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Estimating Genetic Variability in Dual Saline and Submergence Condition of Rice (*Oryza sativa* L.)

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ABSTRACT

Both salinity and submergence are the global problems adversely affecting agricultural productivity in the coastal areas around the world. The current climate change made this situation more complex and is a threat to crop production. The present study was aiming to analyze genetic parameters among yield and yield related traits for ten rice genotypes in both saline and submergence condition. An experiment using a randomized complete block design (RCBD) and five different treatments *viz.,* control, 9dSm^{-1} salinity + without submergence, 6dSm^{-1} salinity + complete submergence, normal water + complete submergence, 9dSm^{-1} salinity + complete submergence was conducted to estimate the genetic variability of ten rice genotypes. All the traits under this study reduced in both saline and submergence condition except days to flowering. In stressed condition, grain yield of all rice genotypes was reduced than no stressed condition. Considering all the treatments BRRI dhan47 showed higher stress tolerance followed by Binadhan-8, RC-191 and RC-221. In the present investigation, the highest genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were 21.42% and 30.16% observed for grain yield plant^{-1} (g), followed by total tillers hill^{-1} (11.92%, 17.42%) indicating that there is enough genetic variability for the traits. High heritability observed in the traits days to flowering followed by plant height and moderate heritability observed in grain yield plant^{-1} followed by filled grains panicle^{-1}. This finding can be used for further breeding programs which helps in crop improvement under both saline and submergence condition.

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Introduction

Rice (*Oryza sativa* L.) is grown under a wide range of agro-climatic condition ranging from favorable to diverse biotic and abiotic stresses. In the 4th Assessment Report the Intergovernmental Panel on Climate Change (IPCC, 2007) states that the world especially South and Southeast Asia is expected to be seriously affected by the adverse impacts of climate change. In the last five years, there has been an increase in the number of floods, salinity and periods of drought, and some of the most devastating cyclones, and water, soil and land resources are continuing to decline. In South and Southeast Asian countries the annual mean temperatures are projected to rise by 4.8°C by 2100, and the global mean sea level will increase by 70 cm during the same period (ADB, 2009). This excludes the additional expected increase in sea level due to melted ice leading to increased coastal salinity, submergence and further yield reduction, even in previously favorable areas (Masutomi *et al.,* 2009). In future, the seawater level as well as the frequencies and intensities of salinity and flooding will increase at an alarming rate due to extreme climatic actions (IPCC, 2008).

Salinity is an acute issue to increase crop production because of opposed environmental change in the coastal areas, particularly in the low-lying coastal regions around the world (Nicholls *et al.,* 2007). Salinity affects plants at all stages of development but the response of rice to salinity varies with growth stage (Mass, 1993). Previous studies were showed that rice is tolerant during germination, very sensitive during early seedling stage (2-3 leaves stage), advances tolerance during vegetative growth stage, also sensitive during pollination and fertilization and then become more tolerant at the maturity stage (IRRI, 1997). There exists tremendous variation for salt tolerance within species in rice providing opportunities to improve crop salt-stress

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tolerance through genetic means (Sabouri and Biabani, 2009). Coastal areas face regular submergence for short periods with saline or freshwater due to the rising sea levels in the wet season. Submergence annually affects the rice production in flood-prone and rain-fed lowland areas of South and Southeast Asia (Abdelbagi *et al.,* 2013). Although rice is a semi-aquatic plant, the prolonged submerged conditions subject plants to the stresses of low light, limited gas diffusion, the effusion of soil nutrients, mechanical damage, and increased susceptibility to pests and diseases and difficult to acquire high yield (Greenway and Setter 1996; Ram *et al.,* 1999). Thus it disturbs the morpho-physiological growth and development of rice plants (Mahmood *et al.,* 2019). Here rice is a suitable crop because it has some adaptive traits for the tolerance of submergence. Such as internal aeration and growth controls, formations of aerenchyma and a barrier to radial O_2 loss (ROL), etc. (Toojinda *et al.,* 2003). So, the perfect rice genotype for coastal areas requires dual tolerance for salinity and submergence for better adaptability. Therefore, it is crucial to select and develop favorable salt and submergence tolerant rice genotypes for crop improvement.

The amount of genetic variability present in the population and the degree to which the desirable characters are heritable is the main component of any breeding programs for broadening the stock of different genes in any population (Kumari *et al.,* 2020). In this study, the knowledge about the degree of several genetic parameters, like PCV and GCV, broad sense heritability, genetic advance as percent of mean are formulated for the improvement of breeding methods to obtain salinity and submergence tolerant high yielding crops. High heritability along with high genetic advance is more useful in estimating genetic gain (Johnson *et al*. 1955).

The aim of the present study was to generate useful information on genetic variability, heritability and genetic advances among yield and yield related traits for ten rice genotypes in both saline and submergence condition. This information may be useful for the improvement of salinity and submergence tolerant rice genotypes in future breeding programs.

Materials and Methods

Genotypes and treatments

Three released genotypes of BINA, two genotypes of BRRI and five advanced breeding lines from IRRI were collected from Bangladesh Institute of Nuclear Agriculture (BINA), Mymensingh and used as study materials for this experiment (Table 1). The experiment was laid out in two factor RCB design with five replications in the net-house of Bangladesh Institute of Nuclear Agriculture (BINA), Mymensingh. Submerged condition considered as factor- Ⅰ and saline water as factor- Ⅱ. Four treatments along with control (T_1: Control environment where no treatment was imposed, T_2: Without submergence pressure 9 dSm^{-1} (9 $dSm^{-1} \approx$ 90 mM NaCl) saline condition was applied to plants at late vegetative stage for 7 days, T_3: Plants submerged in 6 dSm^{-1} saline water at late vegetative stage for 7 days, T_4: Plants submerged in normal water for 7 days at late vegetative stage. T_5: Plants submerged in 9 dSm^{-1} saline water at late vegetative stage for 7 days) were performed on rice genotype in this study. Intercultural operations such as weeding, crop protection measures, water management and fertilization were done by following the IRRI standard procedures (IRRI 2002).

Table 1. List of genotypes used for this study

Sl.	Name of rice lines/variety	Pedigree	Origin
1	RC-191	Advanced line	IRRI
2	RC-193	Advanced line	IRRI
3	RC-217	Advanced line	IRRI
4	RC-221	Advanced line	IRRI
5	RC-229	Advanced line	IRRI
6	Binadhan-8	IR29 × POKKALI	BINA
7	Binadhan-11	Chiherang × IRRI 149	BINA
8	Binadhan-12	Sambha mohasuri × IR 49830	BINA
9	BRRI dhan28	BR6 (IR28) × Purbachi	BRRI
10	BRRI dhan47	IR51511-B-B-34-B × TCCP266-2-49-B-B-3	BRRI

Source of collection: Bangladesh Institute of Nuclear Agriculture (BINA), Mymensingh

Preparation of pots and trays

Net clothes were used for preparation of bags which was well fitted in fiber pots. Net bags were placed at the bottom of the pots. Then the pots were filled with soil containing N, P and K containing fertilizer. Trays were filled with normal tap water and pots were placed in the trays. These trays were served as water bath. For saline treatment Glass fiber trays were filled with ordinary tap water and the soil containing fertilizers were pulverized. Water level was maintained same as the soil level in both types of trays. When the soil began to settle in absorbed water, extra soil was added to maintain correct level (20 cm from bottom to top of the trays) of soil.

Collection of seeds and sowing of pre-germinated seeds

The seeds were kept in the convection oven for 5 days at 50°C for breaking the seed dormancy. The oven treated seeds were soaked with tap water for 24 hours for pre-germination. The pre-germinated seeds (3-4 $seedshill^{-1}$) of test genotypes were sown on the soil surface in soil filled trays. After two weeks of seedling, the seedlings were thinned to two per hill and water level raised 1-2 cm above the soil surface. The water level maintained daily and the plants were protected from pests and diseases by using pesticides.

Preparation of saline water solution

6 pieces cylindrical shape water bath (1m height/piece) each of them contains 271 liter water, crude salt (NaCl), water, pH meter were used to prepare saline water solution. Salinized water solution was prepared up to the desired EC level by dissolving crude salt (NaCl) in water while stirring. In this purpose 3 g/L and 4 g/L crude salt were used to make 6 dSm^{-1} and 9 dSm^{-1} saline solution (Gregorio *et al.,* 1997). 6 dSm^{-1} saline solution was prepared by adding 813 g crude salt in 271 L water. Similarly, 9 dSm^{-1} saline solution was prepared by adding 1219.5 g crude salt in 271 L water. Following is the formula to make saline solution:

Required amount of salt (g)= Salt per liter for 1 dSm^{-1} × Desired Electric Conductivity

Where, 1dS electric conductivity per meter =135.5 g salt per liter.

Treatment setup

For the treatment T_2 to T_5, when the seedlings reached at the late vegetative stage, all water from the trays were siphoned out and given a 24-h break. Then 6 dSm^{-1} and 9 dSm^{-1} saline water solution were prepared in two separate plastic drums. After that, the plants in T_3 and T_5 were submerged in those water drums followed by treatments. Plants in T_4 were submerged in normal water and T_2 gave only 9dSm-1 saline water solution without submergence pressure. The EC of the salinized soil was monitored every day and adjusted when necessary using crude salt and tap water. After 7 days the plants were taken out from the drums and settled in normal environmental condition.

Data collection

The genotypes were evaluated at late vegetative stage for their salinity and submergence tolerance using IRRI standard protocol (IRRI 2002). Data were recorded on individual plant of the experimental tray considering days to flowering, plant height, tiller number per plant, panicle length, filled grain number per plant, unfilled grain number per plant, total dry matter, 100 seed weight, grain yield per plant.

Statistical analysis

MSTAT-C software was used to perform the two-way analysis of variance (Table 2). 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 and r = Number of replications.

Phenotypic variance, $\sigma_p^2 = \sigma_g^2 + EMS$

Where, σ_g^2 = Genotypic variance and EMS = Error mean square

Genotypic and phenotypic co-efficient of variations were calculated according to Burton (1952):

Genotypic co-efficient of variations, GCV (%) = $\frac{\sigma_g}{\mu} \times 100$

Where, σ_g = Genotypic standard deviation and μ= Population mean.

Phenotypic co-efficient of variations, PCV (%) = $\frac{\sigma_p}{\mu} \times 100$

Where, σ_p = Phenotypic standard deviation and μ = Population mean.

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

Heritability, h^2b (%) = $\frac{\sigma_g^2}{\sigma_p^2} \times 100$

Where, σ_g^2 = Genotypic variance and σ_p^2 = Phenotypic variance.

Estimation of genetic advance was done following formula given by Lush (1949) and Johnson *et al.* (1955):

Genetic advance, GA = $\frac{\sigma_g^2}{\sigma_p^2} \times K \times \sigma_p$

Where, K = Selection differential, the value of which is 2.06 at 5% selection intensity and σ_p = Phenotypic standard deviation

Genetic advance in percent of mean was calculated by the formula of Comstock and Robinson (1952) as follows,

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

Where, GA = Genetic advance and μ= Population mean

Results and Discussion

Variance analysis

A two-way Analysis of variance (ANOVA) indicated that the difference among genotypes for all the traits under the study were highly significant for genotypes, treatment and genotypes-treatment interaction,

but the differences among replications for the above-mentioned traits was non-significant (Table 2). Significant variation observed among genotypes for days to 50% flowering, days to maturity, no. of tillers plant^{-1}, no. of effective tillers plant^{-1}, plant height, panicle length, 100 grains weight and yield plant^{-1} (Tiwari *et al.,* 2011; Yaqoob *et al.,* 2012; Rashid *et al.,* 2017). Under the study, it was indicated that the genotypes were possessing intrinsic genetic variations among themselves.

Phenotypic performance of rice genotypes

The Mean effect of 10 rice genotypes on different morphological traits related to yield showed the maximum days to flowering, plant height, total no. of tillers hill^{-1}, effective tillers hill^{-1}, flag leaf length (cm), flag leaf breadth (cm), panicle length (cm), total dry matter production (g) plant^{-1} was found in advanced line RC-217, number of unfilled grains panicle^{-1} in Binadhan-8 and filled grains panicle^{-1}, 100 seed weight (g) plant^{-1}, yield (g) plant^{-1} was found in BRRI dhan47. The performance of all the genotypes with respect to yield and yield contributing traits differed from each other under both saline and submergence condition. Comparing other genotypes, BRRI dhan47 showed the highest tolerance in different treatment of both salinity and submergence. Considering the mean performance result, Binadhan-8, RC-191, RC-221 also identified as tolerant in both saline and submergence condition (Table 3). Considering all the treatment conditions the yield and yield contributing traits reduced in the stressed condition than the normal or no stressed condition. Only days to flowering increased in all the stressed condition (Table 4).

Salinity affects plant growth by increasing osmotic stress which lower the water potential and increase the concentrated solutes around the plant root zone. As a result of ionic imbalance around the root zone plant cannot uptake nutrients and retard growth rate. Thus grain yield and yield components under osmotic and ionic stress are reduced (Munns *et al.,* 1995; Flowers and Flowers, 2005; Verslues *et al.,* 2006). Plant height, number of effective tillers panicle^{-1} and number of filled grains panicle^{-1} decreased with the increase of salinity stress (Table 4). Khan *et al.* (2008) and Saha (2013) reported that plant height of rice decreased under salinity at EC 8 dSm^{-1}. It was examined that the number of effective tillers panicle^{-1} decreased gradually with increase in salinity levels (Desai *et al.,*1975; Saxena and Pandey, 1981). From the study of Islam (2004) it was observed that the of loss of biomass production was lower in tolerant genotypes which increased the assimilation and ultimately produced the higher number of filled grains panicle^{-1}.

Submergence causes poor gas exchange under water through impeding aerobic respiration and photosynthesis (Das *et al.,* 2005; Bailey-Serres and Voesenek, 2008; Colmer and Voesenek, 2009). Zhang *et al.* (2015) observed an increasing panicle number and decreasing grain number panicle^{-1} with the increase of submergence duration. Elanchezhian *et al.* (2013) investigated that the grain yield ranged from 2.65 tha^{-1} to 6.14 tha^{-1} in the control condition, whereas it varied from 0.13 to 3.18 t ha^{-1} under submergence stress.

Estimation of genetic parameters

Agronomic traits are quantitative in nature, and interrelate with the environment under study, therefore the estimation of phenotypic (σ^2p) and genotypic (σ^2g) variances, genotypic coefficient of variance (GCA), phenotypic coefficient of variance (PCA), heritability, genetic advance and genetic advance as percent of mean are essential to find out the additive or heritable portion of variability which are presented in Table 5.

A wide range of genotypic and phenotypic differences were estimated for all the traits studied. The high values of phenotypic variance (144.11) and genotypic variance (75.06) were observed with the character filled grains panicle^{-1}. Akter *et al.* (2018a) also found similar results in case of filled grains panicle^{-1}. The genotypic and phenotypic variance were lower for flag leaf breadth (0.0003 and 0.00004) respectively which is agreed with Chakrabarty *et. al.* (2019).

In general, phenotypic co-efficient of variation (PCV) always higher than genotypic co-efficient of variation (GCV) for all characters studied and this finding agreed with Paikhomba *et al.* (2014); Islam *et al.* (2016); Anis *et al.* (2016); Islam *et al.* (2019a); Kumari *et al.* (2020). Among the characters, the highest phenotypic co-efficient of variation (PCV) and genotypic co-efficient of variation (GCV) value were recorded for grain yield plant^{-1} (30.16% and 21.42%). The lowest PCV and GCV value were equally observed for flag leaf breadth (1.41% and 0.54%). The higher variation between PCV and GCV indicated that there is considerable amount of variation present among the genotypes and all the characters studied that interacted with the environment to some extent. The current study suggests that genotypic variance (σ^2g) and genotypic coefficient of variance (GCV) were lower than their corresponding phenotypic variance (σ^2p) and phenotypic coefficient of variance (PCV) respectively for all the traits studied, indicating that a higher degree of environmental influences interacted during the expression of the traits. Similar findings were reported by (Dutta *et al.,* 2013; Singh *et al.,* 2014; Tuhina-Khatun *et al.,* 2015; Akter *et al.,* 2018b).

The estimation of heritability (h^2b) gives evidence about the substantial amount of genetic variability which is transmitted from parents to off springs. According to Burton *et al.* (1952), heritability classified as low (below 50%), medium (50-70%) and high (above 70%). All the characters studied in the present investigation expressed that heritability ranged from 14.63% for flag leaf breadth to 87.25% for days to flowering. Based on this value, the heritability criteria for the days to flowering, plant height and filled grain panicle^{-1}, grain yield had a moderate heritability, and other characters had low heritability (Table 5). In the current study, flowering time, the plant height, total tiller numbers hill^{-1}, effective tiller numbers hill^{-1}, filled grain panicle^{-1} and grain yield plant^{-1} (g) were the important traits in salt and submergence traits selection. According to Lubis *et al.* (2014), heritability regulates the progress of selection. If the heritability value is higher, the progress of selection is greater. In turns, if the heritability value is lower the progress of selection is slower. High heritability value helps in effective selection for a particular character due to less environmental effect (Kristamtini *et al.,* 2016). Therefore, there is a possibility to change the traits when planted in different environments, as the effect of environmental factors is quite large on the traits (Rashid *et al.,* 2017; Hossain *et al.,* 2018; Mustikarini *et al.,* 2019). Johanson *et al.* (1955) suggested that heritability along with genetic advance would give a more reliable index of selection value than heritability estimates alone.

In the present study genetic advance was highest for plant height (14.85) and lowest for 100 seed weight (0.10) (Table 5) excluding flag leaf breadth which was zero among yield contributing traits. Expected genetic advance as percent of mean indicates the mode of gene action in the expression of traits, which helps in selection. The genetic advance as percent of mean was also highest in case of grain yield plant^{-1} (31.33%), while lowest recorded in flag leaf breadth (0.43%) among the yield contributing traits (Table 5). In the present study, moderate heritability (50.42%) along with low genetic advance as percent mean (31.33%) was noticed for the trait grain yield plant^{-1} (Table 5). Similar results had also been reported by Islam *et al.* (2019b) which indicated that there is a better scope of its improvement through selection, as these characters were primarily governed by additive genetic variation. Other traits like plant height, days to flowering showed high heritability but low genetic advance (GA%) which indicated that non additive gene effects were involved for phenotypic expression of this character. Similar result was found in Karim *et al.* (2007) which support the present findings. The rest of the traits showed moderate or low heritability including low genetic advance as percentage of mean which might be upgraded by selecting superior genotypes of segregating population developed from combination breeding as suggested by Samadia (2005).

Table 2. Analysis of variance for different morphological plant characters of 10 varieties.

Source of variation	df	Days to flowering	Plant height (cm)	Total tillers hill^{-1} (no.)	Effective tillers hill^{-1} (no.)	Flag leaf length (cm)	Flag leaf breadth (cm)	Panicle length (cm)	Filled grains panicle^{-1} (no.)	Unfilled grains panicle^{-1} (no.)	100 grain weight (g)	Grain Yield (g/plant)
Replication	4	12.230	104.24	1.34	0.184	14.98	0.001	38.24	26.77	2.60	0.018	1.268
Treatment (A)	4	1112.49**	2730.15**	298.77**	203.074**	220.72**	0.027**	231.28**	26303.92**	473.81**	15.072**	4256.326**
Variety (B)	9	302.56**	1704.34**	81.16**	41.842**	173.02**	0.002*	75.86**	2846.69**	42.42**	0.486**	293.568**
AB	36	3.441NS	143.15**	33.17**	26.074**	95.98**	0.002*	37.09**	970.22**	17.63**	0.282**	108.147**
Error	196	15.195	30.04	1.55	0.437	9.54	0.001	7.53	43.68	1.24	0.008	0.836

** indicates significant at 0.01 probability level, * indicates significant at 0.05 probability level and NS indicates Not significant

Table 3. Mean effect of genotypes on different morphological traits related to yield of 10 genotypes

Genotype	DF (g)	PH (cm)	TTH (no.)	ETH (no.)	FLL (cm)	FLB (cm)	PL (cm)	FGP (no.)	UGP (no.)	HSW (g)	GY (g/plant)
BRRI dhan28	107.4 c	84.44 d	12.68 bc	10.68 a	21.48 e	1.17 abc	18.72 e	88.4 cd	9.000 bc	1.960 d	14.35 d
RC-191	111.0 ab	84.16 d	11.44 ef	9.160 b	25.7 cd	1.16 abc	22.08 bc	91.0 bc	9.600 b	2.041 c	15.15 bc
RC-193	105.4 cd	87.84 c	9.360 h	7.960 d	28.4 ab	1.16 abc	22.80 b	87.4 cd	9.520 b	1.905 e	12.55 e
Binadhan-8	103.6 d	93.40 b	11.72 de	9.400 b	25.9 cd	1.180 ab	21.80 bc	94.5 ab	11.16 a	2.163 a	15.65 b
BRRI dhan47	110.4 b	94.88 b	10.84 fg	8.360 c	27.4 bc	1.160 bc	21.6 bcd	96.56 a	10.56 a	2.204 a	16.45 a
Binadhan-11	112.1 ab	88.16 c	9.00 h	7.440 e	27.2 bc	1.156 c	22.32 bc	80.68 e	8.840 c	2.097 b	12.19 e
Binadhan-12	112.4 ab	82.68d	12.40 cd	9.040 b	27.1 bc	1.17 abc	20.0 de	67.36 f	7.280 d	1.834 f	6.558 g
RC-217	113.3 a	110.0 a	14.88 a	11.00 a	29.92 a	1.180 ab	25.24 a	66.52 f	7.720 d	1.817 f	7.116 f
RC-229	105.9 c	90.08 c	10.52 g	7.960 d	24.28 d	1.184 a	21.88 bc	86.12 d	8.720 c	2.046 c	12.24 e
RC-221	112.1 ab	82.92 d	13.36 b	10.84 a	22.40 e	1.17 abc	20.60 cd	93.6 ab	11.00 a	2.164 a	14.9 c
Mean	109.34	89.86	11.62	9.18	25.99	1.17	21.70	85.23	9.34	2.02	12.72
CV (%)	3.57	6.10	10.74	7.20	11.88	2.84	12.65	7.76	11.95	4.51	7.19
$LSD_{(0.05)}$	2.17	3.05	0.694	0.368	1.72	0.018	1.53	3.68	0.621	0.050	0.510

** and * indicates significant at 0.01 and 0.05 probability level. Varieties with the different letter (s) are significantly different. DF: Days to flowering, PH: Plant height, TTH: Total tillers hill^{-1}, ETH: Effective tillers hill^{-1}, FLL: Flag leaf length, FLB: Flag leaf breadth, PL: Panicle length, FGP: Filled grains panicle^{-1}, UGP: Unfilled grains panicle^{-1}, HSW: 100 seed weight, GY: Grain yield

Table 4. Mean effect of treatment on different morphological traits related to yield of 10 genotypes

Genotype	DF (g)	PH (cm)	TTH (no.)	ETH (no.)	FLL (cm)	FLB (cm)	PL (cm)	FGP (no.)	UGP (no.)	HSW (g)	GY (g/plant)
T_1	101.1 c	99.76 a	15.14 a	12.10 a	28.82a	1.208 a	24.82 a	116.9 a	13.70 a	2.638 a	26.73 a
T_2	110.8 b	95.50 b	11.80 b	9.480 b	27.32a	1.180 b	23.20 a	100.5 b	11.42 b	2.609 a	17.49 b
T_3	110.8 b	84.58cd	11.42 b	8.860 c	24.06c	1.154 c	19.96 b	65.34 d	6.580 e	1.614 c	5.947 d
T_4	110.8 b	86.74 c	11.50 b	9.040 c	26.04b	1.152 c	20.80 b	79.06 c	7.800 c	1.672 b	7.992 c
T_5	113.2 a	82.72 d	8.240 c	6.440 d	23.72c	1.164 c	19.72 b	64.34 d	7.200 d	1.583 c	5.418 e
Mean	109.34	89.86	11.62	9.18	25.99	1.17	21.70	85.23	9.34	2.02	12.72
CV (%)	3.57	6.10	10.74	7.20	11.88	2.84	12.65	7.76	11.95	4.51	7.19
$LSD_{(0.05)}$	1.53	2.16	0.491	0.261	1.21	0.012	0.108	2.60	0.439	0.035	0.361

** and * indicates significant at 0.01 and 0.05 probability level. Treatments with the different letter (s) are significantly different. Here, T_1= No stress, T_2= Saline condition of 9 dSm^{-1} saline water at reproductive stage, T_3= Submerged in 6 dSm^{-1} saline water at late vegetative stage, T_4= Submerged in normal water and T_5= Submerged in 9 dSm^{-1} saline water at late vegetative stage. DF: Days to flowering, PH: Plant height, TTH: Total tillers hill^{-1}, ETH: Effective tillers hill^{-1}, FLL: Flag leaf length, FLB: Flag leaf breadth, PL: Panicle length, FGP: Filled grains panicle^{-1}, UGP: Unfilled grains panicle^{-1}, TDM: Total dry matter, HSW: 100 seed weight, GY: Grain yield

Table 5. Estimation of genetic parameters for morphological characters related to yield

Characters	δ^2p	δ^2g	PCV (%)	GCV (%)	h^2b (%)	GA	GA (%)
Days to flowering	13.71	11.96	3.39	3.16	87.25	6.66	6.09
Plant height (cm)	75.00	62.45	9.64	8.79	83.27	14.85	16.53
Total tillers hill^{-1}(no.)	4.29	1.92	17.82	11.92	44.79	1.91	16.44
Effective tillers hill^{-1} (no.)	2.41	0.63	16.91	8.65	26.14	0.84	9.11
Flag leaf length (cm)	10.43	3.08	12.43	6.75	29.53	1.97	7.56
Flag leaf breadth (cm)	0.0003	0.00004	1.41	0.54	14.63	0.00	0.43
Panicle length (cm)	4.78	1.55	10.07	5.74	32.47	1.46	6.74
Filled grains panicle^{-1} (no.)	144.11	75.06	14.09	10.17	52.08	12.88	15.11
Unfilled grains panicle^{-1} (no.)	2.29	0.99	16.21	10.66	43.26	1.35	14.45
100 grain weight (g)	0.03	0.01	8.24	4.47	29.39	0.10	4.99
Grain yield plant^{-1} (g)	14.71	7.42	30.16	21.42	50.42	3.98	31.33

Here, δ^2p= Phenotypic variance, δ^2g= Genotypic variance, GCV= Genotypic Co-efficient of Variance, PCV= Phenotypic Co-efficient of Variance, h^2b= Heritability, GA= Genetic Advance, GA (%) = Genetic Advance as percent of mean

Conclusion

It can be concluded that, moderate heritability values (50-70%) along with low genetic advance and genetic advance as percentage of mean were found for the traits grain yield plant^{-1} indicating the presence of additive gene action and selection will be beneficial for such traits. Selection on the basis of traits like days to flowering, plant height which showed high heritability values and grain yield plant^{-1}, filled grains panicle^{-1} which showed moderate heritability values could lead to the improvement of salt and submergence tolerant rice genotypes.

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Conflict of Interests

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

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