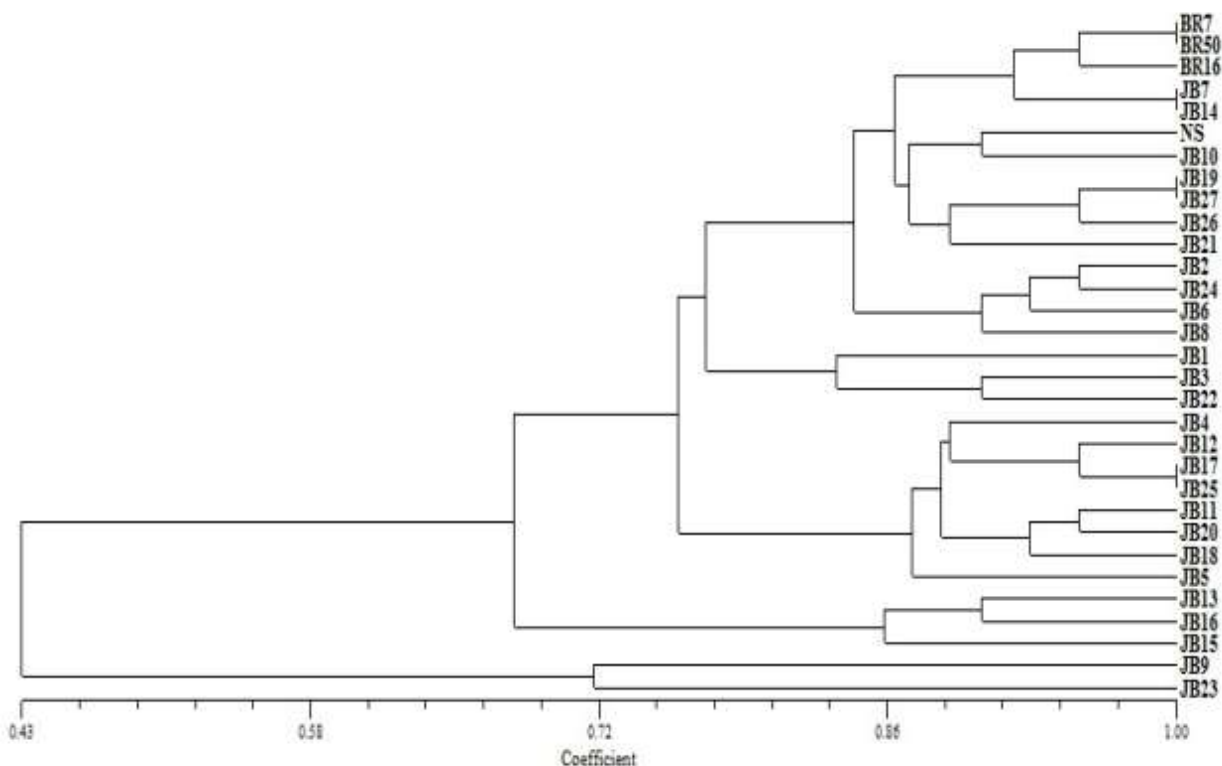
A dendrogram was constructed using UPGMA clustering method based on Dice coefficient and

distributed the germplasm along with BR7, BR16, BRR1 dhan50 and *Nizersail* into three major clusters for the studied qualitative characters (Fig. 5). The genetic distances were ranging from 0.000 to 9.969 and indicated the existence of significant differences among the accessions. The highest genetic distance was recorded as 9.969 between JB7 and JB11, JB10 and JB13, JB11 and JB14 and JB20 and JB21 and the lowest (0.000) between JB7 and JB14, JB17 and JB25 and JB19 and JB27. Cluster III was the major one with maximum genotypes (26), while clusters I had only two genotypes (JBPL9 and JBPL23) and cluster II had three genotypes (JBPL13, JBPL15 and JBPL16), respectively. Besides, Clusters III were consisted of three sub-clusters. The first major sub-cluster of cluster III consisted with 15 genotypes namely JBPL8, JBPL6, JBPL24, JBPL2, JBPL21, JBPL26, JBPL27, JBPL19, JBPL10, JBPL14 and JBPL7 along with the popular varieties BR7, BR16, BRR1 dhan50 and *Nizersail*. The second sub-cluster consisted with 8 genotypes namely JBPL5, JBPL18, JBPL20, JBPL11, JBPL25, JBPL17, JBPL12 and JBPL4. The third sub-cluster of cluster III consisted with three genotypes namely JBPL22, JBPL3 and JBPL1. Hossain (2008) found 10 clusters by using UPGMA clustering method in 78 aromatic and fine grain landraces of rice genotypes. Rahman *et al.* (2009) identified four groups for the qualitative data to evaluate genetic divergence by studying 110 rice varieties. Nascimento *et al.* (2011) observed two major groups by using UPGMA clustering method in 146 accessions of upland rice.

It revealed from the dendrogram that the genotype JBPL7 (acc. no. 2465) and JBPL14 (acc. no. 2464) of cluster III were duplicate. Similarly, genotype JBPL17 (acc. no. 2455) and JBPL25 (acc. no. 2454) as well as genotype JBPL19 (acc. no. 2453) and JBPL27 (acc. no. 2478) of the same cluster were also 100% similar for all the 21 qualitative agro-physiological characters studied (Fig. 5). Besides, BR7 and BRR1 dhan50 were also found duplicate. Similarly, Fukuoka *et al.* (2006) studies aromatic rice landraces and concluded that significant variation may be found among genotypes with the same name. Bisne and Sarawgi (2008)

identified 18 duplicates by evaluating 32 rice accessions, while Nascimento *et al.* (2011) also identified 18 duplicates from 146 rice accessions and in both the case none of these duplicates included in accessions with the same genotype name. Hossain (2008) identified six pairs of duplicates on 78

aromatic and fine grain landraces of rice for 23 qualitative traits and three pairs of these duplicates (Kalijira-1 & Kalijira-2, Kalijira-8 & Kalijira-10, Kalijira-12 & Kalijira-14) had accessions with the same genotype name.



**Fig. 5.** Dendrogram of 27 *Jesso-Balam* rice as constructed by using UPGMA clustering method based on Dice coefficient.

**Conclusion**

The *Jesso-Balam* pure lines possessed exclusive variability and unique features which need safe conservation and sustainable utilization in future rice varieties development for issues like intellectual property rights. Further, the identified variability and unique features can be selected for developing varieties with unique identification, diverse traits and broaden genetic base. Besides, identified qualitative traits like dark green color leaf, strong pubescence on the surface of the leaf blade or purple margin leaf blade etc. can be utilized for developing rice varieties with tolerant to leaf surface related insects and diseases. Apart from this, molecular characterization of the identified accessions needs to be done for QTL mapping and validating candidate genes responsible for unique traits.

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