Evaluation of Germplasm for Reproductive Stage Salinity Tolerance in Rice (*Oryza sativa* L.)

Abstract

The current study was carried out to identify salt tolerant genotypes by screening 76 rice germplasm at reproductive stage salinity stress. The test entries were subjected to salt stress under field conditions and salinity was noted at different intervals of crop growth period *i.e.*, 30 and 67 days after sowing and at the time of harvesting with the pH value of 5.4 and electrical conductivity of 4.3 dSm^{-1}, 5.3 dSm^{-1}and 7.2 dSm^{-1}respectively. The characters namely, salinity score, days to 50 percent flowering, plant height, panicle length, productive tillers/plant, number of filled grains/panicle, total number of grains/panicle, spikelet fertility and grain yield/plant were studied under saline conditions. Variability, heritability and genetic advance as percent of mean showed high genotypic and phenotypic coefficient of variation for grain yield plant^{-1}indicating the presence of considerable amount of variation among the genotypes for potential yield improvement through selection. The trait grain yield per plant had high heritability coupled with high genetic advance as percent of mean indicating that it is regulated by additive gene action and therefore selection could be practiced based on phenotypic performance. Association studies under saline conditions, revealed favorable and significant correlation of grain yield per plant with days to 50% flowering, panicle length, plant height, total number of grains per panicle, number of filled grains per panicle and productive tillers per plant whereas, spikelet fertility and plant height on the other hand, recorded negative non-significant correlation, indicating the undesirable causes of salinity on plant growth and yield potential.

Key words: Reproductive stage, Phenotypiccoefficient of variation (PCV), Genotypic coefficient of variation (GCV), heritability, genetic advance

Introduction

Rice is sensitive to salinity during the reproductive stage especially during pollination and fertilizing period but it is tolerant throughout the vegetative stage. Salinity has an impact on spikelet development and pollengermination during the flowering stage, which in turn influences the number of filled grains/panicle and number of unfilled grains/panicle there by reducing the spikelet fertility. Salinity also reduces panicle length and 1,000 grain weight resulting in reduced productivity (Tran *et al.,* 2017).Rice yield is greatly influenced by salinity, as it hampers growth, photosynthesis and net assimilation rate. Along with the vegetative stages, salt stress affects reproductive stage of rice which reduces yield and yield contributing traits.

Salinity during reproductive stage results sterility and thereby causes reduction in the grain yield.Due to the considerable environmental influences on genotypic expression and the poor narrow sense heritability of salt tolerance, conventional breeding efforts for this trait have been proven to be unproductive. Salinity tolerance is a complex phenomenon governed by multiple stress responsive genes which interacts with other components of stress signal transduction pathways. A better understanding of the morpho-physiological variations induced by salinity in crop plants should facilitate the identification of those involved in tolerance mechanisms.Screening of germplasm atreproductive stage is considered to be the appropriate stage for salt stress because grain yield is crucial factor in rice. The analysis of genetic variance and enormity of genetic divergence existing in the genotypes is therefore highly essential for development of salt tolerant rice varieties. Therefore, the current study was carried out to evaluate the rice germplasm for yield and its attributing traits under reproductive stage salinity.

Materials and methods

Screening for reproductive stage salinity tolerance was studied at Agricultural Research Station (ARS), Machilipatnam, Krishna district of Andhra Pradesh located at 81.7^0 E longitude and 16.10^0 N latitude in Krishna zone.The experimental material consisted of 76 rice genotypes including 4 checks in augmented randomized complete block designduring *Kharif* 2020. The crop was raised under irrigated conditions and all the endorsed package of practices werepromoted to raise a healthy nursery. The thirty days old seedlings were transplanted in the main field with spacing of 20×15 cm. A peizometer was installed in field to measure soil salinity during different growth stages. The pH of the soil was 5.4 and salinity recorded during various intervals of crop growth period was at 30 DAS; 4.3 dSm^{-1}, 67 DAS; $5.3dSm^{-1}$ and at the time of harvesting was $7.2dSm^{-1}$. Data on days to 50% flowering (plot basis), plant height (cm), panicle length (cm), total number of tillers $plant^{-1}$, number of filled grains $panicle^{-1}$, number of total grains $panicle^{-1}$, grain yield $plant^{-1}$ (g), spikelet fertility (%) based on 5 plants per genotype and reproductive stage scoring was also done as per SES of IRRI, 1997 at the time of harvesting were noted (Table 1). The standard method of analysis of variance was applied to the mean data for each character (Federer, 1956). The genotypic and phenotypic coefficient of variation (Burton and Devane, 1953), heritability (Broad sense) (Hanson *et. al.,* 1956) and genetic advance as percent of mean as suggested by Lush (1940) and Johnson *et al*. (1955) were also estimated.

Results and Discussion

1. Analysis of variance

Among the 76 genotypes tested, during reproductive stage salinity tolerance under field conditions, only 67 genotypes were survived and considered for the study on analysis of variance. The results revealed significant differences among the germplasm lines for all characters studied (Table 2), whereas the remaining nine genotypes *viz.,* DRR DHAN 42, Swarna Sub 1, Bahadur, Akshayadhan, Sampada, Krishnahamsa, MandyaVijaya, MST 38 and MST 22 were not survived indicating that their sensitivity to salinity under field conditions.

2. Screening for reproductive stage salinity tolerance

In Table 3 average performance of 67 genotypes for yield and yield component traits under saline conditions is presented. Days to 50% flowering exhibited significant variances among rice genotypes with the range of 95 to 125 days and a mean value of 97 days. Plant height, the utmost important character among the morpho-physiological traits, ranged from 60.00 cm (RP-Bio-226) to 104.80 cm (BPT 3165) with an average of 68.48 cm. Number of productive tillers plant^{-1} ranged from 4.75 (MST 50) to 20.40 (BPT 2595) with an average value of 10.47. Panicle length ranges from 15.50 cm to 28.54 cm with a mean value of 18.81 cm. The genotype, MST 42 (28.54 cm) recorded high panicle length which exhibited significantly superior over the tolerant checks *i.e.,* MTU 1061 (21.90 cm) and CSR 27 (17.47 cm).The trait number of filled grains panicle^{-1} ranged from 25.50 to 300.60 with an average of 114.45 and the genotype BPT 2595 (300.60) recorded highest and significantly superior number of filled grains/panicle than the tolerant checks *i.e.*, MTU 1061 (137.56) and CSR 27 (91.31). Total number of grains/panicle was ranged from 62.60 to 389.90 with the average of 172.39. The genotype BPT 2595 (389.80) recorded the highest and exhibited superiority than the tolerant checks *i.e.*, MTU 1061 (164.49) and CSR 27 (104.22). The character spikelet fertility ranges from 26.41 to 91.39 % with the average of 59.91 %. Grain yield per plant in the current study ranged from 3.13 g to 28.65 g with an average of 14.34 g. Crop productivity is impacted by salinity because it interferes with nitrogen uptake and reduces the growth and ceases the reproduction due to increased Na^+ concentration**.**According to Abdullah *et al*., 2001, the main reason for reduced grain yield under salt stress is lack of transformation of carbohydrates into spikelets during grain development and also, significant reduction in translocation of soluble sugars to the lower spikelets, and inhibition of starch synthetase movement during grain development are the main reasons for lower grain yield under salt stress. The frequency distribution of entire germplasm lines for all the traits was represented in Figure 1**.**

Salinity scoring at reproductive stage

The salinity scoring at the reproductive stage was recorded at the time of harvest as per SES (IRRI, 1997) and the scoring ranged from 3.0 to 9.0. None of the genotypes exhibited high tolerance (1.0) to salinity at the reproductive stage. The genotypes MCM 109, MTU 1290, MTU 1061 exhibited tolerance with yield potential of 23.87 g, 27.84 g and 26.04 g per plant respectively. The genotypes MST 36, MST 42, MST 46, MST 48, MST 51, CO 51, and MTU 4870 exhibited moderate tolerance with grain yield of 15.23 g, 16.61 g, 16.91 g, 14.12 g, 17.29 g and 18.61 g respectively. Further, the hybrid US 301 exhibited susceptible reaction with a grain yield of 11.50 g and the genotype Krishnahamsa recorded as a highly susceptible reaction to salinity under the reproductive stage.

3. Estimates of Genetic Parameters of Variability

Coefficient of variation studies indicate the magnitude of the phenotypic coefficient of variation (PCV) was slightly higher than the corresponding genotypic coefficient of variation (GCV) for all the characters studied, signifying that the influence of environmental expression was less on these characters (Table 4, figure 2 and 3). GCV and PCV are high for grain yield per plant (37.95 and 37.87), then for number of filled grains panicle^{-1} (32.72 and 31.12), for total number of grains/panicle (31.65 and 31.45) and for the number of productive tillers plant^{-1} (23.90 and 23.15). Lowest PCV and GCV was sighted for days to 50% flowering (4.55and 3.67) followed by spikelet fertility (7.67 and 7.53) and panicle length (8.51 and 8.21). The minimum GCV and PCV values for these characters were also stated by Shivani and Reddy (2000) and (Devi *et al.*, 2006).Heritability (Broad sense) ranged from 64.88 (Days to 50% flowering) to 100.00 (Salinity score). Highest and lowest genetic advance as percent of mean was recorded by the characters *viz.*, number of filled grains/panicle (64.54) and days to 50 % flowering (6.08), respectively.High estimates of heritability combined with high genetic advance was observed for grain yield plant^{-1} (99.56, 77.83) followed by total number of grains panicle^{-1} (98.71, 64.36), number of filled grains/panicle (97.55, 64.54), total number of productive tillers (93.80, 46.18), plant height (94.70, 21.20) and salinity score (100, 42.20).High estimates of heritability coupled with moderate genetic advance as percent of mean was recorded for panicle length (92.97, 16.30) and spikelet fertility (96.46, 15.24) whereas, high estimates of heritability coupled with low genetic advance as percent of mean werenoticed for days to 50% flowering (64.88, 6.08). Thus, it was concluded that traits with high heritability along with high genetic advance are governed by additive gene action which could be enhanced through simple selection methods.The traits showing high heritability with low genetic advance indicates the presence of non-additive gene action and high heritability has been revealed due to high environmental effects and selection of these traits must be effective.

4. Correlation among yield and yield component traits under reproductive stage salinity

Thecorrelation coefficient matrix provides an understanding of the relationship between grain yield plant^{-1} and other yield attributing characters under salinity stress (Table 5). Positiveand significant correlationwas noticed for number of productive tillers plant^{-1}with days to 50 percent flowering, number of filled grains, total number of grains and grain yield per plant (Hakim *et al.,*2013);panicle length with plant height, number of filled grains, number of total grains and grain yield/plant; number of filled grains/panicle with total number of grains, grain yield plant^{-1}, plant height, days to 50% flowering, number of productive tillers plant^{-1} and panicle length (Akthar*et al.*, 2010) and (Hossen*et al.*, 2017); number of total grains with grain yield plant^{-1}, days to 50 percent flowering, plant height, number of filled grains, number of productive tillers and panicle length; grain yield plant^{-1} revealed significant and favorable correlation with days to 50 % flowering, plant height, panicle length, number of productive tillers, number of filled grains and total number of grains/panicle at both genotypic and phenotypic level. Similarly, negative andsignificant correlation was noticed for spikelet fertility with total number of grains per panicle at both phenotypic and genotypic levels indicating the adverse effect of salt stress on the grain yield due to non-filling of grains in the panicle which is mainly due to failure of pollination during stress at the reproductive stage.

The association reports on yield and its constituent traits had showed that days to 50 percent flowering, plant height, number of productive tillers plant^{-1},filled number of grains, panicle length and total number of grains noted significant and favorable association with grain yield plant^{-1}. It indicates that the characters taken for study assist in selecting the genotypes which can grow normally and induce high yield potential under saline conditions.

Conclusion:

The current investigation concluded that maximum values of GCV and PCV for grain yield/plant denotes the occurrence of large amount of variation amongst the germplasm lines for potential yield enhancement through selection and also grain yield/plantperceived 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. Association studies for yield and yield constituent traits revealed positivesignificant association of grain yield per plant with days to 50 % flowering, plant height, panicle length, number of filled grains/panicle, total number of grains/panicle and productive tillers/plant, shows that the characters taken for study assist in selecting the genotypes which can grow normally and induce high yield potential under saline conditions whereas, plant height and spikelet fertility recorded negative non-significant correlation indicative of the detrimental effects of salinity on plant growth and yield potential.

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Table 1. Standard evaluation score (SES) of reproductive stage salinity

Score	Observation	Tolerance
1	Normal growth, spikelet sterility at ≤ 5%	Highly tolerant
3	Growth slightly stunted, spikelet sterility at > 5% - 20%	Tolerant
5	Growth moderately stunted, ¼ of leaves brown, panicles partially exerted, spikelet sterility at 21% - 40%	Moderately tolerant
7	Growth severely stunted with about ½ of all leaves become brown, panicles poorly exerted, highly sterility 41% - 70%	Sensitive
9	Growth severely stunted with almost all the leaves become brown and affected, panicles not exerted, delayed heads or papery florets/chaffy panicle with very high sterility at > 70%	Highly sensitive

Table 2. Analysis of variance for yield and yield components in rice (*Oryza sativa* L.) under saline conditions

S. No.	**Source of variation**	**Degrees of freedom**	**Salinity score at reproductive stage**	**Days to 50% flowering**	**Plant height (cm)**	**No. of productive tillers/plant**	**Panicle length (cm)**	**No. of filled grains/panicle**	**Total number of grains/panicle**	**Spikelet fertility (%)**	**Grain yield/plant (g)**
			Mean sum of squares								
1	Block	8	0.001 *	5.113	1.037	0.302	0.335	10.920	62.222	3.425 *	0.283
2	Entries	66	5.526 ***	39.484 ***	156.644 ***	16.994 ***	7.978 ***	4795.253 ***	6682.086 ***	64.503 ***	73.536 ***
3	Checks	3	60.000 ***	209.880 ***	1071.970 ***	106.555 ***	75.162 ***	27364.890 ***	35081.610 ***	103.033 ***	267.074 ***
4	Varieties	62	2.773 ***	31.461 ***	96.621 ***	11.325 ***	4.603 ***	3774.687 ***	5346.885 ***	58.783 ***	65.183 ***
5	Checks *Vs*. Varieties	1	12.750 ***	25.718	1132.137 ***	99.769 ***	15.708 ***	361.480 *	4265.949 ***	303.516 ***	10.806 ***
6	Error	24	0.001	8.546	3.589	0.493	0.228	64.066	47.848	1.451	0.196

* Significant at 0.05 level; ** Significant at 0.01 level

Table 3. Screening of 67 change rice (*Oryza sativa* L.) germplasm for reproductive stage salinity tolerance

S. No.	Genotypes	Days to 50% flowering	Plant height (cm)	No. of productive tillers/plant	Panicle length (cm)	No. of filled grains/panicle	Total number of grains/panicle	Spikelet fertility (%)	Grain yield/plant (g)	Score	Code
1.	27 P 63	114	64.20	8.60	20.62	105.00	154.40	67.25	16.48	5	RS - 1
2.	BPT 3178	113	94.40	13.20	22.50	168.20	286.60	58.68	14.84	7	RS - 2
3.	ADT 49	105	77.30	9.60	22.40	159.00	177.40	90.19	25.92	3	RS - 3
4.	BPT 3139	110	82.80	13.80	22.16	200.00	333.40	59.98	12.83	7	RS - 5
5.	MTU 1282	110	84.90	10.80	24.40	252.00	304.60	82.73	15.70	5	RS - 7
6.	BPT 3141	110	90.00	11.20	21.36	80.40	262.20	30.66	07.11	9	RS - 9
7.	US 301	115	62.00	7.00	16.00	80.00	125.00	64.00	11.50	7	RS - 11
8.	BPT 3146	113	76.00	6.00	15.50	103.00	162.00	63.58	15.40	7	RS - 12
9.	Asandi	103	83.00	10.00	17.90	56.00	96.00	58.33	16.07	7	RS - 14
10.	BPT 2595	125	81.20	20.40	22.44	300.60	389.80	77.11	21.83	5	RS - 16
11.	BPT 2411	110	77.30	20.20	22.10	200.00	240.40	83.19	24.33	5	RS - 18
12.	MCM 103	112	95	18.60	19.50	173.60	202.40	85.90	22.91	5	RS - 20
13.	BPT 3173	107	68.40	14.00	20.94	75.00	213.80	35.07	07.75	9	RS - 21
14.	BPT 2776	107	86.00	11.60	23.50	169.60	265.60	63.85	17.73	7	RS - 22
15.	Kakirekalu	105	101.30	12.00	22.48	142.00	163.00	83.81	15.66	5	RS - 23
16.	BPT 3136	110	74.20	10.20	21.26	154.60	171.60	89.90	28.65	3	RS - 24
17.	Sugandhamati	115	63.90	12.60	19.42	81.20	145.40	55.84	14.58	7	RS - 27
18.	BPT 2660	115	82.20	15.20	23.48	220.00	285.20	79.25	25.62	5	RS - 28

Table 3contd…

S. No.	Genotypes	Days to 50% flowering	Plant height (cm)	No. of productive tillers/plant	Panicle length (cm)	No. of filled grains/panicle	Total number of grains/panicle	Spikelet fertility (%)	Grain yield/plant (g)	Score	Code
19.	BPT 2841	110	81.00	16.40	24.12	90.40	281.00	32.17	09.14	9	RS - 29
20.	BPT 3165	108	104.80	9.40	24.70	159.80	249.40	64.07	17.92	7	RS - 31
21.	BPT 3140	108	79.60	13.20	22.64	119.20	206.60	57.69	16.40	7	RS - 32
22.	BPT 2848	110	83.70	8.20	21.60	171.60	264.80	64.80	18.92	7	RS - 35
23.	BPT 2615	112	74.60	10.20	22.42	227.00	369.80	61.38	16.90	7	RS - 36
24.	RPBIO226	105	60.40	13.60	17.00	101.80	165.60	61.47	14.74	7	RS - 38
25.	MST 49	105	74.60	10.40	21.20	74.80	115.20	64.93	13.83	7	RS - 39
26.	PHI17108	115	70.40	15.40	21.58	71.80	236.60	30.34	11.97	9	RS - 41
27.	BPT 2846	124	76.60	19.20	20.36	86.80	257.40	33.72	10.47	9	RS - 42
28.	MCM 109	105	99	15.20	22.14	212.80	251.40	85.00	23.87	3	RS - 44
29.	Apputhokal	110	70.20	11.60	15.58	57.60	62.60	91.39	27.30	3	RS - 47
30.	Hallabhatta	105	101.20	9.40	19.60	84.80	106.40	79.69	12.25	5	RS - 48
31.	BPT 2766	108	86.00	7.60	25.30	108.40	180.20	60.15	14.57	7	RS - 49
32.	MCM 100	110	100	9.20	21.66	205.60	252.20	81.03	25.47	3	RS - 51
33.	BPT 3111	112	74.60	12.00	20.58	194.60	300.20	64.82	13.30	7	RS - 55
34.	CO 51	101	96.80	13.60	22.70	147.40	169.20	85.98	17.29	5	RS - 57
35.	JKRH 3333	103	77.80	9.20	21.68	166.20	271.40	61.23	15.53	7	RS - 58
36.	IR 64	103	68.20	11.00	18.00	79.20	133.40	59.37	14.77	7	RS - 60
37.	BPT 2782	114	74.10	13.80	20.72	284.40	352.80	79.81	24.88	5	RS - 62
38.	DRRDHAN44	96	61.00	8.40	20.08	30.20	101.60	29.72	7.13	9	RS - 66

Table 3 contd…

S. No.	Genotypes	Days to 50% flowering	Plant height (cm)	No. of productive tillers/plant	Panicle length (cm)	No. of filled grains/panicle	Total number of grains/panicle	Spikelet fertility (%)	Grain yield/plant (g)	Score	Code
39.	BPT 2231	110	69.75	6.00	21.75	107.00	186.50	57.37	12.95	7	RS - 68
40.	Jarava	106	79.00	10.00	21.00	55.00	187.00	26.41	5.88	9	RS - 69
41.	WGL 14	114	73.70	14.00	21.68	128.60	191.40	67.18	12.71	7	RS - 70
42.	DRRDHAN43	112	74.60	16.80	19.70	91.40	151.80	60.21	13.23	7	RS - 72
43.	BPT 1235	95	76.20	19.60	21.18	205.20	318.80	64.36	16.72	7	RS -73
44.	Karma mahsuri	110	86.70	12.00	22.10	66.20	109.60	60.40	14.34	7	RS - 77
45.	MST 40	100	77.30	9.80	18.98	86.40	95.20	90.63	23.93	3	RS - 79
46.	MTU 1318	113	69.00	16.60	19.72	159.20	247.00	64.45	15.44	7	RS - 81
47.	MTU 1290	96	71.90	10.60	21.06	130.60	155.60	83.10	27.84	3	RS - 82
48.	MTU 1271	107	79.10	11.40	22.98	150.20	234.80	63.96	15.92	7	RS - 83
49.	MTU 1238	109	77.40	9.60	22.44	171.60	257.00	67.15	11.00	7	RS - 84
50.	MTU 4870	114	84.60	11.60	20.94	140.60	172.00	81.74	18.61	5	RS - 85
51.	MTU 1315	122	70.00	16.20	19.52	103.60	126.80	81.70	16.40	5	RS - 88
52.	MTU 1253	115	76.60	11.80	21.58	171.40	206.40	82.98	17.58	5	RS - 90
53.	MST 36	98	75.60	8.00	21.32	109.80	126.60	85.95	15.52	5	RS - 91
54.	FL 478	100	61.60	8.80	21.28	89.60	124.40	72.36	14.85	5	RS - 92
55.	MST 42	102	64.75	7.00	28.54	93.00	122.50	75.86	16.61	5	RS - 94
56.	MST 51	100	67.50	9.00	20.40	133.00	159.50	83.38	16.83	5	RS - 95
57.	MST 54	100	63.60	8.60	20.56	71.80	110.20	65.15	11.22	7	RS - 96

Table 3 contd…

S. No.	Genotypes	Days to 50% flowering	Plant height (cm)	No. of productive tillers/plant	Panicle length (cm)	No. of filled grains/panicle	Total number of grains/panicle	Spikelet fertility (%)	Grain yield/plant (g)	Score	Code
58.	MST 48	102	76.60	9.40	22.76	82.40	101.40	81.26	14.12	5	RS - 97
59.	MST 46	96	70.20	8.80	21.08	141.40	163.80	83.48	16.91	5	RS - 98
60.	MST 21	107	63.50	11.00	18.00	50.25	79.50	63.20	11.02	7	RS -100
61.	MST 47	110	62.70	7.40	20.66	58.80	88.40	66.51	14.85	7	RS -101
62.	MST 44	110	64.40	9.80	19.68	63.20	96.20	65.69	10.14	7	RS -102
63.	MST 50	105	65.50	4.75	18.75	25.50	89.50	28.49	3.13	9	RS -107
Susceptible Checks											
64.	BPT 5204	111.33	62.36	18.44	18.77	112.89	191.36	58.99	13.64	7	RS -104
65.	MTU 1121	106.78	78.04	10.9	23.48	161.66	260.76	61.99	15.23	7	RS -103
Tolerant Checks											
66.	CSR 27	100.33	57.86	11.49	17.47	91.31	104.22	87.61	25.80	3	RS - 99
67.	MTU 1061	111.11	77.18	13.98	21.90	137.56	164.49	83.63	26.04	3	RS -106
	Maximum	**125.00**	**104.80**	**20.40**	**28.54**	**300.60**	**389.80**	**91.39**	**28.65**	**9.00**	
	Minimum	**95.00**	**60.00**	**4.75**	**15.50**	**25.50**	**62.60**	**26.41**	**3.13**	**3.00**	
	Mean	**96.61**	**68.48**	**10.47**	**18.81**	**114.45**	**172.39**	**59.91**	**14.34**	**6.44**	
	C. D (5%)	**2.85**	**1.85**	**0.69**	**0.47**	**7.79**	**6.73**	**1.17**	**0.43**	**0.001**	
	C. V (%)	**5.30**	**13.20**	**18.05**	**10.23**	**17.97**	**17.16**	**8.63**	**14.45**	**15.59**	

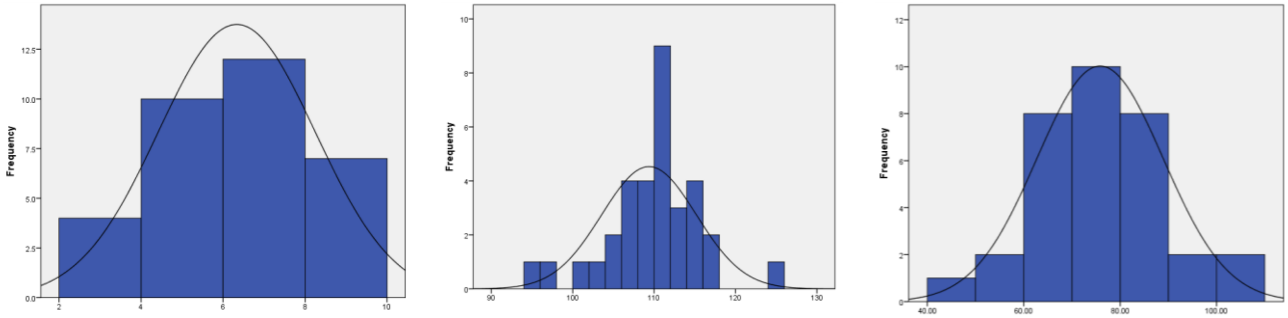
Table 4. Variability, heritability and genetic advance as per cent of mean for yield and yield component traits

S.No	Character	Coefficient of Variation		Heritability (%)	Genetic advance as percent of mean
		PCV (%)	GCV (%)		
1.	Salinity score	20.49	20.49	100.00	42.20
2.	Plant Height (cm)	10.87	10.58	94.70	21.20
3.	Days to 50% flowering	4.55	3.67	64.88	6.08
4.	Number of productive tillers	23.90	23.15	93.80	46.18
5.	Panicle length (cm)	8.51	8.21	92.97	16.30
6.	Number of filled grains/panicle	32.72	31.12	97.55	64.54
7.	Total number of grains/panicle	31.65	31.45	98.71	64.36
8.	Spikelet fertility	7.67	7.53	96.46	15.24
9.	Grain yield/plant (g)	37.95	37.87	99.56	77.83

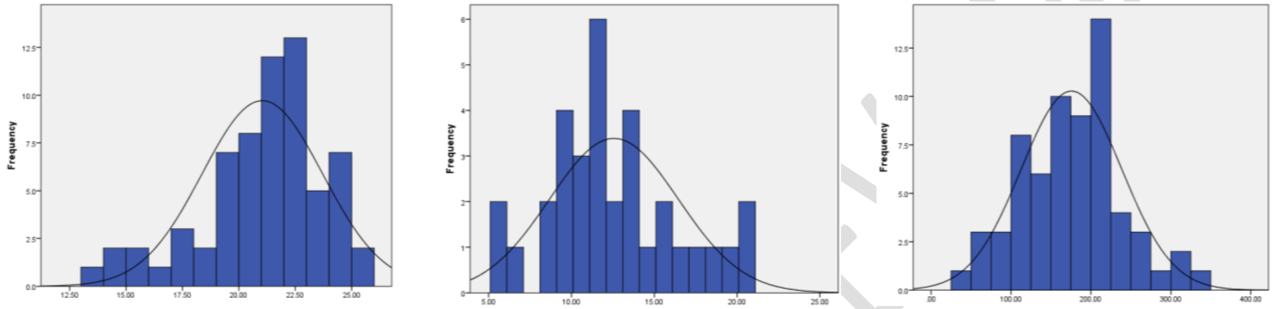
Table 5. Correlation matrix of yield and yield component traits of rice germplasm under salt stress at reproductive stage

Character		Plant height (cm)	Number of productive tillers/plant	Panicle length (cm)	Number of filled grains/panicle	Total number of grains/panicle	Spikelet fertility (%)	Grain yield/plant (g)	Salinity score
Days to 50% flowering	G	0.035	0.666**	-0.136	0.467**	0.524**	-0.111	0.489**	0.283
	P	0.030	0.535**	-0.065	0.384**	0.424**	-0.072	0.391**	0.228
Plant height (cm)	G		0.091	0.472**	0.373**	0.399**	-0.05	0.244*	-0.077
	P		0.116	0.427**	0.361**	0.382**	-0.046	0.242*	-0.075
No. of productive tillers/plant	G			-0.013	0.484**	0.519**	0.032	0.640**	0.108
	P			-0.014	0.476**	0.500**	0.032	0.621**	0.104
Panicle length (cm)	G				0.404**	0.422**	-0.231	0.295*	0.140
	P				0.381**	0.399**	-0.206	0.283*	0.135
No. of filled grains/panicle	G					0.960**	-0.098	0.715**	0.052
	P					0.944**	-0.103	0.703**	0.051
Total number of grains/panicle	G						-0.299*	0.693**	0.053
	P						-0.291*	0.685**	0.052
Spikelet fertility (%)	G							0.037	-0.180
	P							0.037	-0.177
Grain yield/plant (g)	G								0.107
	P								0.107

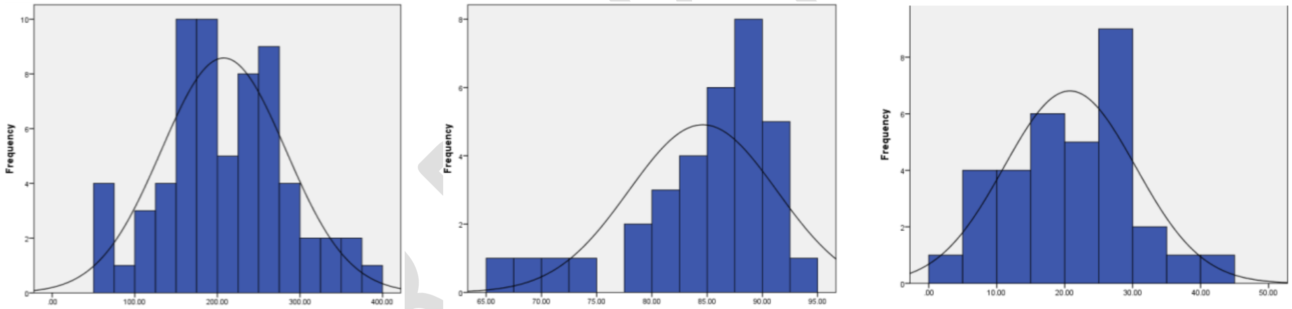
*indicates significant at 0.05 level;** indicates significant at 0.01 level; P = phenotypic correlation, G= genotypic correlation



Reproductive stage salt score **Days to 50% flowering** **Plant height (cm)**



Panicle length (cm) **Number of productive tillers** **Number of filled grains per panicle**



Total number of grains per panicle **Spikelet fertility (%)** **Grain yield per plant (g)**

Figure 1. Frequency distribution of 76 rice germplasm for all the traits under salt stress (EC 7.2 dSm^{-1}) during reproductive stage

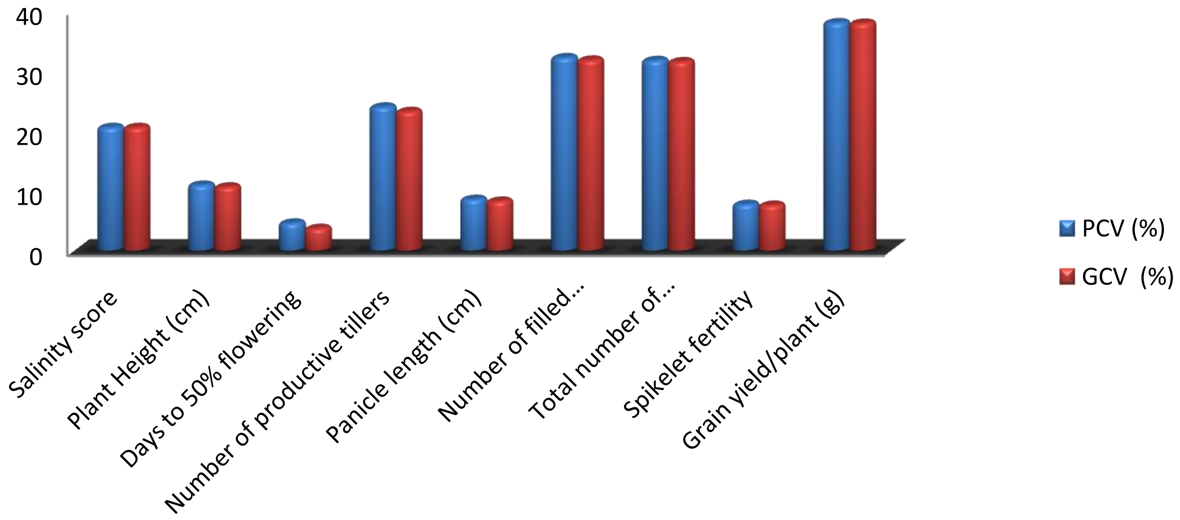


Figure 2. Variability parameters for yield and yield component traits.

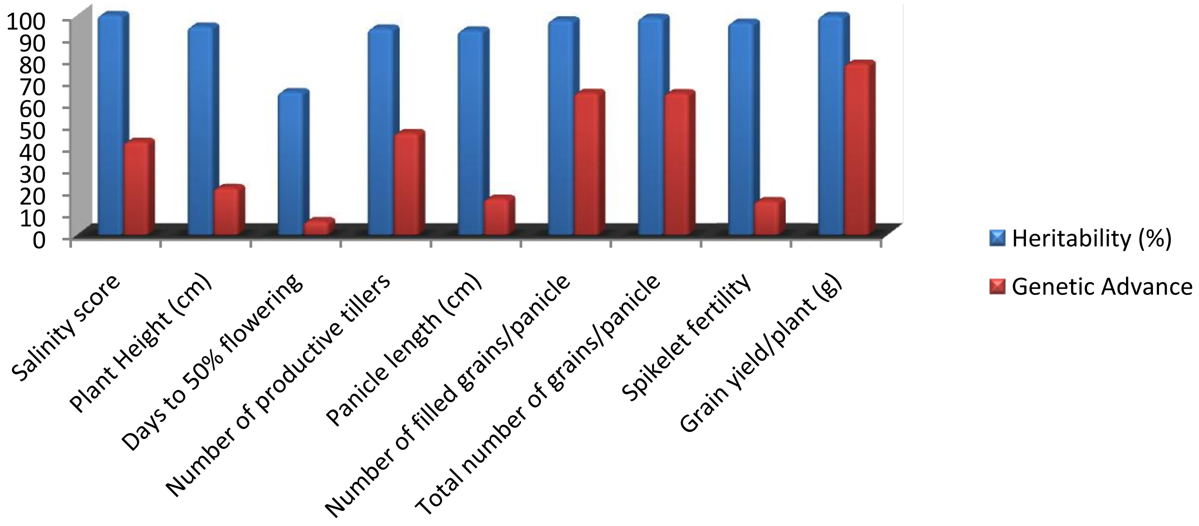


Figure 3. Heritability and Genetic advance as per cent mean for yield and yield component traits