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

ABSTRACT

The purpose of the study was to determine which 86 genotypes of rice were salt tolerant in terms of genetic variability and heritability of yield and yield contributing traits. Analysis of variance exhibited significant differences among the genotypes for all the traits under study. 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). High heritability coupled with high genetic advance were observed in the traits *viz.*, mortality 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).

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

INTRODUCTION

Rice (*Oryza sativa* L.) is the major source of food for one-third of the global population and 70% of Indian population. Salt affected areas in India were found to be 6.7 mha. Out of which 2.9 mha areas were saline and 3.7 mha area were sodic (Mandal *et al.*, 2011). In India, rice is grown in 43.79 million ha area with production and productivity of 116.42 million tonnes and 2.7 tonnes/ha. Salt stress adversely affects crop growth by reducing photosynthetic capacity of plants. High level of sodium in soil causes osmotic stress on cell water relations and increase the toxicity of sodium in the cytosol leading to damage of cell metabolism and photosynthesis (Gupta *et al.*, 2020). Na$^+$ and K$^+$ show similar ionic as well as physical and chemical properties. K$^+$ plays major role in many physiological process and cell metabolism for normal growth and development. Under salt stress conditions, Na$^+$ concentration exceeds the optimal level, reducing K$^+$ uptake in roots. This causes lesser retention of K$^+$ in different plant parts. Na$^+$ enters K$^+$ pathway and alters ion ratio in the cytosol leading to toxicity. Salt tolerant plants maintain low cytosolic Na$^+$ / K$^+$ ratio through some strategies *viz.*, extrusion of excess Na$^+$ through roots and compartmentalization in different parts, which in turn decreases Na$^+$ concentration in cytosol. This osmotic adjustment aids in overcoming adverse salt effects, thus producing considerable yield (Chakraborty *et* *al.,* 2018). Due to continuous cultivation of high yielding varieties there is loss of variability in local cultivars.

Variation is the basis of plant breeding. As success of any crop improvement programme largely depends on the magnitude and range of variability on the available genetic stock. A critical estimate of genetic variability is a prerequisite for initiating appropriate breeding procedures in crop improvement programmes. Hence, it becomes necessary to spilt over-all variability into its heritable and non-heritable components with the help of certain genetic parameters, which may enable the breeders to plan a proper breeding programme. Therefore, the progress of a population mainly depends upon the amount and magnitude to genotypic variability present in the population. 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 genetic variability parameters such as Phenotypic Coefficient of Variation (PCV), Genotypic Coefficient of variation (GCV), Heritability and Genetic Advance as percent Mean (GAM) are useful in identifying the extent of variation present in the population. The present investigation was undertaken to assess the variability parameters contributing to yield and to identify salt tolerant rice genotypes.

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.

Mortality percentage (M%), days to 50 per cent flowering (DFF), plant height (PH), panicle length (PL), the number of productive tillers (NPT), the number of grains per panicle (NGP), the number of unfilled grains per panicle (UFG), spikelet sterility (S%), 1000 grain weight (TW) and seed yield per plant (SY) were recorded. In each entry, observations were recorded on five plants at random and the mean value was computed. Analysis of variance and estimates of coefficient of variation (phenotypic and genotypic) were estimated as per the methodology proposed by Panse and Sukhatme (1967) and Burton (1952). Heritability in broad sense (Lush, 1940) and genetic advance as percent of mean (Johnson *et al*., 1955) were also estimated for the characters studied. The range of heritability was classified as low (10-30%), medium (30- 60%) and high (>60%) as suggested by Johnson *et al*., (1955).The genetic advance for the traits were classified as high (>20%), moderate (10-20%) or low (<10%) as given by Johnson *et al*., (1955). The statistical analysis was carried out using INDOSTAT version 9.2 software.

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.

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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	**66.**	IRIOM300

			NO2		
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.**	Khao Hlan ON	**80.**	KPS 13588
23.	KPS10669	**52.**	IR84984-83-15-481-B		**CHECKS**
24.	KPS10672	**53.**	Manaw Thuka	**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

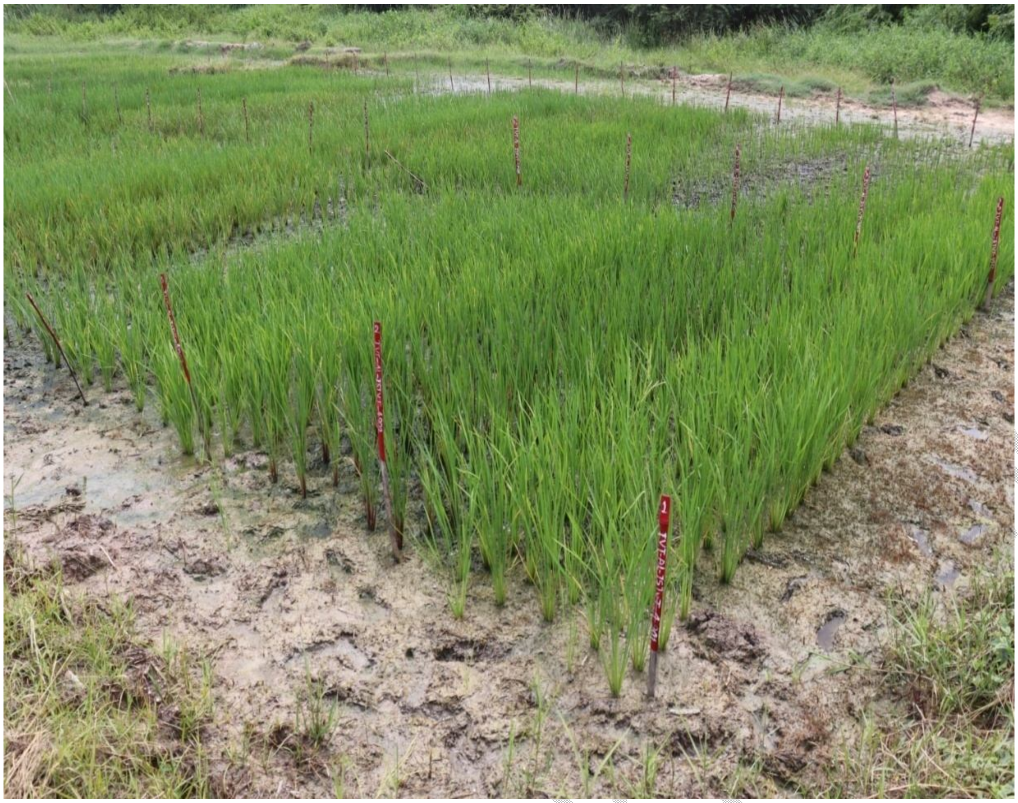

Plate 1. Over view of salinity block

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

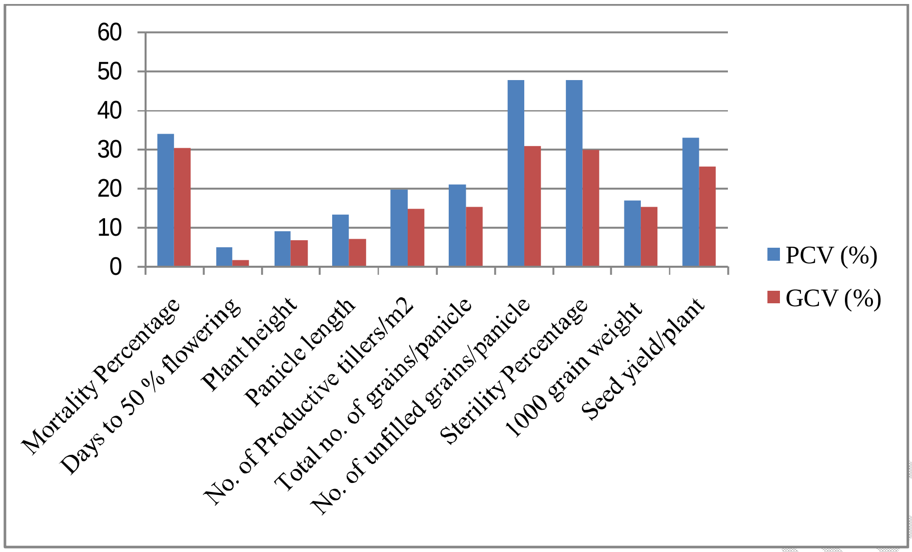

Fig.1. Genotypic and phenotypic coefficients of variation for yield and yield contributing traits in rice genotypes

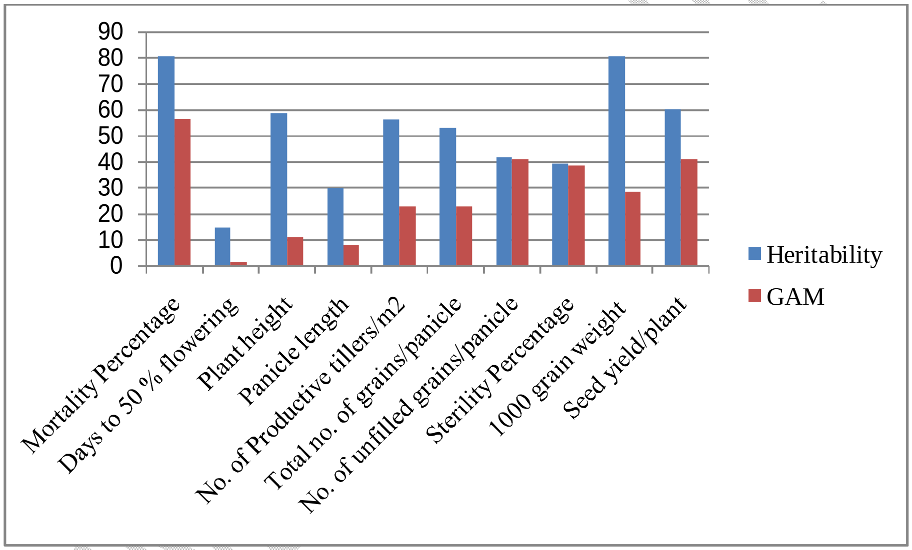

Fig2. Heritability and genetic as per cent of mean (5%) for yield and yield attributing traits in rice genotypes

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

	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

* - 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

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

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

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 %)