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Research Article

Hotspot screening of early maturing rice genotypes and genetic variability studies under sodicity

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Abstract
An experiment was conducted with 39 rice genotypes to screen for salt tolerance and evaluate potential variation among the genotypes under sodic conditions. All the 39 rice genotypes along with two check varieties (TRY2 & TRY5) were screened *in vitro* for salt tolerance by imposing 100 mM $NaHCO_3$ at the seedling stage under hydroponics and a salt injury score was given based on morphological symptoms. Observations on 12 biometrical traits were recorded under field sodic conditions and subjected to variability analysis. The ANOVA revealed that there was a significant difference for the 11 traits among the genotypes except for flag leaf breadth. Among the genotypes, the highest single plant yield was recorded by RG 50 (36.83 g). A correlation study revealed that, single plant yield exhibited significant and positive genotypic and phenotypic relation with panicle harvest index, the number of grains per panicle and panicle length. Path analysis showed that the traits *viz.,* panicle harvest index, plant height and panicle length had a very high and positive direct effect on single plant yield. The traits *viz.,* flag leaf breadth, SPAD meter reading and number of productive tillers per plant had a high and positive direct effect on single plant yield. *In vitro* studies revealed that the genotype RG113 was found to be highly tolerant to salt stress and it also showed a significantly higher yield (35.42 g) under field sodicity. The genotypes RG22, RG150, RG162 and RG188 which showed tolerance under *in vitro* screening and the moderately tolerant genotypes RG26, RG50, RG95, RG107, RG123 and RG176 were exhibiting significant yield under field sodicity conditions. Therefore, in order to breed for high yielding salt-tolerant rice varieties, the identified genotypes could be exploited as donor genotypes.

Keywords: Rice, correlation, path analysis, Hydroponics, sodicity

INTRODUCTION

Rice is a staple food for around 2.5 billion people worldwide, a figure that is expected to rise to 4.6 billion by 2050 (Maclean *et al.,* 2002). Asia produces 640 million tonnes of rice which contributes 90 % of the global production, with India accounting for one-fourth of this total production. Tamil Nadu is one of the most prominent rice-growing states in India. The production and productivity of rice in Tamil Nadu are 6881.16 tonnes and 3379 kg/ha respectively (Anonymous. 2021). Rice plays a vital role in Indian agriculture and has been cultivated in a variety of ecological conditions, exposed to various abiotic stresses. Abiotic stress has a negative impact on agricultural productivity and it could cause severe yield loss of up to 70 per cent in important food crops (Waqas *et al.,* 2019).

Salt stress is one of the major abiotic stresses that affects approximately six per cent of the global farming area of nearly one billion ha (Kakar *et al.,* 2019). Salt stress inhibits plant growth and photosynthetic activity, both of which result in a drastic reduction in yield (Pardo, 2010). Rice is sensitive to salt stress during the early seedling and reproductive stages (panicle initiation, anthesis, and fertilization), but is reasonably resilient during germination, active tillering, and grain filling (Zeng *et al.,* 2001; Singh *et al.,* 2008) and (Singh and Flowers, 2010).

Table 1. Genotypes evaluated in sodicity

Genotype number	Genotype	Parentage	Origin
RG12	*Vellai chithiraikar*	Landrace	Tamil Nadu, India
RG15	*Palkachaka*	Landrace	Tamil Nadu, India
RG17	*Chivapu chithiraikar*	Landrace	Tamil Nadu, India
RG22	IR 36	IR 1561 X IR 24 x *Oryza nivara* x CR 94	IRRI, Philippines
RG26	*Rascadam*	Landrace	Tamil Nadu, India
RG33	*Malayalathan samba*	Landrace	Tamil Nadu, India
RG39	*Kaatu ponni*	Landrace	Tamil Nadu, India
RG50	*Sornavari*	Landrace	Tamil Nadu, India
RG51	RPHP 134	NJAVARA	Kerala
RG53	IR 68144-2B-2-2-3-1-127	IR 72 X ZAWA BONDAY	IRRI, Philippines
RG58	*Kodaikuluthan*	Landrace	Tamil Nadu, India
RG60	*Rama kuruvaikar*	Landrace	Tamil Nadu, India
RG67	RPHP 106	akut phou	MANIPUR
RG69	RPHP 48	Bindli	UTTARKHAND
RG76	*Matta kuruvai*	Landrace	Tamil Nadu, India
RG95	*Jeeraga samba*	Landrace	Tamil Nadu, India
RG103	*Mattaikar*	Landrace	Tamil Nadu, India
RG107	RH2-SM-1-2-1	SWARNA x MOROBERAKAN	Tamil Nadu, India
RG112	IG 35(EC 728858- 117843)	PATE BLANC MN 1	Cote D'Ivoire
RG113	IG 45(EC 728768- 117736)	FORTUNA	Puerto Rico
RG116	RPHP 27	Azucena	IRRI, Philippines
RG117	IG 65(EC 729024- 120958)	GODA HEENATI::IRGC 31393-1	SRILANKA
RG121	IG 74(EC 728622- 117517)	KINANDANG PATONG::IRGC 23364-1	IRRI, Philippines
RG123	IG 2(EC 729808-121874)	BLUEBONNET 50::IRGC 1811-1	IRRI, Philippines
RG130	IG 39(EC 728779- 117750	HONDURAS	HONDURAS
RG133	IG 42(EC 728798- 117774)	KALUBALA VEE	SRILANKA
RG134	IG 9(EC 729682- 121739)	GEMJYA JYANAM::IRGC 32411-C1	IRRI, Philippines
RG135	RPHP 161	Champa Khushi	Vietnam
RG141	IG 44(EC 728762- 117729)	EDITH	UNITED STATES
RG142	Sasyasree	TKM 6 x IR 8	West Bengal
RG150	IG 14(IC 517381- 121422)	MALACHAN::IRGC 54748-1	India
RG160	IG 72(EC 728650- 117587)	TD 25::IRGC 9146-1	Thailand
RG162	IR 64	IR-5857-33-2-1 x IR-2061-465-1-5-5	IRRI, Philippines
RG163	*Mikuruvai*	Landrace	Tamil Nadu, India
RG166	RPHP 140	VYTILLA ANAKOPON	Kerala
RG173	IG 73(EC 728627- 117527)	MAKALIOKA 34::IRGC 6087-1	IRRI, Philippines
RG176	*Kodai*	Landrace	Tamil Nadu, India
RG188	RPHP 80	24(K)	Andhra Pradesh
RG191	G 15(EC 728910- 117901)	SZE GUEN ZIM	CHINA

Heritability measures the transmission of character from parents to their offspring and plays a vital role in the selection process in plant breeding programmes. Genetic advance reveals the information on expected gain resulting from the selection of superior individuals. Heritability and genetic advance are important selection parameters that help in envisioning the gain under selection. Knowledge of association, the direct and indirect effect between yield and associated traits can be helpful in selecting superior genotypes under stress conditions. The selection and identification of tolerant genotypes aided by research on the associations and relationships between various characters and yield will serve as a basis for crop improvement (Fiyaz *et al.,* 2014). With this background, the current study was performed in rice, to assess the variability and association of different biometrical traits with yield under salt stress.

MATERIALS AND METHODS

The experimental material comprising of 39 rice germplasm (**Table 1**) was used in this study. The seeds were sown in raised bed nursery at Anbil Dharmalingam Agricultural College and Research Institute, Tamil Nadu Agricultural University, Trichy under sodic soil conditions (EC – 0.30 dSm $^{-1}$, pH – 9.58 and ESP 42.4) during *rabi*, 2021. Twenty one days old seedlings were transplanted as single seedlings per hill in the main field in 3 m rows replicated twice following a spacing of 20 × 10 cm in Randomized Blocks Design. All cultural practices were adopted as per the recommended package of practices for rice. Observations on 12 traits *viz.*, plant height (cm), the number of productive tillers per plant, flag leaf length (cm), flag leaf breadth (cm), SPAD meter reading, panicle length (cm), panicle exertion (cm), panicle harvest index (PHI), the number of grains per panicle, hundred grain weight (g), single plant yield (g) were recorded on five randomly selected plants from each replication of the genotypes and the days to 50 per cent flowering was recorded on plot basis as per Standard Evaluation System (IRRI. 1996). The mean for all the 12 biometrical characters was subjected to analysis of variance as proposed by Panse and Sukhatme (1969). A correlation was carried out as suggested by Pearson (1897). Partitioning the coefficients into both direct and indirect impacts was done as elaborated by Dewey and Lu (1959). Characterization of path coefficients was done in accordance with Lenka and Mishra (1973) recommendations. All statistical analysis was performed using GENRES software.

All the 39 rice genotypes along with two check varieties (TRY 2 & TRY 5) were screened *in vitro* for salt tolerance at the seedling stage under hydroponics following IRRI standard protocol (Gregorio, 1997) (**Table 1**). The seedlings were raised in Yoshida medium for the first 3 days followed by screening for sodicity with the addition of 100 mM $NaHCO_3$ in the same medium. Earlier, Rajasekar *et al.* (2021) found that 50 per cent mortality of rice genotypes occurs at 100 mM $NaHCO_3$ and the same has been fixed as screening for sodicity.

Salt injury score was recorded after 12 days of treatment. Based on visual symptoms like reduced growth, whitishness of lower leaves, leaf tip death, leaf drying and leaf rolling, the rice seedlings were categorized as highly tolerant, tolerant, moderately tolerant, susceptible and highly susceptible by following the IRRI standard protocol (Gregorio *et al*., 1997).

RESULTS AND DISCUSSION

The analysis of variance revealed that the mean sum of squares due to genotypes was highly significant for all the traits studied except for flag leaf breadth (**Table 2**). There was a significant difference for the 11 traits among the genotypes except for flag leaf breadth. Based on the mean performance, the highest single plant yield was recorded by RG 50 (36.83 g), while the lowest single plant yield was recorded by RG15 (8.00 g). The genotype RG12 recorded superior mean performance for a maximum number of characters *viz.,* flag leaf length, panicle length, the number of grains per panicle, 100 grain weight and grain yield per plant. The genotypes RG50, RG51, RG103, RG112, RG113, RG117, RG123 and RG141 recorded significantly superior mean performance for the trait number of productive tillers per plant. RG12, RG33, RG50 and RG112 recorded superior performance for the trait panicle length. The genotypes RG12, RG39, RG107, RG123, RG133, RG150, RG162 and RG188 recorded significantly superior mean performance for the number of grains per panicle. RG12, RG17, RG26, RG33, RG50, RG60, RG76, RG163, RG166 and RG191 registered a maximum 100 grain weight. The genotypes RG12, RG22, RG26, RG50, RG76,R G95, RG103, RG107, RG113, RG123, RG150, RG162, RG163, RG176 and RG188 recorded significantly superior single plant yield.

Table 2. Analysis of variance for yield and its component traits in rice germplasm

Source	df	Mean squares											
		DFF	PH	NPT	FLL	FLB	SPAD	PL	PE	PHI	NGP	100G Wt.	SPY
Genotypes	38	29.39**	808.45**	38.82**	83.01**	0.12	23.08**	21.48**	13.34**	0.01**	3883.43**	0.57**	134.28**
Replication	1	14.81	15.23	0.18	5.59	0.04	12.28	0.27	9.79	0.01	899.12	0.16	2.45
Error	38	2.53	10.47	4.30	11.97	0.05	1.30	3.07	6.18	0.02	204.33	0.02	3.17

** indicate significance at 1% level.

Where, DFF- Days to 50% flowering; PH- Plant height ; NPT- Number of productive tillers per plant; FLL- Flag leaf length ; FLB- Flag leaf breadth ; SPAD-Soil plant analysis development value; PL-Panicle length ; PE-Panicle exertion ; PHI-Panicle harvest index; NGP-Number of grains per panicle; 100 G wt.- 100 Grain weight ; SPY- Single plant yield.

Table 3. Mean performance of different genotypes under sodicity

S.No.	Genotypes	DFF	PH	NPT	FLL	FLB	SPAD	PL	PE	PHI	NGP	100G Wt.	SPY
1	RG12	87.00	168.80	10.17	52.92*	1.64	43.99	30.42*	5.50	0.91	214.50*	2.78*	33.67*
2	RG15	76.00*	165.67	9.00	50.25*	1.55	48.94*	24.95	6.09	0.62	64.00	1.35	8.00
3	RG17	80.00*	119.17*	9.67	36.00	1.35	43.95	20.75	3.83	0.90	67.59	2.68*	12.75
4	RG22	85.50	135.59	17.00	33.60	1.22	47.12*	22.92	0.82	0.88	123.46	2.01	28.50*
5	RG26	84.50	157.83	13.84	50.58*	1.40	50.70*	25.92	8.17	0.92	91.21	3.69*	33.25*
6	RG33	85.50	119.50*	11.34	34.00	1.40	45.85	27.88*	1.00	0.87	108.96	3.10*	26.90
7	RG39	87.50	163.67	10.50	38.50	1.55	40.99	25.17	0.92	0.88	192.75*	2.24	19.25
8	RG50	83.00	139.17	22.50*	37.67	1.27	41.19	37.09*	4.84	0.85	100.75	3.03*	36.17*
9	RG51	86.50	137.17	25.50*	46.59*	1.27	39.35	26.25	8.02	0.90	97.92	1.25	20.38
10	RG53	87.50	77.17*	16.00	22.55	1.20	53.10*	18.34	0.00	0.96*	111.59	1.74	16.05
11	RG58	77.00*	124.42*	10.00	35.59	1.59	48.50*	22.00	7.73	0.92	124.15	1.10	27.25
12	RG60	81.00	145.50	18.17	33.83	1.43	40.42	25.21	2.58	0.79	117.42	2.59*	20.85
13	RG67	83.00	148.17	12.67	36.02	1.50	41.50	25.70	7.39	0.84	125.50	2.14	21.50
14	RG69	88.00	159.00	12.17	37.42	1.54	45.52	26.42	9.55	0.79	148.92	2.05	18.75
15	RG76	86.00	139.84	18.50	37.58	1.14	42.42	24.29	4.15	0.85	95.00	2.67*	31.50*
16	RG95	87.00	131.17*	12.67	39.42	1.43	44.37	24.34	1.82	0.88	150.00	1.57	30.25*
17	RG103	85.50	140.17	20.50*	35.67	1.00	44.20	22.00	8.12	0.94	118.63	2.24	31.75*
18	RG107	83.00	148.00	12.50	44.67	1.20	44.89	27.34	7.22	0.88	171.25*	1.90	29.50*
19	RG112	77.50*	165.50	25.00*	44.84	1.14	40.99	29.92*	3.94	0.87	181.50*	2.05	25.67
20	RG113	86.50	152.17	21.84*	43.77	1.20	49.77*	23.57	6.63	0.89	123.25	2.18	35.42*
21	RG116	87.50	164.84	13.84	41.20	1.10	38.17	23.97	5.00	0.88	151.63	1.64	22.38
22	RG117	84.00	141.00	19.50*	43.52	0.92	44.40	22.27	8.94	0.82	84.00	1.85	17.75
23	RG121	80.50	146.84	14.00	36.33	0.82	49.35*	19.89	7.85	0.85	84.75	2.37	8.75
24	RG123	86.50	108.00*	21.00*	35.00	1.14	45.59	21.27	4.67	0.96	198.00*	1.86	33.25*
25	RG130	88.00	156.50	19.28	34.33	1.10	46.57	24.60	5.56	0.85	129.00	2.35	21.09
26	RG133	80.50	129.00*	12.50	38.70	1.47	47.24*	22.94	2.22	0.88	217.75*	1.37	26.88
27	RG134	84.50	134.84	14.38	36.41	0.87	44.52	22.88	7.01	0.89	54.35	2.38	15.20
28	RG135	79.50*	136.25	15.50	41.97	1.30	39.89	22.59	2.67	0.79	56.74	1.71	15.17
29	RG141	89.00	127.34*	19.84*	38.83	0.85	42.74	20.78	4.47	0.89	101.50	2.37	16.75
30	RG142	83.50	117.67*	16.00	40.25	0.79	40.80	22.24	3.10	0.84	94.00	1.97	13.00
31	RG150	86.50	147.00	7.83	52.67*	1.50	42.04	23.50	2.94	0.94	174.75*	2.24	33.09*
32	RG160	79.50*	146.83	13.00	43.34	1.00	45.79	24.59	6.80	0.86	104.50	1.83	15.50
33	RG162	88.00	89.50*	12.34	27.94	1.17	44.60	21.90	3.50	0.94	181.50*	2.27	29.50*
34	RG163	82.50	151.67	16.17	48.67*	0.88	41.65	24.62	9.50	0.86	100.00	2.41*	31.00*
35	RG166	85.50	127.34*	15.50	40.44	1.08	43.47	21.95	5.94	0.89	55.50	2.76*	12.50
36	RG173	75.50*	110.17*	12.17	36.12	1.05	43.14	23.92	5.33	0.90	104.00	2.29	26.98
37	RG176	81.50	141.50	18.17	36.84	1.07	47.09*	23.17	7.20	0.88	137.00	1.67	33.25*
38	RG188	86.00	133.25	14.17	34.17	1.35	46.22	22.80	2.52	0.90	152.75*	2.09	33.50*
39	RG191	76.00*	138.00	12.46	33.28	1.63	40.34	26.62	5.79	0.86	81.50	2.55*	14.70
	Grand mean	83.64	138.08	15.31	39.27	1.23	44.39	24.28	5.11	0.87	122.86	2.16	23.78
	C.D. (5%)	3.22	6.55	4.20	7.01	0.484	2.31	3.55	5.03	0.09	28.94	0.27	3.61
	CV	1.90	2.34	13.55	8.81	19.42	2.57	7.21	18.65	5.20	11.63	6.29	7.49

Where, DFF- Days to 50% flowering; PH- Plant height (cm); NPT- Number of productive tillers per plant; FLL- Flag leaf length (cm); FLB- Flag leaf breadth (cm); SPAD-Soil plant analysis development value; PL-Panicle length (cm); PE-Panicle exertion (cm); PHI-Panicle harvest index; NGP-Number of grains per panicle; 100 G wt.- 100 Grain weight (g); SPY- Single plant yield (g).
* Significant at 5% level

In 100 mM $NaHCO_3$ salt stress condition, the genotypes showed variations in visual symptoms. Based on this, the salt injury score was given from 1 (highly tolerant) to 9 (highly susceptible). Compared to the check varieties, the seedlings of RG113 showed high tolerance to sodicity with a salt injury score of 1. The genotypes RG22, RG51, RG67, RG116, RG133, RG150, RG162 and RG188 were observed to be tolerant to sodicity with a salt injury score of 3. The genotypes RG17, RG33, RG 50, RG60, RG69, RG95, RG107, RG117, RG123, RG135, RG142, RG160, RG166, RG176 and RG191 showed moderate tolerance compared to the check varieties with a salt injury score of 5. The genotypes RG17, RG 33, RG39, RG53, RG58, RG76, RG103, RG121, RG130, RG134, RG141, RG163 and RG173 were observed to be susceptible to sodicity compared to the check varieties with a salt injury score of 7. RG12 and RG112 showed high susceptibility to sodicity compared to the check varieties with a salt injury score of 9. Amaravel *et al.* (2019) also screened 97 rice genotypes at the seedling stage under salt stress by hydroponics system on Yoshida nutrient solution with EC of 8 dSm^{-1} and 12dSm^{-1} and identified that the genotypes *Pokkali*, FL 478, *Kuliyadichan*, Gurukot and IR12L-107 revealed a significant level of tolerance to salt stress.

The highly tolerant genotypes RG113 (35.42 g) and the tolerant genotypes RG22, RG150, RG162 and RG188 showed significant yield under field sodicity conditions. The moderately tolerant genotypes RG26, RG50, RG95, RG107, RG123 and RG176 showed significant yield under field sodicity conditions. Even though, RG15 was a moderately tolerant genotype under lab screening, it recorded a lower single plant yield (8 g) under field sodicity conditions. This may be due to susceptibility of the genotype during the reproductive stage. Hotspot screening allows genotypes to select tolerant varieties till maturity. Hitherto, 11 genotypes, RG113, RG22, RG150, RG162, RG188, RG26, RG50, RG95, RG107, RG123 and RG176, with significant yield coupled with sodicity tolerance may be used as a donor for breeding rice varieties tolerant to salt stress. A similar approach has been followed by Rajasekar *et al*. (2021) in which useful rice mutants were identified based on simultaneous screening under hydroponics and field.

In this study, PCV was observed to be higher than the GCV for all the traits observed, but their difference was a minimum except for the traits flag leaf breadth and panicle exertion (**Table 3**). This showed that, apart from flag leaf breadth and panicle exertion, all the other characters were less influenced by environmental factors. High PCV and GCV were expressed by the traits, the number of productive tillers per plant (30.33%, 27.13%), panicle exertion (61.15%, 37.04%), the number of grains per panicle (36.80%, 34.91%), 100 grain weight (24.25%, 25.05%) and single plant yield (36.80%, 34.91%) (**Table 4**). These results were similar to the findings of Venkanna *et al*., (2022) for the number of grains per panicle and 100 grain weight. The traits, plant height (14.65%, 14.47%), flag leaf length (17.55%, 15.18%), panicle length (14.43%, 12.50%) showed moderate PCV and GCV. Similarly, flag leaf breadth (24.05%, 14.19%) exhibited high PCV and low GCV. Days to 50 per cent flowering (4.78%, 4.38%) (Manjunatha *et al.,* 2017), SPAD meter reading (7.87%, 7.43%), panicle harvest index (7.67%, 5.64%) showed low PCV and GCV.

High heritability was observed for the characters, days to 50 per cent flowering, plant height, the number of productive tillers per plant, flag leaf length, SPAD meter reading, panicle length, the number of grains per panicle, 100 grain weight, and single plant yield. Similar results were reported for the characters days to 50 per cent flowering (Devi *et al.,* 2016), plant height (Lingaiah, 2018), panicle length (Devi *et al.,* 2016), the number of grains per panicle (Lingaiah *et al*., 2018) and single plant yield (Venkanna *et al.,* 2022; Lingaiah *et al*., 2018).

Knowledge of heritability is essential for selection based improvement as it indicates the extent of transmissibility of a characters into future generations (Sabesan *et al.,* 2009). High heritability was observed for all the characters studied except for flag leaf breadth, panicle exertion and panicle harvest index which showed moderate heritability. High genetic advance as per cent of mean was observed for the characters plant height, the number of productive tillers per plant, flag leaf length, panicle length, panicle exertion, number of grains per panicle, 100 grain weight and single plant yield.

The selection of traits could be more precisely done by taking into considering genetic advances along with heritability (Johnson *et al.,* 1955). High heritability coupled with high genetic advance as per cent of mean were revealed by the characters plant height (97.44%, 29.42%), the number of productive tillers per plant (80.04%, 50.01%), flag leaf length (74.78%, 27.04%), panicle length (75.01%, 22.30%), the number of grains per panicle (90.00%, 68.22%), 100 grain weight (93.70%, 48.35%) and single plant yield (95.38%, 68.49%) indicating additive gene action. The same results are in accordance with Lingaiah *et al.* (2020) (the number of grains per panicle) and Akshay *et al.* (2022) (plant height, the number of productive tiller per plant and single plant yield). High heritability coupled with low genetic advance as per cent of mean was recorded for days to 50 per cent flowering which indicated that this trait is governed by non-additive gene action, as already reported by Savitha and Ushakumari (2015).

Single plant yield exhibited significant and positive genotypic and phenotypic correlation with Panicle harvest index (0.535, 0.443), number of grains per panicle (0.556, 0.547) and panicle length (0.348, 0.352) (**Table 5**). Similar results were reported by Parimala and Devi (2016), Abhilash *et al.* (2018) and Kalaiselvan *et al.* (2019). Except for panicle exertion, all other traits showed a

Table 4. Variability parameters for biometrical and physiological traits in rice genotypes

S.No.	Characters	Mean	Range		Coefficient of variation		h^2(%)	GAM (%)
			Maximum	Minimum	GCV(%)	PCV(%)		
1	Days to 50 per cent flowering	83.64	89.00	75.50	4.38	4.78	84.14	8.28
2	Plant height (cm)	138.08	168.80	77.17	14.47	14.65	97.44	29.42
3	Number of productive tillers per plant	15.31	25.50	9.00	27.13	30.33	80.04	50.01
4	Flag leaf length (cm)	39.27	52.92	22.55	15.18	17.55	74.78	27.04
5	Flag leaf breadth (cm)	1.23	1.64	0.79	14.19	24.05	34.82	17.25
6	SPAD meter reading	44.39	53.10	38.17	7.43	7.87	89.32	14.47
7	Panicle length (cm)	24.28	37.09	18.34	12.50	14.43	75.01	22.30
8	Panicle exertion (cm)	5.11	9.55	0.00	37.04	61.15	36.70	46.23
9	Panicle Harvest Index	0.87	0.96	0.62	5.64	7.67	54.05	8.54
10	Number of Grains per panicle	122.86	214.50	54.35	34.91	36.80	90.00	68.22
11	100 grain weight (g)	2.16	3.69	1.10	24.25	25.05	93.70	48.35
12	Single plant yield (g)	23.78	36.17	8.00	34.04	34.86	95.38	68.49

positive association with yield. This is in accordance with the findings of Rajeswari and Nadarajan, (2004). Days to 50 per cent flowering was observed to be significant and positively correlated with Panicle harvest index (0.447), while it exhibited a negative correlation with plant height (-0.072), panicle length (-0.123), flag leaf length (-0.131) and panicle exertion (-0.291).

Plant height had a strong negative correlation with Panicle harvest index (-0.561) which is also reported by Li *et al.* (2012) and it also had a strong positive significant correlation with flag leaf length (0.714), panicle length (0.507) and panicle exertion (0.544). Flag leaf length was significant and positively correlated with panicle length (0.315). Similar results were reported by Rahman *et al.* (2013) and it was highly significant and positively correlated with panicle exertion (0.432). Flag leaf breadth recorded a significant and positive correlation with panicle length (0.359) and grains per panicle (0.413).

Panicle length showed a highly significant and negative correlation with the Panicle harvest index and it showed a positive and significant correlation with 100 grain weight as also reported by Li *et al.,* (2012). Panicle harvest index

Table 5. Genotypic and phenotypic correlation coefficients among yield and associated traits in rice germplasm

Traits	DFF	PH	NPT	FLL	FLB	SPAD	PL	PE	PHI	GPP	100G	SPY
DFF	**1.000**	-0.072	0.207	-0.131	-0.204	0.037	-0.123	-0.291	0.447**	0.304*	0.170	0.285
PH	-0.060	**1.000**	-0.005	0.714**	0.280	-0.226	0.507**	0.544**	-0.561**	0.105	0.085	0.040
NPT	0.164	0.012	**1.000**	-0.145	-0.771	-0.181	0.130	0.122	0.084	-0.139	-0.014	0.175
FLL	-0.061	0.637**	-0.007	**1.000**	0.074	-0.225	0.315*	0.432**	-0.346*	0.002	0.026	0.100
FLB	-0.067	0.173	-0.339*	0.118	**1.000**	-0.022	0.359**	-0.547**	-0.343*	0.413**	-0.019	0.194
SPAD	0.013	-0.213	-0.141	-0.160	0.057	**1.000**	-0.400**	0.049	0.125	-0.007	-0.036	0.067
PL	-0.084	0.460**	0.148	0.376**	0.360**	-0.298	**1.000**	0.121	-0.359**	0.149	0.338*	0.348*
PE	-0.103	0.320*	0.157	0.358**	-0.113	0.042	0.084	**1.000**	-0.211	-0.391**	0.033	-0.067
PHI	0.363**	-0.375**	0.101	-0.175	-0.034	0.117	-0.137	-0.112	**1.000**	0.397**	0.169	0.535**
GPP	0.312*	0.102	-0.059	0.081	0.301*	0.006	0.207	-0.196	0.358**	**1.000**	-0.216	0.556**
100G	0.167	0.101	-0.031	0.047	-0.015	-0.052	0.330*	-0.021	0.153	-0.182	**1.000**	0.173
SPY	0.267	0.045	0.192	0.151	0.156	0.069	0.352*	-0.009	0.443**	0.547**	0.172	**1.000**

*and ** indicate significance at 5% and 1% levels, respectively

Where, DFF- Days to 50% flowering; PH- Plant height ; NPT- Number of productive tillers per plant; FLL- Flag leaf length ; FLB- Flag leaf breadth ; SPAD-Soil plant analysis development value; PL-Panicle length ; PE-Panicle exertion ; PHI-Panicle harvest index; NGP-Number of grains per panicle; 100 G wt.- 100 Grain weight ; SPY- Single plant yield.

Table 6. Direct and indirect effects of yield associated components on grain yield at genotypic level

Traits	DFF	PH	NPT	FLL	FLB	SPAD	PL	PE	PHI	GPP	100G Wt.	Correlation co-efficient for SPY
DFF	**-0.226**	-0.113	0.081	-0.009	-0.137	0.023	-0.130	0.249	1.169	-0.456	-0.167	0.285
PH	0.016	**1.563**	-0.002	0.052	0.188	-0.141	0.537	-0.466	-1.467	-0.157	-0.083	0.040
NPT	-0.047	-0.007	**0.394**	-0.010	-0.518	-0.113	0.138	-0.104	0.220	0.209	0.014	0.175
FLL	0.030	1.116	-0.057	**0.072**	0.049	-0.140	0.334	-0.371	-0.904	-0.003	-0.026	0.100
FLB	0.046	0.438	-0.304	0.005	**0.671**	-0.014	0.381	0.469	-0.897	-0.620	0.019	0.194
SPAD	-0.008	-0.353	-0.071	-0.016	-0.015	**0.623**	-0.423	-0.042	0.328	0.010	0.035	0.067
PL	0.028	0.792	0.051	0.023	0.241	-0.249	**1.059**	-0.104	-0.939	-0.224	-0.331	0.348*
PE	0.066	0.850	0.048	0.031	-0.367	0.030	0.129	**-0.857**	-0.552	0.587	-0.032	-0.067
PHI	-0.101	-0.876	0.033	-0.025	-0.230	0.078	-0.380	0.181	**2.617**	-0.596	-0.165	0.535**
GPP	-0.069	0.163	-0.055	0.001	0.277	-0.004	0.158	0.335	1.040	**-1.501**	0.211	0.556**
100G Wt.	-0.039	0.133	-0.006	0.002	-0.013	-0.022	0.358	-0.028	0.442	0.324	**-0.979**	0.173

RESIDUAL EFFECT = 0.2639

Where, DFF- Days to 50% flowering; PH- Plant height ; NPT- Number of productive tillers per plant; FLL- Flag leaf length ; FLB- Flag leaf breadth ; SPAD-Soil plant analysis development value; PL-Panicle length ; PE-Panicle exertion ; PHI-Panicle harvest index; NGP-Number of grains per panicle; 100 G wt.- 100 Grain weight ; SPY- Single plant yield.

showed a highly significant and positive correlation with grains per panicle. A similar result was also reported by Li *et al.* (2012). In the present study, it was observed that all the 39 rice genotypes exhibited considerable variability for most of the qualitative traits and hence they could be exploited as genetic stocks for crop improvement.

The study revealed that panicle harvest index I (2.617), plant height (1.563) and panicle length (1.059) had a very high and positive direct effect on yield (**Table 6**). Flag leaf breadth (0.671), SPAD meter reading (0.623) and the number of productive tillers per plant (0.394) showed a high and positive direct effect on single plant yield. Similar results were earlier reported for the characters *viz.,* the number of productive tillers per plant and plant height by Fiyaz *et al.* (2011). The direct effect of grains per panicle on yield was negative (-1.501) but it showed a high indirect positive effect through on panicle harvest index (1.040).The trait 100 grain weight had a direct negative effect on yield (-0.979) but it showed a high and positive indirect effect through panicle harvest index (0.442), panicle length (0.358) and the number of grains per panicle (0.324). The residual effect is low (0.2639), since the studied traits had limited contribution towards grain yield of rice.

The genotype, RG113 (IG 45(EC 728768- 117736) showed high tolerance to salt stress under *in-vitro* screening besides significant yield (35.42 g) under the field for sodicity. The genotypes, RG22, RG150, RG162 and RG188 were tolerant and showed significant yield. Six genotypes, RG26, RG50, RG95, RG107, RG123 and RG176 were moderately tolerant with significant yield. Hence, all these genotypes with significant yield under sodicity may be used as donors for breeding rice varieties tolerant to salt stress.

Four traits namely, number of productive tillers per plant, number of grains per panicle, 100 grain weight and single plant yield showed high PCV, GCV and High heritability coupled with high genetic advance as per cent of mean. PCV was observed to be higher than the GCV for all these traits, but their difference was minimum. This showed that, all these characters were less influenced by environmental factors. Considering these characters will be rewarding in the selection of genotypes under salt stress conditions. Genotypic and phenotypic correlation coefficient indicated that single plant yield exhibited significant and positive genotypic and phenotypic correlation with panicle harvest index, the number of grains per panicle and panicle length. Path coefficient analysis indicated the importance of panicle harvest index, plant height, panicle length, flag leaf breadth, SPAD meter reading, the number of productive tillers per plant through a positive direct effect on single plant yield. The present study highlighted the importance of the traits *viz.,* the number of productive tillers per plant, the number of grains per panicle, panicle harvest index, plant height, panicle length, flag leaf breadth, SPAD meter reading, 100 grain weight and single plant yield. These traits can be used in selecting parents for a salt tolerant breeding programme in rice.

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