Studies on genetic variability and heritability in rice genotypes (*Oryza sativa*. L.) under salinity

ABSTRACT

Rice (*Oryza sativa* L.) is one of the most important staple food crops in the world because more than half of the world's population depends on rice for their livelihood. By 2050, the world's rice productivity will need to double in order to keep up with population growth. Narrow genetic base in the released variety has made the improvement in plateaus. In order to go more than the yield barrier, the genetic base must be broadened. Heritability and genetic variability were measured in eighty-sixrice genotypes in terms of of yield and yield contributing traits under saline soils. Significant differences were found between the genotypes for all of the studied traits according to analysis of variance. High PCV and GCV were recorded for the traits *viz.*,mortality percentage (%), total number of grains per panicle, number of un-filled grains per panicle, sterility percentage (%) and seed yield per plant (g). The traits showed a significant degree of genetic advancement together with high heritability weremortality percentage (%), 1000 grain weight (g) and seed yield per plant (g). Genetic advance over mean were high for mortality percentage (%), number of productive tillers/m^2, total number of grains per panicle (g), number of un-filled grains per panicle (g), sterility percentage (%), 1000 grain weight (g) and seed yield per plant (g). This study provides information about the variability and heritability measures which may supplement the breeding program to break the yield plateaus.

Key words: Genetic Variability, Genetic advance, Heritability, Salinity, Rice.

INTRODUCTION

Rice (*Oryza sativa* L.) is the primary food sourcefor one-third of the world's population and 70% of Indians,. India was determined to have 6.7 million hectares damaged by salt. Of which 3.7 mha were sodic and 2.9 mha were saline (Mandal *et al*., 2011), 43.79 million hectares of land are utilized to grow rice in India, with a yield of 116.42 million tonnes and 2.7 tonnes per hectare. Salt stress severely affects crop development by lowering photosynthetic potential of plants. High sodium content in soil damages cell metabolism and photosynthesis by increasing the toxicity of sodium in the cytosol and producing osmotic stress on cell-water relations (Gupta *et al.,* 2020). Na^+ and K^+ exhibit comparable ionic, physical, and chemical characteristics. K^+ plays key part in numerous physiological process and cell metabolism for optimal growth and development. When roots are under salt stress, their Na^+ concentration goes over what is ideal, which lowers their ability to absorb K^+. As a result, various plant portions retain less K^+. Toxic effects result from Na^+ entering the K^+ route and changing the ion ratio in the cytosol. Extrusion of surplus Na+ through roots and compartmentalization in distinct regions are two mechanisms used by salt-tolerant plants to maintain low cytosolic Na^+ / K^+ ratios, which in turn lowers Na^+ concentration in the cytosol. By overcoming the negative effects of salt, this osmotic adjustment helps to provide a significant yield (Chakraborty *et al.*, 2018). Local cultivar variability is declining as a result of the ongoing cultivation of high-yielding cultivars.

Plant breeding is based on variation. Any crop improvement program's ability to succeed is mostly determined by the amount and range of genetic stock variability. In crop improvement programs, the initiation of suitable breeding processes requires a crucial estimation of genetic diversity. In order to help breeders plan an appropriate breeding program, it becomes necessary to split overall variability into its heritable and non-heritable components using certain genetic criteria. As a result, the degree and type of genetic variability within a population determines its rate of development. Information of genetic variability among growth as well as yield components in rice has been reported by many workers (Sivasubramanian and Madhava Menon, 1973).

The degree of variation in the population can be determined using genetic variability parameters including Heritability, Phenotypic Coefficient of Variation (PCV), Genotypic Coefficient of Variation (GCV), and Genetic Advance as percent Mean (GAM). Plant breeders have not yet completely utilized the rich pool of useful genes that have collected throughout time in the rice germplasm to improve varietals. In order to support future breeding programs for yield enhancement through expanding the genetic base and genetic recombination, the goals of this study were to evaluate genetic variability, heritability, and genetic advancement.

MATERIAL AND METHODS

During *Rabi,* 2020-21, 86 rice genotypes along with checks were sown in the nursery bed at Agricultural Research Station, Kampasagar (Table 1). Twenty-one day old seedlings were transplanted in a Randomized Block Design, under saline field conditions (pH: 9.30, E.C: 4.68 dSm^{-1}, and ESP: 88.0) with a spacing of 20 x 15 cm. General view of field screening was shown in plate 1. The crop was grown according to the recommended set of cultural practices. During reproductive stage, visual scoring of salt injury was also recorded according to IRRI-SES 2013 (Table 2). Observations on yield and yield attributing characters were recorded while screening for salinity tolerance at the reproductive stage.

Data were collected on the following: percentage of mortality (M%), days to 50% flowering (DFF), plant height (PH), length of panicle (PL), number of productive tillers (NPT), number of grains per panicle (NGP), number of unfilled grains per panicle (UFG), spikelet sterility (S%), 1000 grain weight (TW), and seed yield per plant (SY). Each entry consisted of five randomly selected plants for observations, from which the mean value was calculated.

Analysis of variance and estimates of the phenotypic and genotypic coefficient of variation were estimated using the techniques suggested by Burton (1952) and Panse and Sukhatme (1967). For the features under study, estimates of heritability in the wide sense (Lush, 1940) and genetic advancement as a percentage of mean (Johnson *et al.*, 1955) were also made. According to Johnson *et al.*, (1955), the range of heredity was categorized as low (10–30%), medium (30–60%), and high (>60%).According to Johnson *et al.*, (1955), the genetic progress for the traits was categorized as strong (>20%), moderate (10-20%), or low (<10%). The software INDOSTAT version 9.2 was used to do the statistical analysis.

RESULTS AN DISCUSSION

For the success of any breeding programme, it is essential to know the inherent genetic variability in a given crop species for a particular trait under development is essential. The coefficient of variation is used to estimate the degree of variation existing in the crop species. Estimates of heritability provide information on the amount of transmissible genetic variation among total variation, which defines its responsiveness to selection and the scope of improvement in the new population over the original population through genetic advance. Analysis of variance showed that the mean sum of squares for genotypes were highly significant for all the characters studied (Table 3). It indicates that presence of high variability for the traits in rice genotypes used in the study.

If a character is driven by non-additive gene action, it may have high heritability but low genetic advance, but if it is governed by additive gene action, it will have high heritability (above 60%) and high genetic advance (above 20%), provides much potential for further improvement. As a result, the most significant strategy to make genetic gain through generations is to increase these qualities through selection. For the genotypes, the genotypic and phenotypic coefficients of variation, heritability, genetic advance, and genetic advance as a percentage of the mean were calculated and shown (Table 4.; Fig 1 &2).

The GCV and PCV values for mortality percentage were high at 30.52% and 33.97% respectively. Heritability values for this trait were high at 80.71% with a moderate genetic advance of 15.20% and a high genetic advance as a per cent of mean 56.47%. As this characteristic has a negative impact on yield, it should be subjected to negative selection pressure in order to develop varieties with high yield tolerant to salinity stress.

The GCV and PCV values for days to 50% flowering were both low in magnitude, at 1.92% and 5.02%, respectively. This wide range of variation provides shifting the seasonal timing of reproduction and produce novel varieties that are better adopted to local environment and change in climatic conditions. This trait had a low heritability of 14.70%, with a low genetic advance of 1.53% and a poor genetic advance as a per cent of the mean of 1.52%. As heritability and genetic advance are low, it indicates the preponderance of non-additive gene action, therefore selection for this trait is inefficient due to non-additive gene action.These results are in confirmity with the findings of Parimala and Devi (2019), and Hasan-Ud-Daula and Sarker (2020).

“The GCV and PCV values for plant height were 6.97% and 9.09%, respectively, which were low in magnitude. The trait's heritability value was moderate 58.82%, with moderate genetic advance 10.23% and genetic advance as a percentage of the mean 11.01%. When heritability is moderate and GAM is moderate, it implies that the environment has control over the character, and that improvement can be achieved by intermitting superior genotypes of segregating populations developed through combination breeding. These results are in trend with the findings” of Singh and Verma (2018), and Saha *et al.* (2019)

“The GCV and PCV values for the trait panicle length were 7.30% and 13.34% with low and moderate magnitude respectively. This trait heritability was moderate 30.01%, with low genetic advancement 1.68% and genetic advance as per cent of mean 8.23% respectively. Moderate values of heritability and low genetic advance indicate a lack of inherent variability and limited scope for improvement through selection for these traits among the lines”.Sumanth *et al.* (2017) and Divya *et al.* (2018) also obtained similar results.

“The GCV and PCV values for the trait number of productive tillers/m^2 were 14.94% and 19.89%, respectively, which were moderate in magnitude. This trait had a moderate heritability of 56.40%, and high genetic advance of 39.36%, with high genetic advance as a per cent of mean of 23.11%. The predominance of non-additive gene action is shown by moderate estimates of heritability and high genetic advance. This trait can be improved by heterosis breeding. These results are in confirmity with those” of Parimala and Devi (2019) and Swapnil *et al.* (2020).

“The GCV and PCV values for the trait number of grains per panicle were 15.33% and 21.04% respectively which were moderate and high in magnitude respectively. Heritability values for this trait were moderate at 53.12% and with a moderate genetic advance of 14.42% and high genetic advance as per cent of mean 23.00%. Moderate heritability and high genetic advance for this character indicate predominance of non-additive gene action in the control of this character it can be improved by heterosis breeding. Similar kind of results were reported” by Sameera*et al.* (2016) and Saha *et al.* (2019).

“The GCV and PCV values for the trait un-filled grains per panicle were 30.87% and 47.82%, respectively, which were high. This trait's heritability was moderate 41.74%, with a moderate genetic advance of 8.42% and a high genetic advance as a per cent of the mean 41.05%, indicating a good response to selection”. Hasan-Ud-Daula and Sarker (2020) obtained similar results.

“The GCV and PCV values for trait sterility percentage were both high in magnitude, at 29.98% and 47.67% correspondingly. Negative selection can be utilised efficiently with heritability values of moderate 39.51%, and moderate genetic advance of 13.00%, and high genetic advance as a per cent of mean of 38.84%. As this trait has a negative impact on yield, it should be subjected to negative selection pressure in order to boost develop lines with sterility tolerance to yield”. Hasan-Ud-Daula and Sarker (2020) obtained similar results.

“The GCV and PCV values for the 1000 grain weight were 15.41% and 17.14% respectively which were moderate in magnitude. Heritability values for this trait were high 80.80% with a low genetic advance of 5.68% and high genetic advance as per cent of mean 28.54%. Results indicated possible scope for improvement through selection of this trait and breeder may have reliable benefits in next generation with respect to this trait.These findings were in accordance with those” of Rashid *et al.* (2017) and Sumanth *et al.* (2017).

“The GCV and PCV values for the trait seed yield per plant were 25.69% and 33.08% respectively, both were quite high. This characteristic had a high heritability of 60.31%, with a low genetic advance of 5.40% and a high genetic advance as a per cent of the mean of 41.06%. Yield, as a complex character, was influenced by its attributing factors and was shown to have high heritability and GA, indicating that it is controlled by additive genetic effects and a simple phenotypic selection will hasten the varietal improvement period. Similar results were recorded” by Bhati*et al.* (2015) and Tiwari (2017).

The PCV values in this study were higher or close to the corresponding GCV values for all characteristics. The small differences between PCV and GCV for all the traits indicated that the variability was predominately due to genotypic differences, *i.e.,* fewer environmental influences.

In the present investigation, high values of GCV and PCV were observed in the case of mortality percentage (%), total number of grains per panicle, number of un-filled grains per panicle, sterility percentage (%) and seed yield per plant (g) indicating the presence of inherent variability among the lines. The difference between PCV and GCV was high for un-filled grains and sterility percentage (%), indicating the influence of environment on these traits *i.e.,* indicating the presence of saline environment effects on the treatments under study. These findings of high values of GCV and PCV for un-filled grains per panicle, and sterility percentage (%) were in accordance with the findings of Hasan-Ud-Daula and Sarker (2020). Moderate estimates of GCV and PCV were observed in the case of Sumanth*et al.* (2017) for 1000 grain weight, Parimala and Devi (2019) for number of productive tillers/m^2. Low estimates of GCV and PCV were observed in the case of days to 50 % flowering, plant height (cm), and panicle length (cm), indicating a lack of inherent variability and limited scope of improvement through selection for these traits among the genotypes. Similar results were observed by Parimala and Devi (2019), and Hasan-Ud-Daula and Sarker (2020) for days to 50 % flowering, Singh and Varma (2018), Saha *et al.* (2019) for plant height, Sumanth *et al.* (2017), and Divya *et al.* (2018) for panicle length.

Higher estimates of heritability for characters such as mortality percentage, 1000 grain weight (g) and seed yield per plant (g) indicated that these characters are less influenced by environmental fluctuations. Hence, selection for improvement of such characters may not be useful as broad sense heritability depends on total genetic variance which includes both additive and non-additive variances. Senguttuvel*et al.* (2010), Akinwale *et al.* (2011) and Hasan-Ud-Daula and Sarker (2020) reported the same results for heritability for seed yield per plant.

An estimated heritability values alone is less reliable as these values are prone to alter with change in the environment and experimental material. Hence, the use of high heritability coupled with high genetic advance as per cent of mean is preferred and most probably controlled by additive gene action which may respond to selection.

Genetic advance was low for days to 50% flowering, panicle length (cm), number of un-filled grains per panicle, 1000 grain weight (g) and seed yield per plant (g). Moderate values were observed in the case of traits such as mortality percentage (%), plant height (cm), total number of filled grains per panicle, and sterility percentage (%). A high value of genetic advance was observed in the case of number of productive tillers/m^2. A similar case of the low estimate for days to 50 % flowering was reported by Hasan-Ud-Daula and Sarker (2020) whereas, Divya *et al.* (2018) and Singh and Verma (2018) reported it in case of plant height, Manohara and Singh (2015) for the total number of grains per panicle and Parimala and Devi (2019) for seed yield per plant (g).

"The estimates of genetic advance over mean were high for mortality percentage (%), number of productive tillers/m^2, total number of grains per panicle (g), number of un-filled grains per panicle (g), sterility percentage (%), 1000 grain weight (g) and seed yield per plant (g), indicating that these characters are governed by non-additive gene action and heterosis breeding programme may be useful to improve these traits. These findings align with the reports" of Sumanth*et al.* (2017), Devi *et al.* (2017), Islam *et al.* (2016), Divya *et al.* (2018) Hasan-Ud-Daula and Sarker (2020).

Characters having a high heritability and a high genetic advance over the mean are more reliable for selection. The traits mortality percentage (%), 1000 grain weight (g) and seed yield per plant (g) were observed to be having high heritability coupled with high genetic advance. Partitioning variability into fixable and non-fixable components is critical for understanding the true picture of trait genetic variation. High heritability with moderate GAM may be attributable to additive gene action and manifested as a result of the environment's favourable effect rather than genotype.

CONCLUSION

The current investigation concluded that maximum values of GCV and PCV formortality percentage, number of un-filled grains per panicle, sterility percentage andseedyield/plant denotes the occurrence of large amount of variation amongst the germplasm lines for potential yield enhancement through selection and also grain yield/plant perceived maximum heritability combined with high genetic advance as percent of mean, which revealed that this trait is regulated through additive gene action and thus, the selection might be practiced based on phenotypic performance.

Thus, it was found that traits possessing both strong genetic advancement and high heritability are controlled by additive gene action, which might be improved by applying simple selection techniques. The presence of non-additive gene action is indicated by characteristics exhibiting high heritability with modest genetic advance. High environmental impacts have also revealed high heritability, thus selection for these traits must be successful.

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Table 1. List of rice genotypes and checks utilized in the screening experiment

S.No	Genotype	S.No	Genotype	S.No	Genotype
1.	IR69726-116-1-1	**30.**	KPS10329	**59.**	IR 10F 360
2.	IR77186-122-2-2-3	**31.**	MINGHU163	**60.**	DJ 123
3.	NSICRC240	**32.**	ZHENSHAN 97B	**61.**	Oryzica 1
4.	IRRI154	**33.**	IR64-21	**62.**	FEDEARROZ 50
5.	GSRIR2-9-RI-SU3-Y2	**34.**	IRBB 66	**63.**	TEQING
6.	CT118911-2-2-7-M	**35.**	IR 78222-20-7-148-2-B-B-B-B	**64.**	UPL RI7:IRTP9897-C1
7.	IR13F167	**36.**	IRRI 147	**65.**	Jamir
8.	Sahel177	**37.**	SANHUANGZHAN NO2	**66.**	IRIOM300
9.	Jasmine85	**38.**	IR77298	**67.**	KPS 13575
10.	M202	**39.**	Sambha mahsuri+sub1	**68.**	KPS 13576
11.	KPS10628	**40.**	SUPA	**69.**	KPS 13577
12.	KPS10631	**41.**	IRRI 104	**70.**	KPS 13578
13.	KPS10633	**42.**	N 22 IRGC 19379-1	**71.**	KPS 13579
14.	KPS10640	**43.**	MTU 1010	**72.**	KPS 13580
15.	KPS10642	**44.**	SWARNA	**73.**	KPS 13581
16.	KPS10651	**45.**	NANHI	**74.**	KPS 13582
17.	KPS10654	**46.**	Kinandangpatong	**75.**	KPS 13583
18.	KPS10656	**47.**	SADRI	**76.**	KPS 13584
19.	KPS10657	**48.**	OM4900	**77.**	KPS 13585
20.	KPS10658	**49.**	IR93340	**78.**	KPS 13586
21.	KPS10661	**50.**	IR93354	**79.**	KPS 13587
22.	KPS10667	**51.**	KhaoHlan ON	**80.**	KPS 13588

23.	KPS10669	**52.**	IR84984-83-15-481-B		**CHECKS**
24.	KPS10672	**53.**	ManawThuka	**1.**	FL478
25.	KPS10676	**54.**	BR 28	**2.**	PUSA 44
26.	KPS10683	**55.**	TN1	**3.**	CSR 23
27.	KPS10316	**56.**	IR 6	**4.**	CSR 36
28.	KPS10319	**57.**	Zanton:IRGC31248-1	**5.**	RNR11718
29.	KPS10321	**58.**	URAIBOOL IRGC52785-1	**6.**	KPS2874

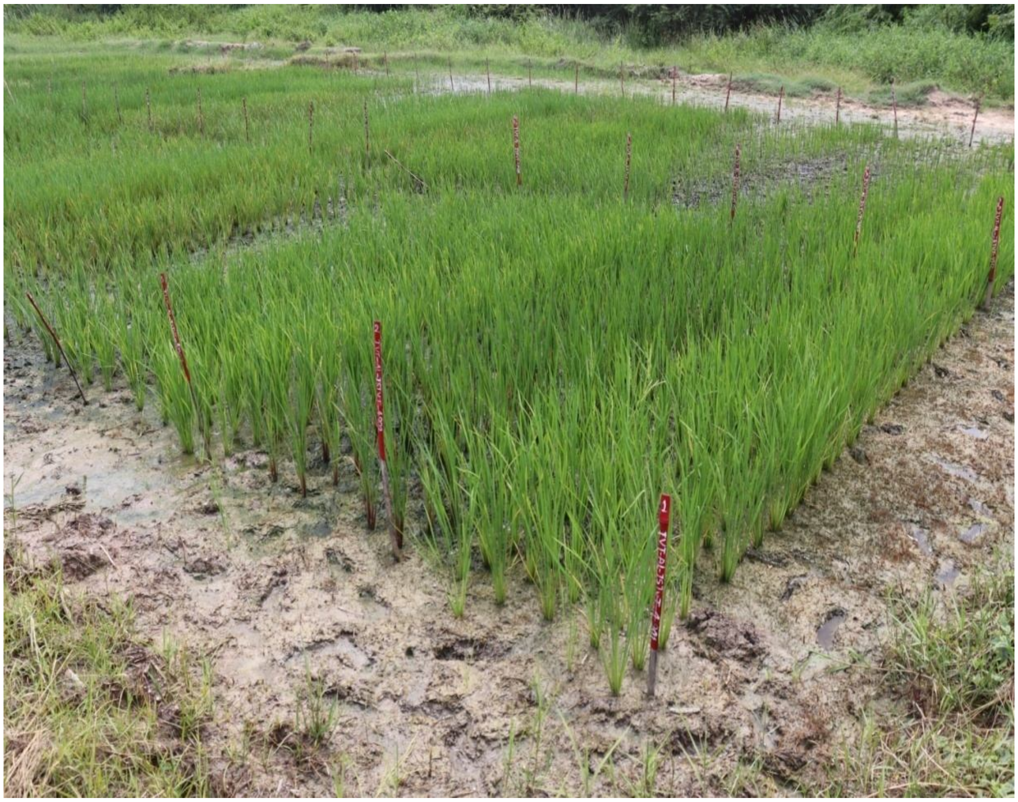

Plate 1. Over view of salinity block

Table 2. Scoring of damage for salt injury in field conditions in rice standard evaluation system scale (IRRI-SES 2013)

Score	**Growth Scale**	**Salinity-induced reaction**
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 cessation of growth, most leaves dry, some plants drying	Susceptible
9	Almost all plants dead or drying	Highly susceptible

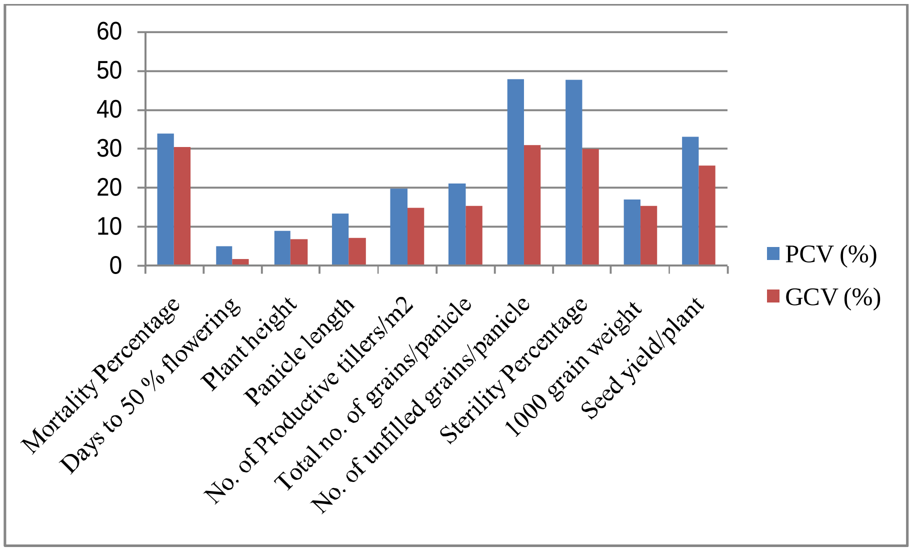

Fig.1. Genotypic and phenotypic coefficients of variation for yield and yield contributing traits in rice genotypes

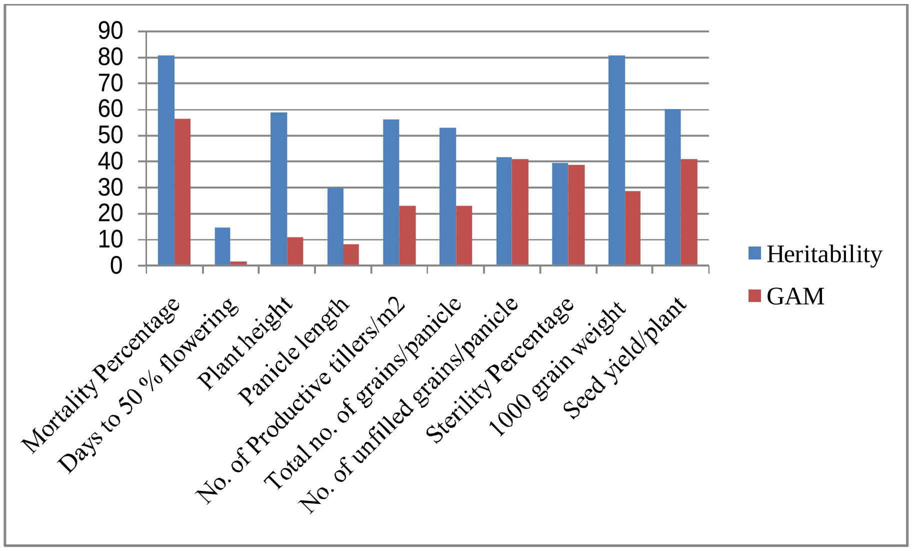

Fig2. Heritability and genetic as per cent of mean (5%) for yield and yield attributing traits in rice genotypes

	DF	M	DFF	PH	NPT/m^2	PL	NGP	UFG	S	TW	SY
Replicates	2	47.16	8.49	37.68	360.81	100.35*	23.49	75.76	40.39	26.79	31.24
Treatments	85	218.48**	33.17*	156.93**	2443.44**	11.78**	358.34**	176.40**	456.52**	30.44**	41.53**
Error (A)	170	16.13	21.88	29.74	500.83	5.16	81.57	56.12	154.10	2.23	7.47
Total	257	83.30	25.51	71.87	1142.24	8.09	172.66	96.05	253.23	11.75	18.92
General Mean		26.91	100.95	93.39	170.35	20.34	62.67	20.51	33.49	19.89	13.11

Table 3. Analysis of variance for yield and its attributing traits in rice genotypes evaluated under saline field conditions

* - significant at 5 per cent level, ** - significant at 1 per cent level   DF- Degrees of freedom

M (%) - Mortality percentage
PH (cm) - Plant height
NPT/ m^2- Number of Productive tillers/m^2
UFG - Number of un-filled grains/panicle
TW (g) - 1000 grain weight

DFF- Days to 50 % flowering
PL (cm) - Panicle length
NGP - Total number of grains/panicle
S (%) - Sterility percentage
SY (g) - Seed yield/plant

S.No.	Traits	PCV (%)	GCV (%)	h^2 (%)	GAP (%)	GAM (%)
1.	Mortality percentage (%)	33.97	30.52	80.71	15.20	56.47
2.	Days to 50 % flowering	5.02	1.92	14.70	1.53	1.52
3.	Plant height (cm)	9.09	6.97	58.82	10.23	11.01
4.	Panicle length (cm)	13.34	7.30	30.01	1.68	8.23
5.	Number of Productive tillers/m^2	19.89	14.94	56.40	39.36	23.11
6.	Total number of grains/panicle	21.04	15.33	53.12	14.42	23.00
7.	Number of un-filled grains/panicle	47.82	30.87	41.74	8.42	41.05
8.	Sterility percentage (%)	47.67	29.98	39.51	13.00	38.84
9.	1000 grain weight (g)	17.14	15.41	80.80	5.68	28.54
10.	Seed yield/plant (g)	33.08	25.69	60.31	5.40	41.06

Table 4. Estimates of genetic parameters for yield and yield attributing traits in rice genotypes evaluated under saline field condition

PCV= Phenotypic coefficient of variation
GCV= Genotypic coefficient of variation

h^2= Broad-sense Heritability
GAP= Genetic advance per cent (at 5%)
GAM= Genetic advance as a per cent of the mean (at 5 %)