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Screening of local landraces of rice (*Oryza sativa* L.) at the seedling stage for salinity tolerance based on genetic divergence analysis

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ABSTRACT

The presence of genetic diversity is a prerequisite for improvement of any crops. Salinity is a severe threat for the production of rice which can be solved by improving tolerant variety through breeding programs. Twenty-five rice genotypes were evaluated to explore the genetic diversity of growth parameters by imposing three levels of salinity treatments (0 dS m^{-1}, 7 dS m^{-1} and 12 dS m^{-1} EC) with three replications following completely randomized design (CRD).The genotypes were categorized into five major sub-clusters considering ten morphological traits using the non-hierarchical Euclidean distances revealed that maximum 10 genotypes *viz*., Moynamoti, Badshavog, Pangash, Suvash, Moghabalam,Sadaswarna, Bina dhan-8, Chinikani, Ashfailand, and Rajashail were found in cluster III while lowest two genotypes namely Lalbat and M-171 were found in cluster IV. The results of the cluster analysis also reported that the inter-cluster distances in all the cases were greater than the intra-cluster distances. The highest intra-cluster diversity was observed in cluster IV (6.30) whereas lowest intra-cluster diversity was found in cluster I (4.16). The maximum inter-cluster distance was found between cluster II and V (15.45) where minimum inter-cluster distance was observed between cluster I and II (6.39). Root fresh weight contributed greatest (19%) to the divergence of genotypes where root length contributed least (0.33%) to the total diversity of the genotypes. The cluster means value for most of the morphological traits was maximum in cluster II reflecting that the genotypes grouped in cluster II could be selected as salt tolerant genotypes at the seedling stages for the cultivation in the coastal area of Bangladesh.

Keywords: Rice, coastal area, genetic diversity, cluster analysis, Euclidean distances

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1 Introduction

Rice (*Oryza sativa* L.) is one of the most important cereal food crops which is consumed by approximately more than three billion people around the world (Kumbhar et al., 2015). Rice is also staple food of Bangladesh and it is the top ranked food crop by production amongst all crops grown in Bangladesh (BBS, 2016). In Bangladesh, the total rice growing area is approximately 10.83 million hectares of land leading to the production of 33.54 million metric tons of rice (Kibria et al., 2017). But now-a-days the production of rice is hampered to a great extent by different abiotic stresses in the world (Fahad et al., 2017). Among different abiotic stress, salinity is the most important abiotic stress, which hampers the plant growth, development and productivity (Nazar et al., 2011; Kordrostami et al., 2017). It is reported that more than 800 million hectares of land are adversely affected by varying degree of salinity around the world (Munns and Tester, 2008). Salinity problem is also a major concern in the southern part of Bangladesh now days (Ahmed et al., 2014b). About 1.06 million hectares of arable lands of Bangladesh are affected by soil salinity and salinity affected area is increasing day by day (SRDI, 2010). Salinity seriously affects the rice production in the southern part of Bangladesh (Kibria et al., 2017). Rice is a salt sensitive crop (Grover and Pental, 2003), though salt sensitivity of rice to salinity varies with different growth stages; rice is particularly very sensitive during the early-vegetative and late-reproductive stages (Chowdhury et al., 2016).

Salinity problems in the country had very little attention in the past to solve in our country (Haque, 2006). But now-a-days population growth rate of Bangladesh is much higher than world growth rate demanding more food is proportion to the population growth (Ahmed et al., 2014a). So, to meet up the food requirement of the bursting population, production of rice has to be increased by at least 60% by the year 2020 by the proper utilization of salinity affected area.

A large number of rice landraces is traditionally cultivated in the southern part of Bangladesh (Tahjib-Ul-Arif et al., 2018). Therefore, landraces could play an important role in the local food security and sustainable development in agriculture by the effectively utilization of saline prone area of Bangladesh (Tang et al., 2002). Genetic improvement of traits mainly depends on the amount of genetic variability present in the population. Generally, genetic diversity in plants has been evaluated by using different morphological and physiological traits (Kumbhar et al., 2015). Now-a-days, the use of multivariate statistical algorithms is an important tool for classification of germplasm and analysis of genetic relationships among breeding material (Mohammadi and Prasanna, 2003). Mahalanobis D^2 statistics is a powerful tool for performing clustering patterns to make a relationship between genetic and geographical divergence and investigating roles of different quantitative traits toward the maximum divergence (Murthy and Arunachalam, 1966).

Screening of rice genotypes for salt tolerance at seedling stages provides more importance (Ali et al., 2014) because stage is readily acceptable as it is based on a simple criterion of selection; it provides rapid screening which is difficult at vegetative and reproductive stage (Gregorio et al., 1997). Therefore, the present study was conducted to evaluate 25 rice genotypes for salinity tolerance based on morphological traits at seedling stage.

2 Materials and Methods

2.1 Plant materials

Twenty five rice genotypes were used as experimental materials in this experiment. Twenty-three genotypes were local genotypes (landraces) collected from southern part of Bangladesh and two genotypes were high yielding varieties collected from Bangladesh Institute of Nuclear Agriculture (BINA) (Table 1).

2.2 Plant cultures and treatments

The experiment was conducted at the growth chamber, located at the Department of Genetics and Plant Breeding, Bangladesh Agricultural University (BAU) in Mymensing. Peter Professional (Peter water-soluble fertilizer 20:20:20 + ferrous sulphate heptahydrate) was used to supply appropriate amount of nutrient for plant growth and development (Roy et al., 2016). The pH of the nutrient solution was maintained to the range of 5.1-5.3 by a pH meter (Hanna HI 2211). After transferring the seedlings in hydroponic system, it is very important to ensure the continuous supply of the nutrients to the plants, therefore, the solution was stirred for two times daily because the iron and some other nutrients get precipitated within 7-8 h and become unavailable to plants. The experiment was laid out by completely randomized design with three treatments (control, 7 dS m^{-1} and 12 dS m^{-1} EC) and three replications (each replication had 10 seedlings).

One hundred and twenty seeds of each genotype were placed into brown bags and kept in the oven at 55 °C for 2-3 d for breaking dormancy. Afterwards, seeds were sterilized by treating with 0.1% $HgCl_2$ and 70% ethanol and washed with distilled water. Afterwards, the sterilized seeds were placed in petridishes having moist filter paper and kept in the dark place for 3-4 d for seed sprouting. Then, 4 day-old seedling was transferred to the hydroponic medium containing nutrient solution and. The EC of the normal nutrient solution was 1.3 dS m^{-1} and after 3 d, nutrient solution was salinized to 7 dS m^{-1} and 12 dS m^{-1} by adding crude salt. For adjusting the EC to 7 dS m^{-1}

Table 1. List of twenty five rice genotypes used in the experiment

Types of Genotypes	Genotypes			
Landraces †	Satin	Chinisagor	M-171	Moghabalam
	Maloti	Badshabhog	Kabuldulan	Chinikani
	Sylhetbalam	Lalbat	Suvash	Sadaswarna
	Lalchikon	Chabli	Moyna	Gottaaman
	Khakshyal	Pangash	Ashfail	Moirom
	Moynamoti	Durgabhog	Ronjit	
Salt tolerant check genotype ‡	BINA dhan-8	BINA dhan-10		

† Collected from Satkhira, Bangladesh; ‡ Collected from Bangladesh Instititue of Nulcear Agriculture

and 12 dS m^{-1}, 2 g and 4.25 g NaCl L^{-1} nutrient solution were added respectively. The salinized conditions were maintained for 15 d. The EC was measured by EC meter (Hanna HI 4321). Afterwards, saline solution again replaced by nutrient solution only and plant grown for next 6 days in normal nutrient solution. The seedlings of the control treatment grown in normal nutrient solution only. The pH and EC of the nutrient solution were monitored regularly. Data collection along with different root and shoot characters were done after 21 d of setting in hydroponic system by successive destructive harvest. Survival rate (%) and percentage of live leaves was calculated by the following equations:

$$\% SR = \frac{TLP}{TP} \times 100 \quad (1)$$

$$\% LL = \frac{TLL}{TL} \times 100 \quad (2)$$

where, $\%SR$ and $\%LL$ are %survival rate and percent live leaves, and TLP, TP, TLL, and LL are number of live plants, total number of plants, number of live leaves, and total number of leaves, respectively.

The length of the root was measured from the shoot initiation to the root tip and shoot length measured by deducting plant length from root length by using centimeter (cm) scale. Leaf chlorophyll content was measured on the fully expanded 2nd leaves of all the plants at 21th days with a chlorophyll meter (SPAD-502 Chlorophyll Meter, Minolta Camera Co. Ltd., Japan). The shoot samples were separated from the root and then, root fresh weight and fresh shoot weight were taken immediately by weighing balance. After the destructive harvest and measurement of all traits, roots and shoots of each genotype were separately enclosed in a brown envelop (20 × 10 cm^2). After that, all envelops were put in an oven at 60 °C for 7 d. The dry weight of root and shoot were taken by weighing balance.

2.3 Statistical analysis

The data were presented as means and different alphabetical lettering indicates the significance difference among the means of different genotypes in the same column at 1% level of significance according to a least significant difference (LSD) test. The genetic divergence was estimated using Mahalanobis's D^2 statistics (Mahalanobis, 1928). All the genotypes were grouped into clusters on the basis of D^2 values, as suggested by Tocher (Rao, 1952). Average intra-cluster and inter-cluster distances were calculated by the formula as suggested by Rao (1952).

3 Results

3.1 Trait-wise mean performance of rice genotypes under salt stress

Salt tolerant genotypes showed better performance of different agronomic parameters than susceptible genotypes when salt is imposed in growth medium (Table 2). The highest live leaves (69.11%) was found in Lalbat followed by Lalchikon (64.88%) where Chabli (24.29%) had the lowest live leaves (%) followed by Kabuldulan (30.99%). Khakshyal showed the maximum survival rate (97.78%) followed by Moirom (91.11%) and the minimum survival rate was observed in Chabli (28.89%) followed by Kabuldulan (32.96%). Among the genotypes, khakshyal and Moyna had the highest total number of roots respectively (6.33 and 5.77) followed by Binadhan-10 (5.55) and the lowest number of roots was reported in Pangash (3.55) followed by Sylhetbalam (3.66%). The maximum root length and shoot length was found in Chinisagor, Binadhan-10, Maloti and Satin where the lowest value of root length and shoot length was displayed by Gottaaman (4.99 cm) and Durgavog (5.04 cm). In case of chlorophyll content, Lalbat showed the highest chlorophyll content (19.83) followed by Moyna (19.61) and M-171-Phillipine (18.71) whereas Chabli had the lowest chlorophyll content (7.426) followed by Kabuldulan (9.641). Among the genotypes, root fresh weight and shoot fresh weight was the highest in Lalbat, Lalchikon, Sylhetbalam and Maloti whereas the lowest root fresh weight and shoot fresh weight was found in Gottaaman followed by Moghabalam. In case of dry weight measurements,

Table 2. Mean performance of different morphological traits of 25 rice genotypes under salt stress

Genotype	LL% †	SR%	TNR	RL	SL	CC	RFW	RDW	SFW	SDW
Satin	40.8 f-i	85.0 b-e	4.11 h-j	9.24 ab	23.0 a	16.3 c-e	9.15 ab	1.24 cd	11.2 b	2.05 b
Maloti	63.0 bc	89.4 a-c	5.00 c-f	8.68 a-c	24.4 a	17.8 a-c	8.6 b-d	1.33 bc	11.7 ab	2.39 a
Sylhetbalam	39.4 f-j	73.8 e-h	3.667 j	8.64 a-c	14.9 gh	16.7 b-e	9.778 a	1.05 e-g	10.46 c	1.5 cd
Lalchikon	64.8 ab	88.3 a-d	5.33 b-e	7.9 c-f	18.1 b-e	15.2 d-g	9.7 a	1.58 a	12.00 a	2.30 ab
Khakshyal	44.1 fg	97.7 a	6.33 a	6.89 f	13.5 hi	9.96 l	8.06 c-e	1.17 de	11.2 b	2.27 ab
Moynamoti	53.7 de	73.3 f-h	4.11 h-j	8.50 a-d	14.6 g-i	13.7 f-i	7.64 d-f	0.74 i	8.6 ef	1.2 ef
Chinisagor	59.2 b-d	95.56 ab	5.22 b-e	9.450 a	19.2 bc	14.9 e-h	7.81 c-f	0.95 gh	10.1 c	1.65 c
Baddshavog	38.2 g-j	63.3 h-j	3.66 j	7.44 c-f	13.5 hi	12.3 i-k	7.65 d-f	0.93 gh	9.22 de	1.73 c
Lalbat	69.11 a	84.4 b-f	4.77 e-g	8.07 b-f	20.2 b	19.8 a	5.74 h-j	0.65 ij	7.00 i	0.84 h
Chabli	24.2 l	28.8 m	4.44 f-i	6.930 -f	9.49 kl	7.42 m	5.66 h-j	0.542 jk	7.52 hi	1.28 df
Pangas	43.0 f-h	46.11 l	3.55 j	7.78 c-f	14.2 g-i	9.960 l	6.29 g-i	0.75 i	9.23 de	1.61 c
Durgavog	35.2 i-k	57.4 i-k	4.33 g-i	5.04 g	8.75 kl	10.7 j-l	6.96 e-g	0.65 ij	9.25 de	1.13 fg
M-171-Phillipine	57.6 c-e	73.3 e-h	4.55 f-h	5.37 g	10.3 jk	18.7 ab	5.54 ij	0.32 l	5.86 j	0.47 i
Kabuldulan	30.9 k	32.9 m	4.33 g-i	7.33 d-f	12.2 ij	9.64 l	6.70 f-h	0.507 k	8.48 e-g	0.842 h
Suvash	45.87 f	66.6 g-i	3.88 ij	7.98 b-f	16.5 d-g	13.8 f-i	6.74 f-h	0.766 i	7.71 hi	2.1 ab
Moyna	61.3 bc	77.59d-g	5.7 b	7.76 c-f	17.82 c-f	19.61 a	8.83 a-c	1.40 b	9.89 cd	2.12 ab
Ashfail	46.1 f	52.2 j-l	4.11 h-j	8.33 b-e	15.15 gh	14.9 e-h	8.03 b-e	0.91 h	7.78 gh	0.96 gh
Ronojit	36.9 h-k	51.1 kl	4.8 d-g	7.12 ef	14.60g-i	12.7 h-j	5.8 g-j	0.49 k	8.66 ef	1.5 cd
Moghabalam	40.2 f-i	84.4 b-f	5.00 c-f	8.72 a-c	15.7 e-h	13.1 f-i	4.90 jk	1.23 cd	7.53 hi	1.33 d-f
Chinikani	45.3 f	66.1 g-i	4.11 hij	8.25 b-e	15.6 f-h	14.9 e-h	8.03 c-e	0.91 h	8.26 f-h	1.45 c-e
Sadasswarna	39.3 f-j	53.3 j-l	5.00 c-f	7.48 c-f	15.3 gh	13.0 g-i	6.17 g-i	0.52 k	8.82 ef	1.51cd
Gottaaman	33.4 jk	34.2 m	3.66 j	4.99 g	7.81 l	10.2 kl	4.24 k	0.266 l	5.10 k	0.43 i
Moirom	43.4 f-h	91.1 ab	3.88 ij	8.60 a-d	18.4 b-d	15.4 d-f	8.50 b-d	1.08 ef	10.1 c	1.55 cd
Binadhan-8	38.15g-j	63.3h-j	5.4 b-d	8.0 b-f	14.98 gh	12.7 h-j	7.57 d-f	1.0 f-h	10.1 c	1.68 c
Binadhan-10	52.3 e	78.3 c-f	5.55 bc	8.67 a-c	24.68 a	17.4 b-d	9.833 a	1.23 cd	11.8 ab	2.25 ab
$LSD_{0.05}$ ‡	3.21	6.78	0.48	0.843	1.37	0.949	0.763	0.106	0.889	0.169
SE (±)	2.03	4.06	0.15	0.22	0.86	0.65	0.28	0.08	0.32	0.11
Sig.	**	**	**	**	**	**	**	**	**	**
CV%	8.47	11.42	12.03	11.78	9.79	7.75	11.21	12.66	10.63	12.16

† LL% = Leaf live (%), SR% = Survival rate, TNR = Total number of roots, RL = Root length (cm), SL = Shoot length (cm), CC = Chlorophyll content, RFW = Root fresh weight (mg), RDW = Root dry weight (mg), SFW = Shoot fresh weight (mg) and SDW = Shoot dry weight (mg); ‡ LSD indicates least significant difference and SE indicates standard error; ** indicates significant at 0.01 probability level

maximum value of root and shoot dry weight was maximum in Maloti, Lalchikon, and Moyna which is similar to Binadhan-10 and the minimum shoot dry weight was found in Gottaaman, Kabuldulan and Ronojit.

3.2 Nature and magnitude of diversity

D^2 values were estimated to assess the genetic diversity among 25 landraces of rice germplasms based on ten growth parameters (Mahalanobis, 1928). Depending upon the range of diversity, 25 rice genotypes were grouped into five clusters (Fig. 1). The distribution pattern revealed that maximum 10 genotypes viz., Moynamoti, Badshavog, Pangash, Suvash, Moghabalam, Sadaswarna, BINA dhan-8, Chinikani, Ashfail and Rajashail were found in cluster III while the lowest two genotypes were included in cluster IV (Lalbat and M-171). Cluster I, II and V included three (Satin, Sylhetbalam and Moirom), six (Maloti, Lalchikon, Khakshyal, Chinisagor, Moyna and Bina dhan-10) and four genotypes (Chabli, Durgavog, Kabuldulan and Gottaaman), respectively.

3.3 Estimation of cluster distance

The average intra and inter cluster distances are presented in Table 3. In all cases, it was observed that the inter-cluster distances were greater than the intra-cluster distances. Maximum intra-cluster diversity was observed in cluster IV (6.30) and minimum intra-cluster diversity was found in cluster I (4.16). In case of inter-cluster distance, the highest value was found between cluster II and V (15.45) followed by cluster II and IV (13.50), and cluster I and V (13.20) where the lowest inter-cluster distance was observed between cluster I and II (6.39) followed by cluster I and III (8.26).

3.4 Individual clusters characterization

Mean performance of different clusters for different morphological traits are presented in (Table 4).There was a wide range of variation in the cluster mean

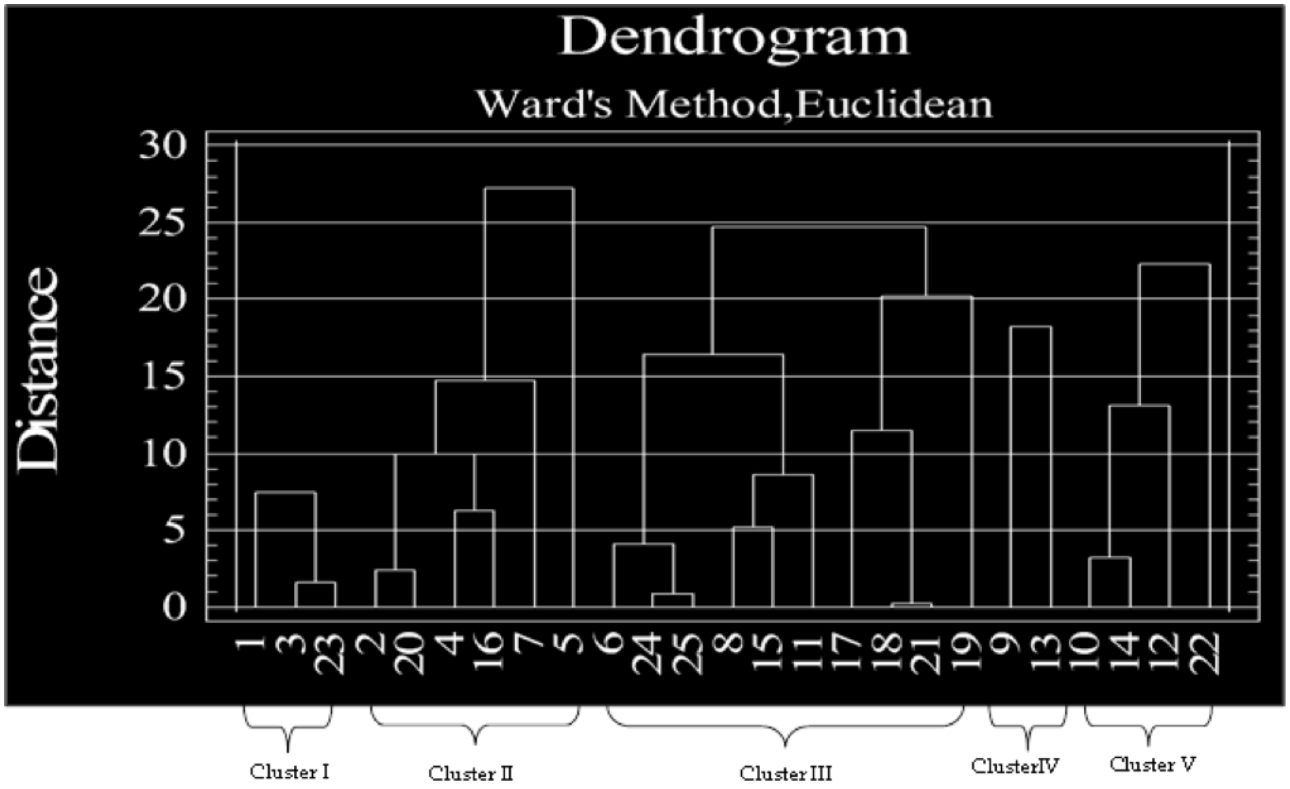

Figure 1. Dendrogram based on summarized data on differentiation among twenty five landraces according to Ward's method (Cluster I includes Satin Sylhetbalam and Moirom; Cluster II includes Maloti, Lalchikon, Khakshyal, Chinisagor, Moyna and Bina dhan-10; Cluster III includes Moynamoti, Badshavog, Pangash, Suvash, Moghabalam, Sadaswarna, Bina dhan-8, Chinikani, Ashfail and Rajashail; Cluster IV includes Lalbat and M-171 and Cluster V includes Chabli, Durgavog, Kabuldulaand Gottaaman)

Table 3. Intra-Inter cluster distance of twenty five rice germplasm

Cluster	I	II	III	IV	V
I	**17.31**	40.84	68.26	139.19	174.18
	–4.16	–6.39	–8.26	–11.8	–13.2
II		**33.37**	102.51	182.23	238.69
		–5.78	–10.12	–13.5	–15.45
III			**32.35**	104.84	66.78
			–5.69	–10.24	–8.17
IV				**39.63**	142.52
				–6.3	–11.94
V					**35.75**
					–5.98

† The bold figures are intra cluster distance

values for all the traits. The mean values of all traits for the respective clusters were categorized into low, moderate and high. The results showed that genotypes having the highest number of live leaves (%) were grouped in cluster IV (63.40) whereas genotypes having the lowest number of live leaves (%) were grouped in cluster V (41.24). For survival rate (%), cluster II (87.84) showed the highest number of genotypes and cluster V (38.38) showed the lowest number of survival rate (%). The highest cluster mean value of total number of roots was found in cluster II (5.54) where the lowest value of total number of roots was found in cluster I (3.89). For root length, genotypes having the maximum root length were grouped into cluster I (8.83) whereas genotypes having the lowest root length were grouped in to cluster V (6.08). The genotypes of cluster II (19.65) also showed the highest shoot length and cluster V (9.58) showed the lowest shoot length for all genotypes. For root length, genotypes having the highest number of root length were grouped into cluster IV (19.27) whereas genotypes having the lowest number of root length were grouped in to cluster V (9.53). With regarding to the root fresh weight, cluster I (9.15) showed the highest mean value and the lowest value was presented in cluster IV (5.65). The maximum root dry weight was found in cluster II (1.28) genotypes where cluster IV and cluster V (0.49) showed the lowest root dry weight. The genotypes having the highest number of shoot fresh weight and shoot dry weight were grouped in cluster II (11.14 and 2.17) whereas genotypes having the lowest shoot fresh weight and shoot dry weight were grouped in cluster IV (6.43 and 0.66). For standard evaluation score, genotype having the highest standard evaluation score was found in cluster V (6.05) whereas genotypes having the lowest standard evaluation score was observed in cluster I (2.51).

3.5 Individual characters contribution towards divergence

The contributions of each character to the total divergence are presented in the Table 5. The results revealed that all the characters did not contribute equally to the total diversity. Root fresh weight contributed maximum (19%) to the divergence of genotypes which was followed by standard evaluation score (18.33%) and shoot dry weight (16.33%). On the other hand, root length contributed least (0.33%) to the total diversity followed by total number of roots (1.67%) and chlorophyll content (2.67%).

4 Discussion

The success of any crop improvement program depends on the amount of diversity present in the crop (Kumbhar et al., 2015). Ranking of genotypes by cluster analysis based on different growth parameters could be applied in salt tolerance breeding to evaluate salt tolerance and may have great advantage over conventional methods. A cluster analysis was performed in this study to facilitate the evaluation of salt tolerance among rice genotypes. The results of the present study reported that the highest number of genotypes was found in cluster III whereas the lowest number in cluster IV and also the lower number of genotypes was found in cluster I, II and V probably due to high correlation among most of the traits and duplication effect of the traits (Fig. 1). The grouping pattern of all the genotypes into various clusters reported the presence of considerable genetic divergence among the genotypes for most of the traits (Kumar et al., 2017). Verma et al. (2006) studied genetic divergence on 108 wheat genotypes and also found eleven clusters based on their various morpho-agronomic traits.

The cluster distance reflects the genetic dissimilarity between and within groups to some extent (Kumar et al., 2017). The inter-cluster and intra-cluster distances range in the present study clearly indicated the existence of variability in the germplasm of dissimilar clusters (Table 3). Similar findings were also reported by Ahmed et al. (2014b). The inter-cluster distances in all the cases were greater than the intra-cluster distances suggesting wider diversity among the genotypes of the distant groups (Table 3). Similar results were reported by (Rahman and Munsur, 2009; Haydar et al., 2007). The overall composition of the clustering pattern in the present study showed that traditional rice genotypes were highly diverse and hence distributed in different clusters. These diverse genotypes could serve as potential germplasm for the improvement of different morphological traits under salinity stress. Similar findings were reported by (Nayak et al., 2004). The maximum intra cluster distance was observed in cluster IV indicating the existence of wide genetic divergence among the constituent genotypes grouped in this cluster. The minimum intra cluster distance was in cluster I (Table 3) indicating the unidirectional selection that lead to uniformity with less deviation between the genotypes in these cluster (Rajesh et al., 2010). Iftekharuddaula et al. (2002) also evaluated the divergence in Boro rice and reported the uniformity of the genotypes within the clusters showing less intra-cluster distances.

The maximum inter cluster distance was observed between cluster II and V showing wider variation among the genotypes between these two groups where the minimum inter cluster distance was found in cluster I and II (Table 3). Ahmed et al. (2014b) also reported that the highest inter-cluster distance between cluster III and V (6.69) by estimating genetic divergence of ten quantitative traits using the non-hierarchical Euclidean cluster in rice germplam.

Table 4. Cluster mean of eleven morphological characters of twenty five genotypes

Characters	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V
Live leaves (%)	41.2	57.5	42.7	63.4	31
Survival rate (%)	83.3	87.8	62	78.8	38.3
Total number of roots	3.89	5.54	4.38	4.67	4.19
Root length	8.83	8.23	7.97	6.72	6.08
Shoot length	18.8	19.6	15	15.3	9.58
Chlorophyll content	16.2	15.8	13.1	19.2	9.53
Root fresh wt.	9.15	8.83	6.89	5.65	5.89
Root dry wt.	1.13	1.28	0.83	0.49	0.49
Shoot fresh wt.	10.6	11.1	8.61	6.43	7.59
Shoot dry wt.	1.72	2.17	1.52	0.66	0.93
Standard Evaluation Score (SES)	2.51	2.52	4.75	2.76	6.05

Rajesh et al. (2010) reported that the inter-varietal hybridization among genotypes of these two clusters (II and V) would be beneficial combine the agronomically superior features.

Table 5. Percent distribution of morphological characters towards divergence

Characters	Towards divergence (%)
Live leaves (%)	14.6
Survival rate (%)	7.0
Total number of roots	1.67
Root length	0.33
Shoot length	5.67
Chlorophyll content	2.67
Root fresh wt.	2.66
Root dry wt.	19.0
Shoot fresh wt.	11.6
Shoot dry wt.	16.3
SES	18.3
Total	100

The results of cluster mean (Table 4) revealed that the genotypes in cluster II showed the highest survival rate (%), total number of roots, shoot length and root dry weight, shoot fresh weight and shoot dry weight indicating that the genotypes of this cluster II should get priority as parent for the improvement of salinity tolerance. The cluster IV showed maximum mean value for the highest live leaves (%), chlorophyll content. Thus, genotypes from this cluster could be good for the improvement of salinity tolerance traits in rice. In addition, genotype having the highest number of standard evaluation score was observed in cluster V whereas genotype having the lowest number of standard evaluation score was observed in cluster I indicating the genetic divergence between clusters I and V. Kumar et al. (2017) also reported maximum value of flag leaf length, 1000-grain weight, seed vigor index and germination% after harvesting in cluster VII, cluster II for flag leaf width, spike length, number of grains per spike and germination (%) before harvesting and cluster IV for grain yield per plant and number of tillers per plant. Genetic divergence analysis is important tool to estimate genetic diversity among selected genotypes which determine family relationships and genetic affinity or distance of genotypes from each other studying cluster analysis (Roger, 1972). Sreelakshmi et al. (2011) studied for genetic divergence using Mahalanobis D^2 statistic indicated wider genetic diversity among germplams. The results of present study showed that the maximum contribution of root fresh weight followed by standard evaluation score and shoot dry weight to the divergence of genotypes indicating their importance during traits selection for the improvement of salinity tolerance (Table 5). Choudhury et al. (1999) also mentioned that plant height contributes the highest for genetic divergence. Reddy et al. (2015) reported that number of seeds per pod, 100-seed weight, plant height, days to maturity and seed yield per plant together contributed for about 81.31% of the total divergence and hence these traits to be emphasized during selection (Rajesh et al., 2010). These findings are similar in agreement with earlier reported by other workers (Nimbalkar et al., 2002; Tsegaye et al., 2012; Hailegiorgis et al., 2011; Ali et al., 2008).

5 Conclusions

This study gave information about desirable traits that contributes to the divergence between the genotypes for salinity tolerance. The genotypes in cluster I namely Satin, Sylhetbalam, Moirom may be used for the improvement of root length and root fresh weight and the genotypes of the cluster II (Maloti, Lalchikon, Khakshyal, Chinisagor, Moyna, Binadhan-10) could be used for the improvement of survival rate (%), total number of roots, shoot length and root dry weight, shoot fresh weight and shoot dry weight in rice under salinity stress. These genotypes may be used in future breeding program for further improvement

of salinity tolerance. Relative contribution of root length showed maximum contribution in divergence. However, root fresh weight has least contribution in divergence.

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Conflict of Interest

The authors declare that there is no conflict of interests regarding the publication of this paper.

References

Ahmed A, Shaon SG, Islam MS, Saha PS, Islam MM. 2014a. Genetic divergence analysis in HRDC rice *(Oryza sativa* L.) hybrids in Bangladesh. Bangladesh Journal of Plant Breeding and Genetics 27:25–32. doi: 10.3329/bjpbg.v27i2.27842.

Ahmed I, Kadir MN, Ahmed MH. 2014b. Surface water salinity intrusion assessment of south-west region of Bangladesh - A GIS based approach. International Journal of Surface and Groundwater Management 1:90–95.

Ali MN, Yeasmin L, Gantait S, Goswami R, Chakraborty S. 2014. Screening of rice landraces for salinity tolerance at seedling stage through morphological and molecular markers. Physiology and Molecular Biology of Plants 20:411–423. doi: 10.1007/s12298-014-0250-6.

Ali Y, Atta BM, Akhter J, Monneveux P, Lateef Z. 2008. Genetic variability, association and diversity studies in wheat *(Triticum aestivum* L.) germplasm. Pakistan Journal of Botany 40:2087–2097.

BBS. 2016. Yearbook of Agricultural Statistics. Bangladesh Bureau of Statistics, Ministry of Planning. Government of the People's Republic of Bangladesh.

Choudhury DA, Hamid A, Bhowmik A, Mian GU, Islam MS. 1999. Genetic divergence in indigenous rice *(Oryza sativa* L.) varieties of Bangladesh. Bangladesh Journal of Plant Breeding and Genetics 12:33–36.

Chowdhury AD, Haritha G, Sunitha T, Krishnamurthy SL, Divya B, Padmavathi G, Ram T, Sarla N. 2016. Haplotyping of rice genotypes using simple sequence repeat markers associated with salt tolerance. Rice Science 23:317–325. doi: 10.1016/j.rsci.2016.05.003.

Fahad S, Bajwa AA, Nazir U, Anjum SA, Farooq A, Zohaib A, Sadia S, Nasim W, Adkins S, Saud S, Ihsan MZ, Alharby H, Wu C, Wang D, Huang J. 2017. Crop production under drought and heat stress: plant responses and management options. Frontiers in plant science 8:1147. doi: 10.3389/fpls.2017.01147.

Gregorio GB, Senadhira D, Mendoza RD. 1997. Screening rice for salinity tolerance. IRRI Discussion Paper Series No. 22. Plant Breeding, Genetics, and Biochemistry Division, IRRI .

Grover A, Pental D. 2003. Breeding objectives and requirements for producing transgenics for major field crops of india. Current Science 84:310–320.

Hailegiorgis D, Mesfin M, Genet T. 2011. Genetic divergence analysis on some bread wheat genotypes grown in Ethiopia. Journal of Central European Agriculture 12:344–352. doi: 10.5513/JCEA01/12.2.922.

Haque SA. 2006. Salinity problems and crop production in coastal regions of bangladesh. Pakistan Journal of Botany 38:1359–1365.

Haydar A, Ahmed MB, Hannan MM, Razvy MA, Mandal MA, Salahin M, Karim R, Hossain M. 2007. Analysis of genetic diversity in some potato varieties grown in Bangladesh. Middle-East Journal of Scientific Research 2:143–145.

Iftekharuddaula KM, Akter K, Bashar MK, Islam M. 2002. Genetic parameters and cluster analysis of panicle traits in irrigated rice. Bangladesh Journal of Plant Breeding and Genetics 15:49–55.

Kibria MG, Hossain M, Murata Y, Hoque MA. 2017. Antioxidant defense mechanisms of salinity tolerance in rice genotypes. Rice Science 24:155–162. doi: 10.1016/j.rsci.2017.05.001.

Kordrostami M, Rabiei B, Kumleh HH. 2017. Biochemical, physiological and molecular evaluation of rice cultivars differing in salt tolerance at the seedling stage. Physiology and Molecular Biology of Plants 23:529–544. doi: 10.1007/s12298-017-0440-0.

Kumar A, Gaurav SS, Kumar A, Rathi V. 2017. Genetic divergence analysis of agronomic traits in bread wheat *(Triticum aestivum* L.) genotypes. International Journal of Current Microbiology and Applied Science 6:2683–2686. doi: 10.20546/ijcmas.2017.608.320.

Kumbhar S, Kulwal P, Patil J, Sarawate C, Gaikwad A, Jadhav A. 2015. Genetic diversity and population structure in landraces and improved rice varieties from india. Rice Science 22:99–107. doi: 10.1016/j.rsci.2015.05.013.

Mahalanobis PC. 1928. A statistical study at Chinese head measurement. The Journal of the Asiatic Society of Bengal 25:301–377.

Mohammadi SA, Prasanna BM. 2003. Analysis of genetic diversity in crop plants—salient statistical tools and considerations. Crop Science 43:1235–1248. doi: 10.2135/cropsci2003.1235.

Munns R, Tester M. 2008. Mechanisms of salinity tolerance. Annual Review of Plant Biology 59:651–681. doi: 10.1146/annurev.arplant.59.032607.092911.

Murthy BR, Arunachalam V. 1966. The nature of divergence in relation to breeding systems in some crop plants. Indian Journal of Genetics and Plant Breeding 26:188–198.

Nayak AR, Chaudhury D, Reddy JN. 2004. Genetic divergence in scented rice. Oryza 41:79–82. doi: 10.3329/bjb.v44i2.38506.

Nazar R, Iqbal N, Masood A, Syeed S, Khan NA. 2011. Understanding the significance of sulfur in improving salinity tolerance in plants. Environmental and Experimental Botany 70:80–87. doi: 10.1016/j.envexpbot.2010.09.011.

Nimbalkar C, Navale P, Biradar A. 2002. Generalized D2 and genetic diversity in wheat. Journal-Maharashtra Agricultural Universities 27:43–45.

Rahman MM, Munsur MAZ. 2009. Genetic divergence analysis of lime. Journal of the Bangladesh Agricultural University 7:33–37. doi: 10.3329/jbau.v7i1.4795.

Rajesh T, Paramasivam K, Thirumeni S. 2010. Genetic divergence in land races of rice. Electronic Journal of Plant Breeding 1:199–204.

Rao CR. 1952. Advanced statistical methods in biometric research. A Division Of Macmillan Publishing Co, Inc New York; Collier-Macmillan.

Reddy VG, Jayalakshmi V, Sreenivas T. 2015. Research note genetic divergence studies in pigeonpea inbreds. Electronic Journal of Plant Breeding 6:515–520.

Roger JS. 1972. Measure of genetic similarity and genetic distance. Studies in genetics VII. University of Texas publication 7213:145–153.

Roy PR, Tahjib-Ul-Arif M, T A. 2016. Exogenous ascorbic acid and hydrogen peroxide alleviates salt-induced oxidative stress in rice *(Oryza sativa* L.) by enhancing antioxidant enzyme activities and proline content. Advances in Environmental Biology 10:148–155.

SRDI. 2010. Saline Soils of Bangladesh. Soil Resource Development Institute, Ministry of Agriculture, Bangladesh.

Sreelakshmi C, Kumar CS, Shivani D. 2011. Research note genetic analysis for yield and its components in hybrid pigeonpea. Electronic Journal of Plant Breeding 2:413–416.

Tahjib-Ul-Arif M, Sayed M, Islam M, Siddiqui M, Begum S, Hossain M. 2018. Screening of rice landraces *(Oryza sativa* L.) for seedling stage salinity tolerance using morpho-physiological and molecular markers. Acta Physiologiae Plantarum 40:70. doi: 10.1007/s11738-018-2645-4.

Tang S, Jiang Y, Li Z, Yv H. 2002. Genetic diversity of isozymes of cultivated rice in China. Acta Agronomica Sinica 28:203–207.

Tsegaye D, Dessalegn T, Dessalegn Y, Share G. 2012. Analysis of genetic diversity in some durum wheat *(Triticum durum* Desf) genotypes grown in Ethiopia. African Journal of Biotechnology 11:9606–9611.

Verma AK, Singh PK, Vishwakarma SR, Tripathi RM. 2006. Genetic divergence in wheat *(T. aestivum* L.). Journal of Farm Sciences 15:32–34.

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