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GENETIC DIVERSITY ASSESSMENT OF QUANTITATIVE TRAITS IN LANDRACES OF *AUS* RICE

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ABSTRACT

Genetic diversity of 46 land races of Aus rice was studied under irrigated condition through Mahalanobis D^2 statistic for grain yield and yield contributing characters. The genotypes were grouped into seven clusters. The highest inter-genotype distance was observed between the genotypes Lalgalong and Langrabeni and the lowest between Saita and Korchamuri respectively. The intra cluster distances were low for all the clusters ranging from 0.64 in cluster IV to 1.17 in cluster I. The highest inter cluster value was 11.45 (between cluster III and V) and the lowest was 4.36 (between cluster VI and VII). The highest cluster means for effective tiller number and grain yield per hill were obtained from cluster III. On the other hand, the highest leaf width and highest spikelet fertility from cluster IV, tallest plant and highest grain breadth from cluster VI, highest 1000-grain weight from cluster V whereas the lowest mean value for days to 50% flowering and days to maturity were found in cluster VI. The genotypes from cluster III could be hybridized with the genotypes of other clusters for producing transgressive segregants. Canonicalvector analysis revealed that days to 50% flowering and days to maturity were contributed maximum to the genetic divergence. Principal Coordinate Analysis (PCoA) revealed that the genotypes Begun bitchi, Rang mahal, Laxmijhota, Katar, Chiknal, Manikmendal, Baismugur were found far away from the centroid of the cluster and can be selected as parents for further breeding programs. The results suggested that Lalgalong (acc. no. 1655) and Langrabeni (acc. no. 1645) can be crossed with the genotypes of cluster III and cluster VI to develop more promising as well as high yielding variety for *Aus* season.

Keyword: Genetic diversity; *Aus* rice; quantitative traits.

INTRODUCTION

Rice (*Oryza sativa*) is one of the most important food crops and a primary source of food for more than half of the world's population (Khush 2005). According to the United Nations (UN) estimates, the current world population 6.1 billion is expected to reach 8.0 billion by 2025. Most of this increase (93%) will take place in the developing world. Global rice production must reach 800 million tons of paddy rice to meet projected demand in 2025 (Peng *et al.* 1999) which is about 200 million tones more than rice produced in 2006. This additional rice must come mainly from irrigated land in Asia, because improving rice yield in most rainfed regions is constrained by drought, flooding and poor soil quality (Cassman 1999). Bangladesh is already under pressure both from huge and increasing demands for food, and from problems of agricultural land and water resources depletion. Bangladesh needs to increase the rice yield in order to meet the growing demand for food emanating from population growth.

There are four distinct ecotypes of rice viz. Boro, Aus, Transplanted Aman and Deep water Aman in Bangladesh. Bangladesh has a good source of indigenous rice cultivars. About 4000 T. Aman, 2500 Boro and 1500 Aus landraces have been conserved in BRRI rice gene bank. Only a few decades ago large numbers of farmers were growing local cultivars as their main crop. Those cultivars have good adaptation but are poor yielder. Actually cultivation of these landraces was gradually replaced by high yielding modern varieties during last twenty years. These landraces adapted in different parts of this country, some of which have very nice quality, fineness, aroma, taste and high protein contents (Dutta *et al.* 1998). But information on the genetic diversity of local landraces particularly for Aus rice is very scanty. Precise information on the extent of genetic diversity among population is crucial in any crop improvement program, as selection of plants based on genetic diversity has become successful in several crops (Ananda and Rawat 1984; De*et al.* 1988). The assessment genetic diversity is a powerful tool to select or determine the appropriate parents for hybridization programs to develop high yielding variety. With the development of advanced biometrical techniques such as multivariate analysis based on the Mahalanobis (1936) statistics, quantification of divergence among the biological population and assessing the relative contribution of different components to the total divergence at intra and inter-cluster levels have now become possible. Genetic diversity study also permits to select the genetically diverse parents from different clusters to obtain the desirable recombinant in the segregating generations upon crossing. The present study was, therefore, undertaken to assess the variability and diversity of 46*Aus* rice germplasm of Bangladesh and classify them into clusters for selecting genotypes as prospective parents to develop transgressive segregants for developing new rice variety.

MATERIALS AND METHODS

Forty six rice landraces (Table 1) of *Aus* season selected from the gene bank of Bangladesh Rice Research Institute (BRRI), Gazipur were grown under irrigated condition with three replications using one row of 5.4 m long each per entry/accession and single seedling per hill with a spacing of 25 X 20 cm between rows and plants, respectively during 2014. Fertilizers were applied @ 60:20:40:40 kg NPKS/ha. Total quantity of TSP, MoP and Gypsum were applied at the final land preparation. Urea was applied in three installments at 7, 25 and 35 days after transplanting (DAT). Control measures for pests, diseases and weeds were taken whenever necessary. Thirteen morpho-agronomic and yield contributing characters were recorded. The data were analyzed following principal component analysis (PCA) and Mahalanobis's (1936) generalized distance (D^2) extended by Rao (1952). Intra and inter cluster distances were calculated by the method of Singh and Chaudhury (1985). All statistical analyses were carried out using Genstat 5.5. The PCoA of 46 accessions was calculated by EIGEN program of NTSYS-pc version 2.2 (Rohlf, 2002).

RESULTS AND DISCUSSION

A total of 46 *Aus* rice germplasm were grown for genetic diversity study. The eigen values (latent roots) and percentage of total variation accounted for them obtained from principal component analysis (PCA) are presented in Table 2. The result revealed that the first four components in the PCA with eigen values >1, contributed 73.35% of the total variations among the genotypes for 13 agro-morphological characters. Sohrabi*et al.*

(2012) and Chakravorty*et al.* (2013) observed the contribution of 76.7 and 75.9% of the first six and four components to the total variation in rice, respectively. Siddique *et al.* (2011) observed about 77.91% of the total variation accounted by the first two principle components in traditional rice (*oryza sativa* L.) cultivars of hilly areas in Bangladesh.

The 46 rice genotypes of *Aus* germplasm were grouped into seven clusters on the basis of non-hierarchal clustering method using Mahalanobis' D^2 statistic for 13 agro-morphological characters (Table 3). Similarly, Sohrabi*et al.* (2012) reported six clusters in 50 Malaysian upland rice accessions for 12 growth traits, yield and yield components. However, the result was in conformity with the cluster pattern of the genotypes obtained though Principal Component Analysis. Again, the inter-genotypic distance (D^2) was obtained from principal coordinate analysis. The highest inter-genotype distance (2.6813) was observed between the genotypes Lalgalong and Langrabeni and the lowest (0.2094) between the genotypes Saita and Korchamuri, respectively.

Table 1. The list of 46 *Aus* rice germplasm

Local name	Code name	Acc #	Place of collection	Local name	Code Name	Acc. #	Place of collection
Dal Kaisha	V1	564	Joypurhat	Kali Bori (1)	V24	1633	Jessore
Garia	V2	569	Joypurhat	Panock	V25	1641	Chittagong
MarikMandu	V3	572	Joypurhat	Chiknal	V26	1642	Noakhali
Shoni	V4	575	Joypurhat	Ingra	V27	1643	Comilla
Nayan Tara	V5	654	B. Baria	LangraBeni	V28	1645	Chittagong HT
Begun Bichi	V6	1202	Gopalganj	LalGalong	V29	1655	Chittagong HT
Bolium	V7	1205	Gopalganj	Holat	V30	1656	Comilla
Noroi(4)	V8	1210	Madaripur	Kamini Sail	V31	1662	Chittagong HT
Laxmilota	V9	1211	Faridpur	Mele	V32	1671	Chittagong HT
Saita	V10	1213	Faridpur	GoriSaita	V33	1675	Faridpur
Porangi (7)	V11	1216	Faridpur	Goyal	V34	1680	Faridpur
Manikmoda	V12	1323	Meherpur	Saita	V35	1681	Faridpur
Paik juta	V13	1528	Dinajpur	Kala manik	V36	1682	Faridpur
BenaFul	V14	1529	Dinajpur	KoeJuri	V37	1683	Faridpur
Tepakain	V15	1532	Dinajpur	Kautukmoni	V38	1684	Faridpur
Hasha	V16	1534	Dinajpur	Korchamuri	V39	1687	Faridpur
Ajabbeti	V17	1546	Chittagong	Boilam	V40	1688	Faridpur
Bnamka	V18	1549	Chittagong	Parangi	V41	1689	Faridpur
Baturi	V19	1550	Chittagong	HaitaiSaeta	V42	1691	Faridpur
MorySaita	V20	1626	Comilla	Manikmendal	V43	1692	Faridpur
RangMahal	V21	1629	Dhaka	Baismagur	V44	1696	Faridpur
LaxmiJhota	V22	1630	Chittagong	Sribalium	V45	1699	Faridpur
Katar	V23	1632	Chittagong	Pankhiraj	V46	1700	Faridpur

The distribution pattern of cluster indicated that the highest number of genotypes (17) included in clusters VII, while cluster III had only two genotypes. The clustering pattern also revealed that the genotypes constellated in the cluster were not originated from the same geographic region. Chakravorty*et al.* (2013), Hosan*et al.* (2010) and Rajesh *et al.* (2010) also found no parallel relationship between genetic and geographical divergence on rice landraces.

The average intra-(bold) and inter-cluster distances (D^2) are presented in Table 4. All the inter-cluster distances were larger than the intra-cluster distance indicating presence of wider diversity among genotypes of distance groups. The intra-cluster distances were low for all the seven clusters ranging from 0.647 in cluster III to 1.178 in cluster I which indicated homogeneous nature of the genotypes within the same clusters. The results were supported by the findings of Siddique *et al.* (2011) and Iftekharuddaula *et al.* (2002) in rice. The highest inter cluster value was 11.45 (between cluster III and V) and the lowest value was 4.36 (between cluster VI and VII), which clearly indicated the presence of variability in the germplasm of different clusters.

Table 2. Latent roots (Eigen value) and their variation for 13 agro-morphological characters of 46 *Aus* landraces

Principal component axes	Latent roots	Variation accounted (%)	Cumulative variation (%)
I	4.497	34.58	34.58
II	1.843	14.18	48.76
III	1.781	13.70	62.46
IV	1.416	10.89	73.35
V	1.012	7.79	81.14
VI	0.813	6.25	87.39
VII	0.528	4.07	91.46
VIII	0.395	3.04	94.50
IX	0.269	2.07	96.57
X	0.218	1.68	98.25
XI	0.159	1.22	99.47
XII	0.065	0.50	99.97
XIII	0.004	0.03	100

Table 3. Distribution of 46 ***Aus* landraces into seven clusters for 13 agro-morphological characters**

Cluster	**No. of genotypes**	**Name of genotypes**
I	5	Nayantara, Begun bichi, Benaful, Panock, Langrabini
II	11	Dalkaisha, Garia, Marikmandu, Shoni, Porangi, Paik juta, Hasha, Baturi, Chiknal, Porangi, Haitaisaita
III	2	Mori saita, Holat
IV	4	Ajjabbeti, Rang mahal, Laxmijata, Katar
V	3	Boilum, Laxmilata, Pankhiraj
VI	4	Noroi, Kamini sail, Baismugur, Sribalam
VII	17	Saita, Manikmoda, Tepakain, Binmaka, Kali boroi, Ingra, Lalgalong, Mele, Gorisaita, Goynal, Saita, Kala manik, Koejuri, Kautukmoni, Korchamuri, Boilam, Manikmendal

Table 4. Average intra-(bold) and inter-cluster distances (D^2) for 13 agro-morphological characters of 46 *Aus* landraces

Clusters	**I**	**II**	**III**	**IV**	**V**	**VI**	**VII**
I	**1.178**						
II	6.01	**0.678**					
III	8.45	9.11	**0.652**				
IV	5.68	9.11	7.77	**0.647**			
V	8.42	6.96	11.45	10.60	**0.671**		
VI	7.86	8.39	5.22	6.69	11.22	**0.704**	
VII	6.14	5.03	7.16	6.80	8.50	4.36	**0.668**

The cluster-mean values for all the 13 agro-morphological characters are presented in Table 5. The data revealed that different clusters exhibited the highest and lowest mean values of individual characters and none of the single cluster showed the highest or lowest mean values of all the characters. However, the highest cluster means for effective tiller number (14) and grain yield per hill (12.98) were obtained from cluster III. On the other hand, the highest cluster means for leaf length (60.82 cm) from cluster I, highest leaf width (1.56 cm) and highest spikelet fertility (90.04%) from cluster IV, tallest plant (155.20 cm) and highest grain breadth (2.27 cm) from cluster VI, highest 1000-grain weight (28.63) from cluster V whereas the lowest mean value for days to 50% flowering (91.73) and days to maturity (121.76) were found in cluster VI.

Table 5. Cluster means of 46 *Aus* rice germplasm for 13 agro-morphological characters

Characters	Cluster number						
	I	II	III	IV	V	VI	VII
Leaf length (cm)	60.82	49.58	55	59.45	47.33	52.15	51.38
Leaf width (cm)	1.52	12.16	1.07	1.56	1.13	1.31	1.2
Effective tiller no./hill	6.56	13.24	14	7.25	3.9	9.75	11.6
Days to 50% flowering	102.4	91.76	104	104.75	92.67	98.75	91.73
Plant height (cm)	124.5	123.19	143	139.4	114.83	155.2	143.85
Panicle length (cm)	25.98	24	25.1	25	18.83	26.9	24.59
Spikelet fertility (%)	88.85	83.87	72.34	90.04	73.1	85.01	87.93
Days to maturity	132.8	122	134	135.25	122.67	129.25	121.76
1000 grain weight (g)	21.74	25.91	22.8	15.1	28.63	26.52	28.21
Grain length (mm)	8.5	8.72	8.01	6.65	8.16	8.61	8.68
Grain breadth (mm)	1.97	2.09	2.1	1.79	2.26	2.27	2.19
Length-breath ratio	2.88	2.94	2.75	2.53	2.39	2.76	2.72
Yield/hill (g)	11.31	11.37	12.98	9.91	6.6	11.42	10

Thus the results suggest that the crosses between the genotypes belonging to the cluster III, with that of clusters IV, V and VI, would exhibit maximum transgressive segregation along with good characters. As a result, the genotypes under cluster III with clusters IV, V and VI, might be selected as parents for future breeding program depending upon the objectives. Hosan *et al.* (2010), Siddique *et al*. (2010, 2013) and Sohrabi *et al*. (2012) earlier reported similar trend of conclusions on rice using Mahalanobis' D^2 statistics. Therefore, the genotypes under cluster III, cluster IV, cluster V, cluster VI might be selected for future breeding program. The results of the canonical analysis showed that 47.12% of the total variation was accounted for canonical root 1 and 25.85% by canonical root 2 (Table 6).

The coefficients pertaining to the different characters in the first two canonical roots are presented in Table 7. It was revealed from canonical vector analysis that days to 50% flowering and days to maturity were contributed maximum to the genetic divergence for the characters of the germplasm studied. Earlier, Mahalingam *et al.* (2012) and Rajesh *et al.* (2010) found similar results. Siddique *et al.* (2011) also found that flag leaf length, flag leaf width, days to 50% lowering, days to maturity, unfilled grain per panicle, grain length and grain length breadth ratio contributed maximum towards divergence in traditional rice (*Oryza sativa* L.) cultivars of hilly areas in Bangladesh.

The two and three dimensional graphical view of Principal Coordinate Analysis (PCoA) showed the spatial distribution of the genotypes. The genotypes Begun bitchi, Rang mahal, Laxmijhota, Katar, Chiknal, Manikmendal, Baismugur were found far away from the centroid of the cluster and the rest of the genotypes were placed more or less around the centroid (Fig. 1 and 2).

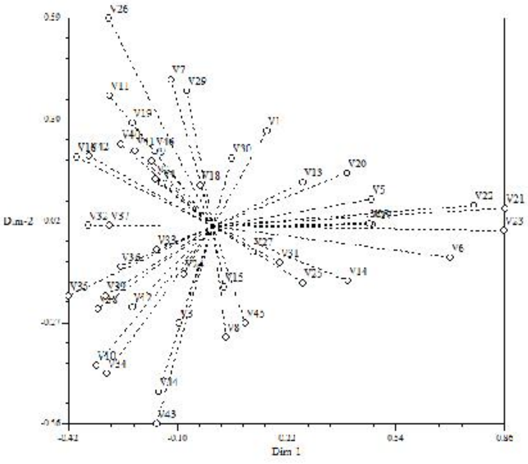
Table 6. Values of canonical roots and percentage of variation of 13 agro-morphological characters of 46 *Aus* landraces

Canonical roots	Values of the canonical roots	% of variation absorbed by the canonical roots
1	10.17	47.12
2	5.58	25.85
3	2.70	12.54
4	2.09	9.68
5	0.78	3.65
6	0.25	1.16
Total		100.0

Table 7. Latent vectors for 13 agro-morphological characters of 46 *Aus* landraces

Characters	Vector I	Vector II	Combined ranking*
Leaf length (cm)	+0.3497	-0.1405	3
Leaf width (cm)	+0.3338	-0.1705	4
Effective tiller number per hill	-0.1931	-0.1053	7
Days to 50% flowering	+0.4173	+0.0253	1
Plant height (cm)	+0.0178	-0.4801	10
Panicle length (cm)	+0.1939	-0.4826	6
Days to maturity	+0.4119	+0.0188	2
1000-grain weight (g)	-0.3535	-0.2167	12
Grain length (mm)	-0.3190	-0.3186	13
Grain width (mm)	-0.3026	-0.1748	11
Spikelet fertility (%)	+0.1142	-0.4315	9
Grain length width ratio	-0.0371	-0.2748	8
Grain yield per hill (g)	+0.1208	-0.1870	5

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



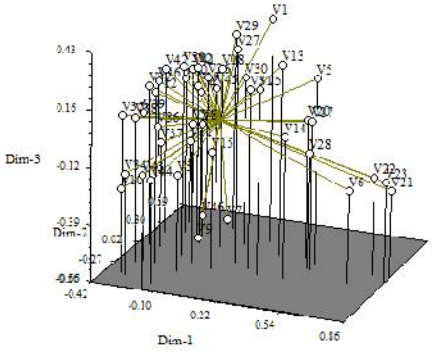


Figure 1: Two-dimensional graph of 46 upland rice accessions based on 13 quantitative traits.

Figure 2: Three-dimensional graph of 46 upland rice accessions based on 13 quantitative traits.

The results indicated that the genotypes were placed far away from the centroid were more genetically diverse while the genotypes were placed near the centroid possessed more or less similar genetic background. However, centroid may be defined as the vector representing the middle point of the cluster which contained at least one number for each variable. The connecting lines between the each genotype and the centroid represented eigen vectors for the respective genotypes.

CONCLUSION

The landraces of rice germplasm can be a source of valuable new genes. There are high degree of diversity existed among the studied *Aus* landraces which can be utilized in different varietal improvement/development program in future. Considering results from genetic distance, the genotypes Begun bitchi, Rang mahal, Laxmijhota, Katar, Chiknal, Manikmendal, Baismugur could be selected as parents for further breeding programs. The genotype Lalgalong (acc. no. 1655) and Langrabeni (acc. no. 1645) can be crossed with the genotypes of cluster III and cluster VI to develop more promising as well as high yielding variety for *Aus* season.

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