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Morphological based screening and genetic diversity analysis of the local rice (*Oryza sativa* L.) landraces at the seedling stage for salinity tolerance

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ABSTRACT

Salinity is considered as one of major threats in rice production around the world. This experiment was conducted to screen out the salt tolerant rice genotypes following modified hydroponic method and IRRI standard protocol (SES scoring). Twenty-five rice genotypes were evaluated for the screening purpose for salinity tolerance considering morphological parameters. Three levels of salinity treatments (EC-0 dSm^{-1}, EC-7 dSm^{-1} and EC- 12 dSm^{-1}) were used for the phenotypic analysis and genotypes were categorized according to SES scoring based on visual salt injury in rice seedlings at 21th days of saline treatment. Salt injury symptoms varied among the landraces with different concentration of salt. All plant parameters reduced significantly in all genotypes with increasing salinity although less reduction was found in some genotypes at higher salinity also and identified those genotypes as salt tolerant. After 21 days of salinization, five genotypes (Maloti, Chinisagor, Lal bat, Moyna, Binadhan-8 and Binadhan-10) were found as slat tolerant at both 7 dSm^{-1} and 12 dSm^{-1} according to standard evaluation score based on visual salt injury at seedling stage. The phenotypic co-efficient of variation (PCV) was higher than genotypic co-efficient of variation (GCV) for all the traits studied indicating that they all are interacted with the environment to some extent. The highest heritability was found for all traits in the range of 73.82% to 96.08% indicating that the traits are less influenced by environment and these traits can be considered for the improvement of salinity tolerance. High heritability coupled with high genetic advance as percent of mean was observed for standard evaluation score (96.08%, 130.51%), root dry weight (95.72%, 135.08%) and shoot fresh weight (94.63%, 68.38%) indicating the role of additive gene expression for these traits and would facilitate better scope for improvement of these traits through direct selection. The correlation and path analysis showed that live leaves (%), survival rate (%), shoot length, chlorophyll content, root fresh weight, root dry weight had significant negative correlation with standard evaluation score as well as had direct positive effect on standard evaluation score indicating their importance for the improvement of salt tolerance ability of plant.

Key Words: *Rice, Salinity, Heritability, Genetic advance and Path analysis*

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I. Introduction

Rice (*Oryza sativa* L.) is a most important staple food plant for more than half of the world's population belonging to the family Poaceae and subfamily Oryzoidea (Kordrostam *et al.*, 2017). It has been considered as foremost food of the Bangladeshi people; about 80% of the total cultivated lands in Bangladesh are used for rice cultivation and its total production is 34.71 million metric tons (BBS, 2016). Although most of the part of our country is suitable for rice cultivation in our country but a major part namely southern part is still uncultivated for rice cultivation due to different abiotic stress and salinity is one of them. Salinity reduced the productivity of crop plants because most of the crop plants are sensitive to salinity caused by high concentrations of salts in the soil, and the area of land affected by it is increasing day by day (Shrivastava and Kumar, 2015). The salinity area is increasing with time from 0.83 mha to 1.056 mha in 36 years (SRDI, 2003) due to rise in sea level and global temperature. Rice is considered as sensitive to salinity, particularly at the young seedling stage and reproductive stage (Razzaque *et al.*, 2017). Several studies also indicated that rice is tolerant during seed germination but becomes very sensitive during early seedling stage (2-3 leaf stage), gains tolerance during vegetative growth stage (Mokhtar *et al.*, 2015). Salt stress caused toxicity in plants leading to different metabolic changes, like loss of chloroplast activity, decreased photosynthetic rate and increased photorespiration rate resulting the production of reactive oxygen species (ROS) production (Parida and Das, 2005).

Population of our country increasing day by day but land is restricted. It is so much essential to identify the precarious soil and use those lands under cultivation through the introduction of suitable varieties. Therefore, approach should be taken both increase the production per unit and increase the land quality under production including the problematic soil. Therefore, for the improvement of local food security and sustainable agriculture, landraces played very important role, in addition to their significance as genetic resource for rice genetic improvement (Tang *et al.*, 2002). Landraces provided specific adaptability genes for specific environmental conditions and the incorporation of adaptability genes from landraces could ensure higher grain yield for the region (Prabakaran *et al.*, 2010). Screening of rice germplasms for salt tolerance at seedling stage based on morphological parameters readily acceptable as it is based on a simple criterion of selection; it provides rapid screening of large number of materials (Arif *et al.*, 2017). Hydroponic systems have been utilized as one of the standard methods for plant biology research and are also used in commercial production for several crops (Nguyen *et al.*, 2016) following to facilitate the use of good quality experimental procedures that are crucial to the success of salinity studies (Gregorio *et al.*, 1997). Therefore, present study was carried out with the screening and genetic variability analysis of rice genotypes for salinity tolerance and identification of salt tolerant genotypes at seedling stage.

II. Materials and Methods

The experiment was conducted at the growth chamber, located at the Department of Genetics and Plant Breeding, Bangladesh Agricultural University (BAU), Mymensingh-2202, Bangladesh. A total of twenty five rice genotypes were used in this experiment. Twenty-three genotypes were local varieties (landraces) collected from southern part of Bangladesh and two genotypes (Binadhan-8 and Binadhan-10 used as salt tolerant check genotypes) were collected from Bangladesh Institute of Nuclear Agriculture (BINA) (Table 01).

Probable one hundred and twenty seeds of each genotype were placed in petridishes having moist filter paper and kept in the dark place for 3-4 days for sprouting. Then the 4-5 days old seedlings were transferred to hydroponic medium by wrapping the seedling with sponge and placed into the holes of the rubber sheet. In this experiment, peter professional (water soluble fertilizer) was used to supply appropriate amount of nutrient. The solution was stirred for two times daily to ensure the continuous supply of the nutrients to the plants. The nutrient solution was changed after every 7 seven days. Two salt treatments (7 dSm^{-1} and 12 dSm^{-1}) were imposed in the nutrient solution after five days of seedling transfer into the hydroponic system by adding NaCl. For the adjustment of EC to 7 dSm^{-1} and 12 dSm^{-1}, 2g and 4.25g NaCl per liter nutrient solution were added respectively. The EC was measured by EC meter. Plants were exposed to salinity for 10 days from the adding of salt into the nutrient

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solution, afterwards they were grown with the normal nutrient solution and the seedlings were up to 21 days. The modified standard evaluation score (SES) of IRRI was used to access the visual symptoms of soil toxicity (Table 02). The scoring discriminates the tolerant, moderately tolerant and susceptible rice varieties. The scoring was done at 21st day of experimental setting. Data collection along with different root and shoot characters were done after 21 days of setting in hydroponic system by successive destructive harvest.

Table 01. List of twenty five rice genotypes used in the experiment

Sl. No.	Genotypes	Types	Place of Collection
V1	Satin	Landraces	Satkhira
V2	Maloti		
V3	Sylhetbalam		
V4	Lalchikon		
V5	Khakshyal		
V6	Moynamoti		
V7	Chinisagor		
V8	Badshavogh		
V9	Lalbat		
V10	Chabli		
V11	Pangash		
V12	Durgabhog		
V13	M-171		
V14	Kabuldulan		
V15	Suvash		
V16	Moyna		
V17	Binadhan-8	High yielding salt tolerant genotype	Bangladesh Institute of Nuclear Agriculture (BINA)
V18	Ronjit	Landraces	Satkhira
V19	Moghabalam		
V20	Binadhan-10	High yielding salt tolerant genotype	Bangladesh Institute of Nuclear Agriculture (BINA)
V21	Sadaswarna	Landrace	Satkhira
V22	Gottaaman		
V23	Moirom		
V24	Chinikani		
V25	Ashfail		

Measurement of morphological parameters

Live leaves (% LL) plant was observed by close visual observation. Just after the removal of the plants from the hydroponic system, 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 leaf of all the plants per pot with a chlorophyll meter (SPAD-502 Chlorophyll Meter, Minolta Camera Co. Ltd., Japan) at the harvest time. Total number of roots was also measured by close visual observation. A sharp needle or forceps were used in counting the root number. Immediately after harvesting, the shoot samples were separated from the root and the fresh weight of root and shoot was taken separately by using an electric balance. After the destructive harvest and measurement of all traits, roots and shoots of each variety among with replicates were separately enclosed in a brown envelop (20 x10 cm). Similar tactics were also followed in case of shoot. After that, all envelops were put in an Oven. In the oven they were kept at 60º C for 7 days and then the dry weight of root and shoot also was measured separately by using an electric balance.

The susceptibility index (SI) of morphological parameters were evaluated such as live leaves susceptibility index (LLSI), survival rate susceptibility index (SRSI), shoot length susceptibility index (SLSI), root length susceptibility index (RLSI), chlorophyll content susceptibility index (CCSI), total number of roots susceptibility index (TNRSI), root fresh weight susceptibility index (RFWSI), shoot

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fresh weight susceptibility index (SFWSI), root dry weight susceptibility index (RDWSI) and shoot dry weight susceptibility index (SDWSI), by the following formula:

$$\text{Susceptibility index (SI)} = \frac{\text{Control plant value} - \text{salt treated plant value}}{\text{control plant value}} \times 100$$

Table 02. Modified Standard Evaluation Score (SES) for visual salt injury (1-9 scale) (IRRI, 1997)

Score	Observation	Tolerance level
1	Normal growth, no leaf symptoms	Highly tolerant
3	Nearly normal growth, but leaf tips of few leaves whitish and rolled	Tolerant
5	Growth severely retarded , most leaves rolled; only a few are elongating	Moderately tolerant
7	Complete cessations of growth, most leaves dry; some plants dying	Susceptible
9	Almost all plants dead or dying	Highly susceptible

Table 03. SES score of twenty eight rice genotypes under salinized condition grown in hydroponic system at the seedling stage

Sl Number	Genotypes	EC- 7 dSm^{-1}		EC- 12 dSm^{-1}	
		SES score	Tolerance	SES score	Tolerance
1.	Satin	3.51	MT	6.16	S
2.	Maloti	2.75	T	3.12	T
3.	Sylhetbalam	3.51	T	4.06	MT
4.	Lalchikon	6.66	S	7.13	S
5.	Khakshyal	4.46	MT	8.03	HS
6.	Moynamoti	6.67	S	7.87	HS
7.	Chinisagor	2.37	T	3.33	T
8.	Badshavogh	5.9	MT	7	S
9.	Lalbat	3.18	T	3.27	T
10.	Chabli	8.2	HS	9	HS
11.	Pangash	6.46	S	9	HS
12.	Durgavog	7.03	S	7.93	S
13.	Moyna	2.75	T	3.12	T
14.	Binadhan-8	2.23	T	3.46	T
15.	Ronojit	5	MT	8.55	HS
16.	Moghabalam	2.73	T	6.91	S
17.	Binadhan-10	2.75	T	3.06	T
18.	Sadaswarna	3.45	T	8.73	HS
19.	Gottaaman	8.2	HS	9	HS
20.	Moirom	6.71	S	8.06	HS
21.	Chinikani	5.3	MT	9	HS
22.	Ashfail	7.13	S	9	HS
23.	M-171	3.27	T	3.33	T
24.	Kabuldulan	8.36	HS	9	HS
25.	Suvash	2.7	MT	9	HS

Note: 1-9 Scale, where 1 = highly tolerant (HT), 3 = tolerant (T), 5 = moderately tolerant (MT), 7 = susceptible (S) and 9 = highly susceptible

Statistical analysis

MSTATC was used to perform data analysis on morphological parameters for normal and salinized environments. Analysis of variance (ANOVA), path co-efficient and correlation co-efficient were performed using the plant breeding statistical program (MSTATc). Genetic parameters such as genotypic co-efficient of variation (GCV) and phenotypic co-efficient of variation (PCV), heritability, genetic advance were estimated by using the formula.

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Estimation of genotypic and phenotypic variances

Genotypic and phenotypic variances were estimated according to the formula given by Johnson *et al.*, (1955).

Genotypic variance, $\sigma_g^2 = \frac{GMS - EMS}{r}$

Where,

GMS = Genotypic mean square; EMS = Error mean square; r = Number of replication

Phenotypic variance, $\sigma^2_p = \sigma^2_g + EMS$

Where,

σ^2_g = Genotypic variance; EMS = Error mean square

Estimation of heritability

Heritability in broad sense (h^2b) was estimated according to the formula suggested by Johnson *et al.* (1955) and Hanson *et al.* (1956).

Heritability, $h^2_b = \frac{\sigma^2_g}{\sigma^2_p} \times 100$

Where,

h^2_b=Heritability in broad sense; $\delta^2 g$ = Genotypic variance; $\delta^2 p$ = Phenotypic variance

Estimation of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV)

Genotypic and phenotypic coefficient of variations were estimated according to Burton (1952) and Singh and Chaudhary (1985).

Genotypic coefficient of variations, $GCV = \frac{\sqrt{\sigma_g^2}}{\overline{X}} \times 100$

Where,

σ^2_g= Genotypic variance; $\overline{X}$= Population mean

Phenotypic coefficient of variations, $PCV = \frac{\sqrt{\sigma_P^2}}{\overline{X}} \times 100$

Where,

σ^2_p = Phenotypic variance; $\overline{X}$= Population mean

Estimation of genetic advance

Estimation of genetic advance was done following formula given by Johnson *et al.* (1955) and Allard (1960).

Genetic advance, $GA = h^2_b.K.\sigma_p$

Where,

h^2_b = Heritability in broad sense; K= Selection differential, the value of which is 2.06 at 5% selection intensity; σ_p = Phenotypic standard deviation

Estimation of genetic advance in percentage of mean, GA (%)

Genetic advance in per cent of mean was calculated by the formula of Comstock and Robinson (1952) as follows:

Genetic advance in percentage of mean, $GA\ (\%) = \frac{GA}{\overline{X}} \times 100$

Where,

GA = Genetic advance; $\overline{X}$= Population mean

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III. Results

Categorizing of rice genotypes based on SES score at seedling stage

Injury scoring of rice genotypes was performed by Standard Evaluation Score (SES) (IRRI, 1997) (Table 02) chart based on the visual salt injury at seedling stage. Scoring was done at 21st days of experimental setting and the range of scoring was 1 to 9. Table 03 showed the tolerance level of different rice genotypes under saline and non-saline conditions. In salinized setup, wide variation was found among different genotypes. None of the genotypes showed high salt tolerance level at EC-7 dSm^{-1} or EC-12 dSm^{-1}. Seven genotypes (Maloti, Chinisagor, Lalbat, M-171, Moyna, Binadhan-8, Binadhan-10) were identified as tolerant at both EC-7 dSm^{-1} or EC-12 dSm^{-1}, four genotypes (Shyletbalam, Suvash, Mogha and Sadaswarna) identified as tolerant at EC-7 dSm-1 but those were found as susceptible and highly susceptible at higher salinity (EC-12 dSm^{-1}), rest of the genotypes were found as moderately tolerant, susceptible and highly susceptible to salt at EC- 7 dSm^{-1} and at EC- 12 dSm^{-1} (Table 03).

The analyses of variance (ANOVA) of different morphological parameters of rice landraces for salt tolerance are shown in Table 04. The ANOVA indicated that the difference among genotypes for all the traits under study viz., live leaves (%LL), survival rate (%SR), shoot length (SL), root length (RL), chlorophyll content (CC), total number of roots (TNR), root fresh weight (RFW), shoot fresh weight (SFW), root dry weight (RDW) and shoot dry weight (SDW) were moderately significant.

Table 04. Analysis of variance for different morphological characters of twenty five rice genotypes

Items	d.f	LL (%)	SR (%)	TNR	RL	SL	CC
Replication	2	31.16	307.12	1.231	0.776	52.565	16.689
Variety (A)	24	1188.48**	3546.69**	5.016**	12.564**	175.551**	97.677**
Treatment (B)	2	5984.56**	40305.21**	163.498**	349.478**	2711.611**	4178.427**
A x B	48	466.68**	696.83**	1.938**	3.128**	32.262**	56.807**
Error	148	37.61	118.50	0.335	1.328	5.393	4.673

Traits	d.f	RFW (100mg)	RDW (100mg)	SFW (100mg)	SDW (100mg)	SES
Replication	2	1.196	0.117	0.047	0.176	0.797
Variety (A)	24	21.845**	1.090**	29.592**	2.784**	20.289**
Treatment (B)	2	339.788**	8.111**	607.618**	37.351**	343.894**
A x B	48	3.220**	0.148**	6.807**	1.143**	7.651**
Error	148	1.105	0.016	0.549	0.068	0.272

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), SDW = Shoot dry weight (mg), ** indicates significant at 0.01 probability level.

Effect of salt on morphological traits

Rice is a salt sensitive cereal crop which shows considerable variation in different salt tolerance level. Twenty five rice genotypes were screened for salinity tolerance based on their phenotypic characteristics under salt stress and control condition. Seedlings grown in saline condition showed several symptoms of salt injury such as yellowing and drying of leaves, reduction in root and shoot growth, reduced stem thickness and in many cases dying of seedlings were also observed. Moreover, some other symptoms such as leaf roll and tip whitening etc.

Susceptible genotypes were more affected than tolerant genotypes under salt stress for different agronomic traits such as live leaves (%LL), survival rate (%SR), shoot length (SL), root length (RL), chlorophyll content (CC), total number of roots (TNR), root fresh weight (RFW), shoot fresh weight (SFW), root dry weight (RDW) and shoot dry weight (SDW) (Table 05). LL (%) was drastically reduced in all rice genotypes with the increasing of salinity and some genotypes viz., Chabli, Khakshyal and M-171 had showed greater live leaves susceptibility index (LLSI) under 12 dSm^{-1} NaCl stress where minimum LLSI was found in salt-tolerant Maloti and Moyna. Under salt stress conditions, survival rate (%) was significantly decreased in all the rice genotypes compared to control condition. Some genotypes showed greater survival rate susceptibly index (SRSI) viz. Chabli, Moriom and M-171 (Table 04) where salt tolerant Maloti, Chinisagor and Lalbat had reported least SRSI compared to rest 21

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genotypes. Under salinity stress, maximum total number of roots susceptibility index (TNRSI) were increased with the increasing of salinity but tolerant genotypes showed less TNRSI compared to the susceptible genotypes. The maximum TNRSI were found in Sylhetbalam, Chabli and Chinikani where minimum TNRSI were observed for Chinisagor, Lalbat and Moyna. Salt concentration notably reduced Root length (RL) and shoot length (SL) of rice seedlings in all genotypes under saline condition but the salt tolerant genotypes namely Chinisagor, maloti and Binadhan-10 showed lowest RLSI and SLSI where a maximum RLSI and SLSI had reported in salt susceptible genotypes viz, Chabli, Moriom, Badshavogh, M-171 and Ashfail. Chlorophyll content (SPAD) in rice seedlings showed different response under salinity stress and significantly decreased in all rice genotypes with the increasing of higher salinity. With the increasing of salinity Chabli, Moriom, Badshavogh, M-171 and Ashfail showed maximum chlorophyll content susceptibility index (CCSI) (100%) where minimum CCSI were observed for Chinisagor, Moyna and Binadhan-10. Fresh weight (FW) and dry weight (DW) of root and shoot were considerably reduced in all genotypes under salinity stress. Salt susceptible genotypes viz., Chabli, Moriom and M-171 showed maximum root fresh weight susceptibility index (RFWSI) and shoot fresh weight susceptibility index of (SFWSI) whereas lowest RFWSI and SFWSI under salinity stress were found in salt tolerant Chinisagor, Lalbat, Binadhan-8 and Binadhan-10. Similarly, maximum root dry matter susceptible index (RDWSI) and shoot dry matter susceptible index (SDWSI) were also found in highly salt susceptible genotypes namely Chabli, Pangash, Ashfail and Moriom whereas some salt tolerant genotypes viz, Maloti, Chinisagor, Moyna and Binadhan-10 showed less RDWSI and SDWS under salinity stress compared to other genotypes.

Estimation of genetic parameters for morphological traits

The genetic parameters viz., genotypic variances, phenotypic variances, phenotypic co-efficient of variation (PCV), genotypic co-efficient of variation (GCV), heritability, genetic advance and genetic advance in percentage GA (%) for all the studied morphological traits were estimated and presented in Table 06. In this study all the traits showed significant genotypic and phenotypic variance. From the results of analysis of genotypic and phenotypic variances, the phenotypic co-efficient of variation (PCV) were higher than genotypic co-efficient of variation (GCV) for all the traits. Among the traits, survival rate (%) exhibited high estimates of PCV (1261.23) and GCV (1142.73) followed by live leaves (%) (421.23 & 383.62) and shoot length (62.11 & 56.72) where lowest phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were observed for root dry weight (0.37 & 0.36) followed by shoot dry weight (0.97 & 0.91) and total number of roots (1.90 & 1.56). All the traits studied in this experiment exhibited high heritability ranging from 73.82% to 96.08%. The highest heritability was found in standard evaluation score (96.08%) followed by root dry wt. (95.72%), shoot fresh wt. (94.53%), shoot dry wt. (93.01%), shoot length (91.32%), leaf live (91.07%), survival rate (90.60%), chlorophyll content (86.90%), root fresh wt. (86.22%) and root length (73.82%). Only estimation of heritability is not enough to provide clear indication and screening of desirable genotypes. Hence knowledge about genetic advance is essential along with heritability. The highest GA was found in survival rate (66.28) followed by live leaves percentage (38.50) and the lowest genetic advance was found in root dry weight (1.21) and shoot dry weight (1.89) followed by total number of roots (2.33). Expected genetic advance as percent of mean indicates the mode of gene action in the expression of traits, which would be helpful for selection program. The highest genetic advance as percent of mean was found for root dry weight (135.08) followed by standard evaluation score (130.51%) while the lowest was found in root length (44.30%) followed by total number of roots (55.85%).

Estimation of correlation coefficients

Correlation co-efficient among different traits of twenty five rice genotypes at phenotypic and genotypic level revealed significant and negative relations of standard evaluation score with live leaves (%), survival rate (%), root length, shoot length, chlorophyll content, root fresh weight, root dry weight, shoot fresh weight and shoot dry weight for all the genotypes (Table 07). Afterwards, negative and non-significant co-relation was found total number of roots which referred to a complex linked of relation among the pair of combinations. It was also observed that the genotypic correlation coefficients were higher than their respective phenotypic co-relation coefficient in most cases, however, in some cases, the phenotypic correlation coefficients were higher than their corresponding genotypic correlation coefficients.

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Table 05. Performance of rice genotypes in response to different morphological traits at seedling stage under salinized (7 dsm^{-1} & 12 dsm^{-1}) and non- salinized condition

Genotype	Treatment	LL	SR	TNR	RL	SL	CC	RFW	RDW	SFW	SDW
Satin	Control	74.9	100.0	5.7	60.2	55.3	40.4	52.0	49.2	47.2	49.4
	EC-7	31.1	85.0	4.3	40.1	43.2	29.2	37.5	36.6	34.4	36.2
	EC-12	16.6	70.0	2.3	29.6	34.0	22.0	28.5	28.2	26.2	27.6
	% SI at 7 dsm^{-1}	58.5	15.0	23.5	33.3	21.9	27.7	27.8	25.6	27.0	26.8
	% SI at 12 dsm^{-1}	77.9	30.0	58.8	50.8	38.5	45.6	45.1	42.8	44.4	44.1
Maloti	Control	73.5	100.0	6.0	59.8	55.3	40.4	51.8	49.2	47.1	49.4
	EC-7	63.9	100.0	4.7	56.2	53.6	38.2	49.3	47.0	44.8	47.1
	EC-12	51.7	68.3	4.3	41.5	38.0	27.9	35.8	33.9	32.6	34.1
	% SI at 7 dsm^{-1}	13.1	0.0	22.2	6.1	3.0	5.5	4.8	4.3	4.8	4.7
	% SI at 12 dsm^{-1}	29.6	31.7	27.8	30.7	31.2	30.8	30.9	31.0	30.9	30.9
Sylhetbalam	Control	63.6	91.7	6.3	53.9	50.6	36.9	47.1	44.9	43.0	45.0
	EC-7	30.6	70.0	2.7	34.4	35.7	24.3	31.5	30.5	28.7	30.2
	EC-12	24.1	60.0	2.0	28.7	30.2	20.3	26.4	25.7	24.1	25.4
	% SI at 7 dsm^{-1}	51.9	23.6	57.9	36.1	29.5	34.3	33.3	32.1	33.2	32.9
	% SI at 12 dsm^{-1}	62.0	34.5	68.4	46.7	40.3	45.0	43.9	42.9	43.9	43.6
Lalchikon	Control	75.5	93.3	6.0	58.3	52.5	38.9	49.9	47.1	45.3	47.5
	EC-7	65.5	100.0	5.7	57.1	54.2	39.0	50.1	47.8	45.6	47.8
	EC-12	53.6	71.7	4.3	43.2	39.7	29.1	37.3	35.4	33.9	35.6
	% SI at 7 dsm^{-1}	13.3	-7.1	5.6	2.1	-3.2	-0.1	-0.3	-1.3	-0.6	-0.8
	% SI at 12 dsm^{-1}	29.0	23.2	27.8	25.9	24.4	25.3	25.2	24.9	25.1	25.1
Khakshyal	Control	82.2	100.0	6.7	63.0	56.5	42.1	53.9	50.8	48.9	51.2
	EC-7	34.5	100.0	6.3	46.9	51.1	34.8	44.3	43.4	40.8	42.8
	EC-12	15.7	93.3	6.0	38.4	45.9	30.1	38.1	38.0	35.4	37.2
	% SI at 7 dsm^{-1}	58.1	0.0	5.0	25.5	9.6	17.3	17.8	14.6	16.6	16.4
	% SI at 12 dsm^{-1}	80.9	6.7	10.0	39.1	18.8	28.5	29.2	25.2	27.6	27.4
Moynamoti	Control	70.8	80.0	6.0	52.3	46.1	34.8	44.4	41.8	40.3	42.2
	EC-7	56.5	73.3	3.3	44.4	40.4	29.4	38.0	35.9	34.4	36.1
	EC-12	34.0	66.7	3.0	34.5	34.7	24.1	31.1	30.0	28.4	29.8
	% SI at 7 dsm^{-1}	20.3	8.3	44.4	15.1	12.5	15.6	14.3	14.0	14.6	14.3
	% SI at 12 dsm^{-1}	52.1	16.7	50.0	33.9	24.6	30.7	29.9	28.2	29.5	29.2
Chinisagor	Control	78.6	100.0	6.0	61.5	55.8	41.1	52.8	49.9	48.0	50.2
	EC-7	55.6	100.0	5.7	53.7	53.1	37.5	48.1	46.3	44.0	46.1
	EC-12	43.5	86.7	4.0	44.7	45.1	31.3	40.4	38.9	36.9	38.7
	% SI at 7 dsm^{-1}	29.3	0.0	5.6	12.7	4.9	8.8	8.9	7.4	8.3	8.2
	% SI at 12 dsm^{-1}	44.6	13.3	33.3	27.3	19.2	23.9	23.6	22.0	23.1	22.9
Badshavogh	Control	60.8	90.0	6.3	52.4	49.6	36.1	46.0	43.9	42.0	44.0
	EC-7	27.7	53.3	3.3	28.1	28.3	19.9	25.4	24.5	23.3	24.4
	EC-12	26.2	46.7	1.3	24.7	24.2	16.8	21.9	21.0	19.9	20.9
	% SI at 7 dsm^{-1}	54.4	40.7	47.4	46.3	43.0	44.8	44.7	44.1	44.5	44.5
	% SI at 12 dsm^{-1}	56.9	48.1	78.9	52.8	51.1	53.5	52.4	52.2	52.7	52.4
Lalbat	Control	93.5	100.0	6.0	66.5	57.5	43.3	55.8	52.2	50.4	52.8
	EC-7	64.3	80.0	5.0	49.8	44.9	33.2	42.6	40.3	38.7	40.5
	EC-12	49.6	73.3	3.3	42.1	39.6	28.3	36.7	34.9	33.3	34.9
	% SI at 7 dsm^{-1}	31.2	20.0	16.7	25.2	21.9	23.3	23.5	22.9	23.2	23.2
	% SI at 12 dsm^{-1}	47.0	26.7	44.4	36.7	31.2	34.6	34.3	33.2	34.0	33.8
Chabli	Control	72.9	86.7	6.3	55.3	49.4	37.0	47.2	44.6	42.9	44.9
	EC-7	0.0	0.0	4.7	1.6	2.1	2.8	2.1	2.3	2.4	2.3
	EC-12	0.0	0.0	2.3	0.8	1.0	1.4	1.1	1.2	1.2	1.1
	% SI at 7 dsm^{-1}	100.0	100.0	26.3	97.2	95.8	92.5	95.5	94.8	94.4	94.9
	% SI at 12 dsm^{-1}	100.0	100.0	63.2	98.6	97.9	96.3	97.7	97.4	97.2	97.5
Pangas	Control	67.6	88.3	6.0	54.0	49.4	36.5	46.6	44.2	42.4	44.4
	EC-7	47.3	50.0	3.0	33.4	28.8	21.7	28.0	26.2	25.3	26.5
	EC-12	14.3	0.0	1.7	5.3	2.3	3.1	3.6	3.0	3.2	3.3
	% SI at 7 dsm^{-1}	30.0	43.4	50.0	38.0	41.7	40.4	39.9	40.7	40.3	40.3
	% SI at 12 dsm^{-1}	78.8	100.0	72.2	90.1	95.3	91.5	92.3	93.2	92.4	92.6
Durgavog	Control	58.8	85.0	6.0	49.9	47.0	34.3	43.7	41.7	39.9	41.8
	EC-7	36.5	80.0	4.0	40.2	41.4	28.5	36.7	35.5	33.6	35.3
	EC-12	10.5	7.3	3.0	7.0	5.8	5.2	6.0	5.7	5.6	5.8
	% SI at 7 dsm^{-1}	37.9	5.9	33.3	19.5	11.9	16.9	16.1	14.7	15.8	15.6

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Genotype	Treatment	LL	SR	TNR	RL	SL	CC	RFW	RDW	SFW	SDW
	% SI at 12 dsm^{-1}	82.1	91.4	50.0	86.1	87.7	84.7	86.3	86.4	85.9	86.2
M-171	Control	68.8	91.7	5.0	55.2	50.6	36.9	47.6	45.0	43.2	45.3
	EC-7	61.7	75.0	4.7	47.1	42.3	31.3	40.2	37.9	36.5	38.2
	EC-12	42.6	53.3	4.0	33.3	30.2	22.5	28.7	27.1	26.1	27.3
	% SI at 7 dsm^{-1}	10.3	18.2	6.7	14.6	16.5	15.1	15.4	15.7	15.4	15.5
	% SI at 12 dsm^{-1}	38.1	41.8	20.0	39.6	40.3	39.0	39.7	39.7	39.5	39.7
Kabuldulan	Control	60.0	75.6	7.0	47.5	43.4	32.6	41.2	39.0	37.6	39.3
	EC-7	33.0	23.3	4.0	20.1	15.8	13.3	16.4	15.2	15.0	15.5
	EC-12	0.0	0.0	2.0	0.7	0.9	1.2	0.9	1.0	1.0	1.0
	% SI at 7 dsm^{-1}	45.0	69.1	42.9	57.7	63.5	59.2	60.1	61.1	60.2	60.5
	% SI at 12 dsm^{-1}	100.0	100.0	71.4	98.6	97.9	96.4	97.8	97.4	97.3	97.5
Suvash	Control	70.9	88.3	5.7	55.0	49.7	36.8	47.1	44.5	42.8	44.8
	EC-7	66.7	68.3	4.3	46.4	39.7	30.2	38.8	36.2	35.0	36.7
	EC-12	0.0	43.3	1.7	15.0	20.0	12.2	15.7	16.0	14.7	15.5
	% SI at 7 dsm^{-1}	6.0	22.6	23.5	15.5	20.0	18.0	17.8	18.7	18.1	18.2
	% SI at 12 dsm^{-1}	100.0	50.9	70.6	72.7	59.7	66.8	66.6	64.1	65.8	65.5
Moyna	Control	74.8	100.0	6.7	60.5	55.7	41.0	52.4	49.7	47.7	49.9
	EC-7	63.6	71.7	6.0	47.1	41.6	31.6	40.1	37.7	36.5	38.1
	EC-12	45.8	61.1	4.7	37.2	34.3	25.4	32.3	30.7	29.4	30.8
	% SI at 7 dsm^{-1}	15.0	28.3	10.0	22.2	25.4	23.0	23.5	24.0	23.5	23.7
	% SI at 12 dsm^{-1}	38.8	38.9	30.0	38.5	38.4	38.0	38.4	38.3	38.2	38.3
Binadhan-8	Control	65.4	93.3	6.0	54.9	51.4	37.4	47.9	45.6	43.7	45.7
	EC-7	27.0	53.3	5.3	28.6	29.1	21.0	26.2	25.4	24.2	25.3
	EC-12	22.0	43.3	5.0	23.5	23.9	17.5	21.6	21.0	20.0	20.9
	% SI at 7 dsm^{-1}	58.7	42.9	11.1	48.0	43.4	43.9	45.3	44.2	44.5	44.7
	% SI at 12 dsm^{-1}	66.3	53.6	16.7	57.3	53.5	53.4	54.9	53.9	54.1	54.3
Ronojit	Control	62.6	88.3	6.0	52.3	48.9	35.7	45.6	43.4	41.6	43.5
	EC-7	48.3	40.0	4.0	30.8	24.9	19.9	25.2	23.3	22.8	23.8
	EC-12	0.0	25.0	4.7	9.9	13.2	9.2	10.8	11.1	10.4	10.7
	% SI at 7 dsm^{-1}	22.8	54.7	33.3	41.2	49.0	44.3	44.8	46.2	45.1	45.4
	% SI at 12 dsm^{-1}	100.0	71.7	22.2	81.1	73.0	74.1	76.4	74.5	75.1	75.3
Moghabalam	Control	64.8	100.0	7.0	57.3	54.8	39.7	50.6	48.3	46.2	48.4
	EC-7	38.2	93.3	5.0	45.5	47.9	32.8	42.1	41.0	38.6	40.6
	EC-12	17.7	60.0	3.0	26.9	30.0	20.0	25.6	25.2	23.6	24.8
	% SI at 7 dsm^{-1}	41.0	6.7	28.6	20.5	12.4	17.3	16.7	15.3	16.4	16.1
	% SI at 12 dsm^{-1}	72.7	40.0	57.1	53.0	45.3	49.7	49.4	47.9	48.9	48.7
Binadhan-10	Control	74.9	100.0	6.3	60.4	55.6	40.8	52.3	49.5	47.5	49.8
	EC-7	49.1	71.7	6.0	42.2	40.0	29.4	37.2	35.5	34.0	35.6
	EC-12	33.1	63.3	4.3	33.6	33.8	23.9	30.4	29.4	27.9	29.2
	% SI at 7 dsm^{-1}	34.5	28.3	5.3	30.1	28.1	27.9	28.8	28.3	28.4	28.5
	% SI at 12 dsm^{-1}	55.7	36.7	31.6	44.4	39.3	41.4	41.8	40.7	41.3	41.3
Sadaswarna	Control	68.1	83.3	6.0	52.5	47.3	35.2	45.0	42.5	40.9	42.8
	EC-7	50.0	46.7	4.7	33.8	28.4	22.3	28.1	26.3	25.6	26.7
	EC-12	0.0	30.0	4.3	11.4	15.3	10.3	12.3	12.7	11.8	12.3
	% SI at 7 dsm^{-1}	26.5	44.0	22.2	35.6	40.0	36.8	37.5	38.2	37.5	37.7
	% SI at 12 dsm^{-1}	100.0	64.0	27.8	78.2	67.7	70.6	72.6	70.2	71.2	71.4
Gottaaman	Control	64.0	75.0	5.0	48.0	42.7	31.9	40.9	38.5	37.1	38.8
	EC-7	36.3	27.7	4.0	22.6	18.1	14.9	18.6	17.2	16.9	17.5
	EC-12	0.0	0.0	2.0	0.7	0.9	1.2	0.9	1.0	1.0	1.0
	% SI at 7 dsm^{-1}	43.3	63.1	20.0	52.8	57.6	53.2	54.6	55.3	54.4	54.8
	% SI at 12 dsm^{-1}	100.0	100.0	60.0	98.6	97.9	96.3	97.8	97.4	97.2	97.5
Moirom	Control	73.8	100.0	6.3	60.1	55.5	40.6	52.0	49.4	47.3	49.6
	EC-7	30.3	100.0	2.7	44.3	49.0	32.0	41.8	40.9	38.2	40.3
	EC-12	26.2	73.3	2.7	34.1	36.7	24.5	31.7	31.0	29.1	30.6
	% SI at 7 dsm^{-1}	59.0	0.0	57.9	26.2	11.7	21.2	19.7	17.1	19.3	18.7
	% SI at 12 dsm^{-1}	64.6	26.7	57.9	43.3	33.9	39.8	39.0	37.3	38.6	38.3
Chinikani	Control	71.5	93.3	6.3	57.0	52.2	38.5	49.3	46.7	44.8	46.9
	EC-7	64.5	65.0	4.3	44.6	38.0	29.0	37.2	34.7	33.6	35.2
	EC-12	0.0	40.0	1.7	13.9	18.5	11.4	14.6	14.8	13.6	14.3
	% SI at 7 dsm^{-1}	9.8	30.4	31.6	21.8	27.3	24.8	24.5	25.6	25.0	25.1
	% SI at 12 dsm^{-1}	100.0	57.1	73.7	75.7	64.5	70.5	70.4	68.3	69.7	69.5
Ashfail	Control	73.1	91.7	6.3	57.0	51.7	38.3	49.0	46.4	44.6	46.6

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Genotype	Treatment	LL	SR	TNR	RL	SL	CC	RFW	RDW	SFW	SDW
	EC-7	65.3	65.0	4.3	44.9	38.1	29.1	37.3	34.8	33.8	35.3
	EC-12	0.0	0.0	1.7	0.6	0.7	1.0	0.8	0.8	0.9	0.8
	% SI at 7 dsm^{-1}	10.7	29.1	31.6	21.3	26.3	24.1	23.8	24.8	24.3	24.3
	% SI at 12 dsm^{-1}	100.0	100.0	73.7	99.0	98.6	97.4	98.4	98.2	98.1	98.2

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), SDW = Shoot dry weight (mg), SI (susceptibility index) was estimated as [(control value-salt treatment value)/control value*100].

Table 06. Estimation of genetic parameters for morphological characters of twenty five rice genotypes

Traits	PCV (δ^2p)	GCV (δ^2g)	PCV (%)	GCV (%)	Heritability (%)	GA	GA (%)
Leaf Live (%)	421.23	383.62	44.75	42.70	91.07	38.50	83.9
Survival Rate (%)	1261.23	1142.73	51.97	49.47	90.60	66.28	97.0
Total no. of roots	1.90	1.56	29.99	27.21	82.33	2.33	50.8
Root length	5.07	3.75	29.13	25.03	73.82	3.43	44.3
Shoot length	62.11	56.72	50.05	47.83	91.32	14.83	94.1
Chlorophyll Content	35.67	31.00	42.46	39.58	86.90	10.69	76.0
Root fresh wt. (100mg)	8.02	6.91	38.43	35.68	86.22	5.03	68.2
Root Dry wt. (100mg)	0.37	0.36	68.50	67.02	95.72	1.21	135.0
Shoot fresh wt. (100mg)	10.23	9.68	35.08	34.12	94.63	6.24	68.3
Shoot Dry wt. (100mg)	0.97	0.91	64.24	61.96	93.01	1.89	123.0
SES	6.94	6.67	65.94	64.63	96.08	5.22	130.5

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), SDW= Shoot dry weight (mg).

Table 07. Correlation coefficients of different morphological traits at phenotypic and genotypic level

Traits	CR	SR (%)	TNR	SR	SL	CC	RFW	RDW	SFW	SDW	SES
LL (%)	r_p	0.69**	0.38	0.33	0.59**	0.79**	0.35	0.42*	0.24	0.26	-0.67**
	r_g	0.69**	0.38	0.33	0.60**	0.79**	0.35	0.42*	0.24	0.26	-0.68**
SR (%)	r_p		0.45*	0.51**	0.66**	0.63**	0.53**	0.70**	0.55**	0.52**	-0.89**
	r_g		0.46*	0.51**	0.66**	0.62**	0.54**	0.70**	0.55**	0.53**	-0.90**
TNR	r_p			0.09	0.31	0.19	0.21	0.42*	0.43*	0.44*	-0.33
	r_g			0.11	0.32	0.19	0.21	0.44*	0.43*	0.45*	-0.34
RL (cm)	r_p				0.79**	0.39*	0.55**	0.62**	0.52**	0.52**	-0.41*
	r_g				0.80**	0.41*	0.57**	0.63**	0.53**	0.52**	-0.42*
SL (cm)	r_p					0.66**	0.61**	0.67**	0.63**	0.64**	-0.60**
	r_g					0.66**	0.62**	0.68**	0.64**	0.65**	-0.60**
CC	r_p						0.43*	0.40*	0.20	0.18	-0.70**
	r_g						0.44*	0.40*	0.19	0.19	-0.70**
RFW	r_p							0.77**	0.85**	0.68**	-0.57**
	r_g							0.78**	0.85**	0.69**	-0.58**
RDW	r_p								0.79**	0.79**	-0.62**
	r_g								0.79**	0.79**	-0.62**
SFW	r_p									0.84**	-0.50*
	r_g									0.85**	-0.50*
SDW	r_p										-0.43*
	r_g										-0.44*

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), SDW= Shoot dry weight (mg) & CR indicates correlation; *Significant at 5% level of probability; **=Significant at 1% level of probability; r_p indicates phenotypic correlation and r_g indicates genotypic correlation.

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Estimation of path coefficient

An estimate of simple correlation would not provide the true contribution of the characters towards the yield and this simple correlation could be partitioned into direct and indirect effects through path coefficient analysis. Path analysis allows separating the direct effect and their indirect effects through other attributes by apportioning the correlations for better interpretation of cause and effect. The path coefficient analysis showed that leaf live, total no. of roots, shoot length, root length, root dry weight and shoot dry weight had direct positive effect on standard evaluation score at genotypic level where live leaves (%), total no. of roots, shoot length, root length, root dry weight had direct positive effect on standard evaluation score at phenotypic level (Table 08; Table 09). The residual effect was 0.1458 and 0.1204 at phenotypic and genotypic level respectively in case of the present study.

Table 08. Partitioning of correlation coefficients into direct and indirect effects on important traits of twenty five rice genotypes at genotypic level by path coefficient analysis

Traits	LL	SR	TNR	RL	SL	CC	RFW	RDW	SFW	SDW	SES
LL (%)	0.05	-0.58	0.02	0.02	0.08	-0.25	-0.04	0.03	-0.02	0.001	-0.68**
SR (%)	0.03	-0.83	0.03	0.03	0.09	-0.20	-0.06	0.06	-0.06	0.003	-0.90**
TNR	0.02	-0.38	0.07	0.01	0.04	-0.06	-0.02	0.03	-0.05	0.002	-0.34
RL	0.01	-0.43	0.01	0.06	0.11	-0.13	-0.07	0.05	-0.06	0.003	-0.42*
SL	0.03	-0.55	0.02	0.05	0.14	-0.21	-0.08	0.06	-0.07	0.004	-0.60**
CC	0.04	-0.52	0.01	0.02	0.09	-0.32	-0.05	0.03	-0.02	0.001	-0.70**
RFW	0.01	-0.45	0.01	0.03	0.08	-0.14	-0.12	0.07	-0.09	0.004	-0.58**
RDW	0.02	-0.58	0.03	0.04	0.09	-0.13	-0.09	0.09	-0.09	0.005	-0.62**
SFW	0.01	-0.46	0.03	0.03	0.09	-0.06	-0.10	0.07	-0.11	0.005	-0.50*
SDW	0.01	-0.44	0.03	0.03	0.09	-0.06	-0.08	0.07	-0.09	0.00	-0.44*

Residual effect = 0.1204

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), SDW = Shoot dry weight (mg) & CR indicates correlation; *=Significant at 5% level of probability and **=Significant at 1% level of probability

Table 09. Partitioning of direct and indirect effects of morphological characters of 25 rice genotypes at phenotypic level by path coefficient analysis

Traits	LL	SR	TNR	RL	SL	CC	RFW	RDW	SFW	SDW	SES
LL (%)	0.01	-0.55	0.05	0.01	0.06	-0.20	-0.05	0.03	-0.01	-0.001	-0.67
SR (%)	0.00	-0.80	0.02	0.02	0.07	-0.16	-0.08	0.05	-0.03	-0.002	-0.89
TNR	0.005	-0.36	0.06	0.005	0.03	-0.05	-0.03	0.03	-0.02	-0.002	-0.33
RL	0.00	-0.41	0.005	0.05	0.08	-0.08	-0.08	0.04	-0.03	-0.002	-0.41
SL	0.00	-0.53	0.01	0.04	0.10	-0.17	-0.09	0.04	-0.03	-0.002	-0.60
CC	0.01	-0.50	0.01	0.01	0.07	-0.25	-0.06	0.03	-0.01	-0.000	-0.70
RFW	0.004	-0.43	0.01	0.03	0.06	-0.11	-0.15	0.05	-0.05	-0.003	-0.57
RDW	0.005	-0.56	0.026	0.03	0.07	-0.10	-0.11	0.07	-0.04	-0.003	-0.62
SFW	0.003	-0.44	0.026	0.03	0.07	-0.05	-0.12	0.05	-0.06	-0.003	-0.50
SDW	0.003	-0.42	0.02	0.02	0.07	-0.04	-0.10	0.05	-0.05	-0.004	-0.43

Residual effect = 0.1458

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), SDW = Shoot dry weight (mg) & CR indicates correlation, *=Significant at 5% level of probability, **=Significant at 1% level of probability

IV. Discussion

Germination, growth and development as well as productivity of rice are severely affected by salinity. The present study showed that the genotypes under non-salinized condition were uniform in green color and height whereas seedlings grown under saline condition showed different visual symptoms of salt injury regarding of live leaves (%), survival rate (%), root length, shoot length, total number of

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roots, chlorophyll content, root fresh weight, shoot fresh weight, root dry weight and shoot dry weight. Under saline condition, the genotypes showed great variation in phenotypes ranging from 1 (highly tolerant) to score 9 (highly susceptible) according to the SES of IRRI (Gregorio *et al.*, 1997) and the genotypes viz., Maloti, Chinisagor, Lalbat, M-171, Moyna, Binadhan-8, Binadhan-10 identified as salt tolerant at both salt concentrations (7 dsm^{-1} and 12 dsm^{-1}). Islam *et al.* (2007) and Razia (2012) also reported wide variation in phenotypes in rice from tolerant (score 3) to highly susceptible (score 9) using modified Standard Evaluation Score (SES) of IRRI standard protocol (IRRI, 1997). Bhowmik *et al.* (2009) also found large variation among the rice germplasms for salinity tolerance. Analysis of variance indicated that the difference among genotypes for all the traits studied were significant (Table 04) viz., live leaves (%), survival rate (%), total number of roots, root length, shoot length, chlorophyll content, root fresh weight, root dry weight, shoot fresh weight, and shoot dry weight. Kordrostam *et al.* (2017) indicating the significant differences of seedling characteristics among the 44 rice varieties and among the salinity levels and different physiological and biochemical responses of the varieties from one salinity condition to another.

Generally it was reported that plant survival is not a major problem under moderate stress but under higher stress, it could be a good selection criterion (Niones, 2004). The results from the study revealed that survival rate of plant decreasing with the increasing of salinity except tolerant cultivars. This may be due to the inability of plant to uptake water and nutrients from soil under saline conditions. A similar study reported that high salt concentration reduces the ability of roots to extract water with available soil nutrients and disarrange many physiological in plant such as nutrient uptake, assimilation resulting mortality of the plant and finally reduces survival rate (%) of plant (Munns and Tester, 2008). Live leaves (%) of plant were decreases with the increasing of salinity level resulting the reduction of shoot length as well as chlorophyll content in all the genotypes in present study. This reduction of % LL was observed due to the leaf rolling, drying of leaves, brownish and whitish of leaf tip under saline condition. Generally shoot growth is more sensitive than root growth to high salt concentration due to the induced osmotic stress reducing leaf area. Shoot growth stunted under high salt stress due to the inhibition of symplastic xylem loading of calcium by salt in the root (Läuchli and Grattan, 2007). The results from the study revealed that genotypes (Chinisagor, Lalbat, M-171, Maloti, Moyna, Binadhan-8 and Binadhan-10) which were tolerant showed higher shoot growth and chlorophyll content and which were susceptible showed lower shoot growths under saline treatment (Table 05). This is probably due to the salt tolerant ability of the tolerant genotypes by adopting some morphological, physiological or biochemical mechanisms. These results are in agreement with those of (Islam *et al.*, 2009) and (Abeer *et al.*, 2013) in rice. Parida and Das (2005) reported that the decrease in chlorophyll content in response to salt stress is a widespread phenomenon. Salt stress causes the oxidative stress which reduced the number and size of chloroplasts and destroys it (Santos, 2004; Khafagy *et al.*, 2009). Therefore, the variation of chlorophyll content under salt stress condition could be used as an indicator for the improvement of salt tolerance (Naumann *et al.*, 2008). Salinity restricted root growth resulting decreased root length in all genotypes under salinity stress and the tolerant genotypes (Chinisagor, Lalbat, Moyna, Maloti and Binadhan-10) showed higher root length compared to the sensitive genotypes under saline condition. Similar results of reduced root length under salinity were reported by (Acosta-Motos *et al.*, 2015). The probable reason for reduced root length may be due to the effect of salinity on final cell size as well as rate of cell production (Azaizeh *et al.*. 1992). The inhibition of plant growth and development due to salinity salinity stress leading to the notable reduction of shoot and root fresh weight in all genotypes but the reduction was lower in salt-tolerant rice genotypes (Chinisagor, Lalbat, Binadhan-8 and Binadhan-10) than the sensitive one. Salinity stress causes the reduction of root fresh weight (FW) of root and shoots (Chunthaburee *et al.*, 2016). Shannon and Grieve (1998) also reported that shoot and root biomass of rice significantly decreased with increasing salt stress. The lowest dry weight of root and shoot was observed in sensitive genotypes than the tolerant genotypes under high salinity. The reason behind this could be the higher biomass production by the tolerant genotypes (Chinisagor, Lalbat, Binadhan-8 and Binadhan-10) resulting higher yield under salinity stress. Sweet *et al.* (1990) reported that salinity causes the solidity of cell wall and alter the cell wall structure which leads to the reduction of dry weight accumulation in plant. It was also reported that dry shoot and root weight decreased significantly with the increase of salinity levels in rice (Hakim *et al.*, 2010).

The results of the study reported wide genetic variation for all the traits of rice genotypes. The phenotypic co-efficient of variation (PCV) was higher than genotypic coefficient of variation (GCV) for

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all the traits (Table 06) reflect the environmental influence in the phenotypic expression of the traits to some extent. Akanda *et al.* (1997) also reported similar findings for the screening of rice genotypes for salt tolerance. The difference between genotypic and phenotypic coefficient of variability indicates the environmental influence. The higher values of PCV and GCV further facilitate the possibility of improvement of those genotypes through selection of desired characters. The highest GCV was found in survival rate (%) and live leaves (%) indicated wide range of variability for these traits. However, root dry weight followed by shoot dry weight and total number roots showed very low GCV indicating lack of inherent variability and so improvement by utilizing these traits could not be so effective among the genotypes.

Heritability could be an important parameter in plant breeding to select the high heritable plant trait. The results from the present study reported that live leaves (%), survival rate (%), total number of roots, root length, shoot length, chlorophyll content, root fresh weight, root dry weight, shoot fresh weight and shoot dry weight standard evaluation score of twenty five rice genotypes showed high heritability (Table 06). High heritability values indicate that the characters under study are less influenced by environment for their phenotypic expression and selection can be applied by using these traits to improve rice genotypes for salt tolerance. Therefore, the plant breeder may select a genotype based on phenotypic expression for the desired characters of individual plant through simple selection method. Gana *et al.* (2013) also found the similar result. He reported that high heritability was expressed among twelve morpho-physiological characters of thirty nine varieties. High heritability along with high genetic advance was noticed for survival rate (%) followed by live leaf percentage reported that the indication of additive gene action and selection based on these parameters could be important for salinity improvement. Hosseini *et al.* (2012) also found high genetic advance for plant height, root dry weight and shoot length. It indicates that accumulation of more additive genes will be leading to further improvement for their performance. Significant and negative relations between standard evaluation score (SES) and live leaves (%), survival rate (%), shoot length, root fresh weight, root dry weight and shoot dry weight were significant at 1% level of probability at the seedling stage further confirmed the importance of these parameters as useful selection criteria for screening of salt tolerance genotypes. Afterwards, negative and non-significant co-relation was found between total number of roots and SES which referred to a complex linked of relation among the pair of combinations. The higher value of genotypic correlation coefficients than phenotypic co-relation coefficient in most cases, indicating strong inherent association between the characters studied and suppressive effect of the environment on the phenotypic expression of these characters reducing phenotypic correlation values (Bai *et al.*, 1992). However, in some cases, the lower value of genotypic correlation coefficients than phenotypic correlation coefficients suggesting both environmental and genotypic correlation has same effect and finally maximizes their expression at phenotypic level. The path coefficient analysis showed that live leaves (%), total no. of roots, shoot length, root length, root dry weight and shoot dry weight had direct positive effect on standard evaluation score at genotypic level where live leaves (%), total no. of roots, shoot length, root length, root dry weight had direct positive effect on standard evaluation score at phenotypic level indicating their importance in determining complex characters. Similar findings have also been reported by (Osman *et al.*, 2012). When correlation coefficient is negative and the direct effect is highly positive, a restricted simultaneous selection model is to be followed, i.e. restrictions are to be imposed to nullify the undesirable effect in order to make use of the direct effect (Singh *et al.*, 1997; Rashid *et al.*, 2010). The residual effect determines how best the causal factors account for the variability of the dependent factor such as standard evaluation score.

V. Conclusion

The results of our study showed that great variation was found in different morphological parameters of twenty five rice genotypes at seedling stage. The morphological parameters were reduced almost in all genotypes with the increasing of salinity. Some landraces Chinisagor showed higher salt tolerance ability similar to salt tolerant check genotypes Binadhan-8 and Binadhan-10 under salinity stress. So this genotype could be used as a potential donor of saltol gene for the development of high yielding salt tolerant rice genotypes further. The molecular characterization further could be helpful to the breeders for further planning of breeding rice for salinity tolerance. Besides Maloti, Chinisagor, Lalbat and Moyna identified as salt tolerant under salinity stress and these genotypes could also be used in

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marker assisted backcrossing for the improvement of salinity tolerance in rice genotypes. On the contrary, genetic variability reported that live leaves (%), survival rate and shoot length could be important parameter for the development of salinity tolerance ability of plant. The result of correlation and path analysis concluded that that live leaves (%), survival rate (%), shoot length, chlorophyll content, root fresh weight, root dry weight had significant negative correlation with standard evaluation score as well as employed positive direct effect on standard evaluation score suggesting the selection for these traits would be helpful for the screening and improvement of salt tolerance ability of plant.

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