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Research Article

Deciphering combining ability for yield and its components under saline environment in rice (*Oryza sativa* L.)

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Abstract

Line x tester analysis was performed with six lines and four testers and resulted 24 hybrids along with parents were evaluated for salinity conditions. Analysis of variance showed significant differences between lines, testers and crosses for all the parameters except 1000 grain weight. SCA mean squares were substantially larger than GCA mean squares, showing a prevalence of dominance gene action in parents and hybrids for tolerance to salinity conditions. Among the lines and testers, KPS 10642, KPS 10640, KPS 10651, RNR 11718 and CSR 36 were proven to be a good combiners for increasing yield under salt stress conditions. The hybrids viz., KPS 10651 x CSR 36, KPS 10651 x RNR 11718, KPS 10642 x KPS 2874, KPS 10651 x CSR 23, KPS 10640 x CSR 36, KPS 10640 x CSR 23, KPS 10642 x RNR 11718, KPS 10642 x CSR 36 and KPS 10642 x CSR 23 were found to be good specific combiners. The crosses KPS 10651 x RNR 11718, KPS 10642 x KPS 2874, KPS 10651 x CSR 36, KPS 10651 x CSR 23 and KPS 10640 x CSR 36 demonstrated significant results with respect to mean and *sca* effects.

Keywords: Rice, combining ability, hybrid, line x tester, salinity

INTRODUCTION

Rice is prone to a range of abiotic stresses like drought, salinity, flooding, temperature extremes and heavy metal stress, to name a few and all of these have an impact on plant growth and yield. Of these, soil salinity is having a major impact at the global level on rice production and productivity with yield losses upto 30–50% annually (Eynard *et al.*, 2005). It is highly sensitive at the seedling and reproductive stages. Despite being a glycophyte, it is observed to show susceptibility to saline conditions throughout the vegetative stage. This is due to the changes that occur in the plant physiological processes which effect the growth, development and yield especially during the pollination and fertilisation stages (Reddy *et al.*, 2017). These physiological changes delay

heading stage in rice, which further decreases other yield components (Grattan *et al.*, 2002). Salinity in the soil can be controlled by using reclamation techniques, which may raise production costs. As a result, saline-tolerant cultivars must be developed *i.e.*, plants having in-plant resistance against salinity would be the best alternative. Salt tolerance being a polygenic trait is controlled by many genes. Combining ability determines the pattern of genetic effects in the manifestation of quantitative traits by identifying possibly superior parents and hybrids (Zhang *et al.*, 2015). For selecting ideal parents, the breeder has access to multiple of biometrical methods. Combining ability analysis is a prominent tool amid various breeding tools to analyze combining ability

effects and helps in the selection of appropriate parents and crosses for heterosis exploitation (Gopikannan and Ganesh, 2013). The combining ability of the parents simply, General Combining Ability (*gca*) is caused by additive gene effects and additive x additive epistasis. Whilst, the combining ability of hybrids, i.e., Specific Combining Ability (*sca*) is caused by a non-additive gene effect that can be caused by dominance, epistasis, or both, and is irreversible (Koze, 2017). The goal of this experiment was to examine the combining ability in hybrids and rice parental lines for seed yield and yield components under salinity conditions to aid in the selection of parents and breeding rice cultivars that can withstand salinity stress.

MATERIALS AND METHODS

The salinity tolerant parental lines were chosen based on prior screening experiments, and their yield performance was validated under salinity conditions with E.C. 4ds/m and pH 9.2. A total of 24 test crosses were developed by following Kempthorne (1957), Line x Tester method using six lines and four testers. The hybrids, testers and lines (Table 1) were evaluated along with check varieties at Agricultural Research Station, Kampasagar at Nalgonda during *Rabi*, 2019-2020.

The experiment was carried out under salt stress circumstances following appropriate management practices in a randomized complete block design (RCBD) with three replications during *Kharif*, 2021. Twenty-five days old seedlings were transplanted into the screening experiment field with a spacing of 20 x 15 cm. Parameters for yield and its attributing features were observed, days to 50% flowering and seedling mortality were collected on a plot basis. During the reproductive stage, visual scoring

of salt injury was also recorded according to IRRI-SES 2013 (Table 2). 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. The GCA and SCA variances were calculated using the method given by Kempthorne (1957). The general and specific combining ability effects of Sprague and Tatum (1942) were utilized to find good combiners among parental genotypes and good combiners from crosses. INDOSTAT version 9.2 was used to conduct the statistical analysis.

RESULTS AND DISCUSSION

Hybrids were classified into different categories based on visual SES scores. Out of 24 hybrids, three were categorised as highly tolerant, five as tolerant, six as moderately tolerant and ten as sensitive under saline conditions at ARS, Kampasagar (Table 3). Similarly, Sudharani *et al.* (2013) classified the newly developed rice hybrids into different categories based on their reaction to salinity.

Analysis of variance showed significant differences for all the traits, which indicates that presence of considerable genetic variability among the experimental material under study. Line mean squares were significant for all the parameters except for panicle length, un-filled grains per panicle, 1000 grain weight and spikelet sterility. In case of

Table 1. List of parents and check varieties utilized in the experiment

S.No.	GENOTYPES	S.No.	GENOTYPES	S.No.	GENOTYPES
	LINES		TESTERS		CHECKS
1.	KPS 10628	1.	CSR 23	1.	MTU 1010
2.	KPS 10631	2.	CSR 36	2.	BPT 5204
3.	KPS 10633	3.	KPS 2874	3.	IR 64
4.	KPS 10640	4.	RNR 11718		
5.	KPS 10642				
6.	KPS 10651				

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

Table 3. Grouping of 24 hybrids based on its visual salt injury score

S.No.	Hybrid	Salt injury score	Reaction	S.No.	Hybrid	Salt injury score	Reaction
1.	KPS 10628 x CSR 23	5	MT	13.	KPS 10640 x CSR 23	7	S
2.	KPS 10628 x CSR 36	3	T	14.	KPS 10640 x CSR 36	1	HT
3.	KPS 10628 x KPS 2874	3	T	15.	KPS 10640 x KPS 2874	3	T
4.	KPS 10628 x RNR 11718	5	MT	16.	KPS 10640 x RNR 11718	1	HT
5.	KPS 10631 x CSR 23	7	S	17.	KPS 10642 x CSR 23	7	S
6.	KPS 10631 x CSR 36	1	HT	18.	KPS 10642 x CSR 36	7	S
7.	KPS 10631 x KPS 2874	7	S	19.	KPS 10642 x KPS 2874	3	T
8.	KPS 10631 x RNR 11718	7	S	20.	KPS 10642 x RNR 11718	7	S
9.	KPS 10633 x CSR 23	3	T	21.	KPS 10651 x CSR 23	7	S
10.	KPS 10633 x CSR 36	7	S	22.	KPS 10651 x CSR 36	5	MT
11.	KPS 10633 x KPS 2874	7	S	23.	KPS 10651 x KPS 2874	5	MT
12.	KPS 10633 x RNR 11718	5	MT	24.	KPS 10651 x RNR 11718	5	MT

HT- Highly Tolerant

T- Tolerant

MT- Moderately Tolerant

S- Susceptible

testers, the traits viz., mortality percentage, the number of productive tillers, the number of grains per panicle, un-filled grains per panicle and 1000 grain weight had significant differences, while the other parameters had non significance. Such results indicated a wide range of variability among parental lines and testers. In addition, tester mean squares were much higher than those of lines for the total number of grains per panicle, the number of un-filled grains per panicle, spikelet sterility percentage, 1000 grain weight and seed yield per plant of the studied traits. Such results revealed that testers contributed much more to the total variation as compared to lines. The interaction between lines and testers showed significance for all the traits. Crosses mean squares were significant for all the studied characteristics except panicle length and 1000 grain weight, indicating the wide diversity among the material utilized in the experiment.

The results of this investigation revealed that most of the traits, showed ratios of GCA/SCA variances were <1 and σ^2 SCA helps in determining the inheritance of most of the examined traits, suggesting that non-additive gene action accounted for the major portion of the total genetic variability associated with these parameters (Table 4). Mortality percentage, days to 50% flowering, plant height, panicle length, un-filled grains per panicle, 1000 grain weight and seed yield per plant were all influenced by non-additive gene action. Heterosis breeding helps in the improvement of these parameters with non-additive gene action. Many researchers Saidaiah *et al.* (2010), Thorat *et al.* (2017), Singh *et al.* (2020) and Sandhya kishore *et al.* (2017), reported that σ^2 SCA was important in the inheritance of seed yield per plant and other yield traits in rice. The parameters controlled by additive gene action were the number of productive tillers, the number

of grains per panicle and spikelet sterility and these traits can be improved by employing pureline selection or pedigree breeding. Similar results are reported that σ^2 GCA was important in the inheritance of these parameters by Widyastuti *et al.* (2017) and Zewdu *et al.* (2020) while studying rice hybrids.

General combining ability, which is also the parent's breeding value, has proven to be a beneficial technique for selecting parents for hybridization, whereas specific combining ability aids in the identification of superior cross combinations. The results of *gca* effects on parental phenotypes have been represented in Table 5. Low per cent of mortality and reduced number of days to 50% flowering with negative *gca* effects are desirable in the view of developing hybrids. CSR 23, CSR 36, KPS 10631 and KPS 10651 showed negative significant among the parents for the trait mortality percentage and KPS 10651, KPS 10642, CSR 36 and KPS 2874 for the trait days to 50% flowering. The highest seed yield is the economic character for the hybrids to adopt more even under stress conditions. The genotypes KPS 10651, KPS 10640 and KPS 2874 recorded highly positive significant *gca* effects for seed yield. Among the parental genotypes, KPS 10651 and KPS 10640 were found to be a good general combiner for the traits viz., the number of productive tillers, the number of grains per panicle and seed yield with positive significant *gca* effects. Lower spikelet sterility was desirable for improving yield. The parents KPS 10642, KPS 10640 and KPS 10651 were found to be good combiners for spikelet sterility with significant negative *gca* effects. Unfilled grain should be less in number or negligible for the enhancement of economic yield under stress conditions. For this, the parents should have negative *gca* effects. Line KPS 10642 was recorded

Table 4. ANOVA for combining ability (line x tester) for yield and its components

Source of variation	Degrees of freedom	Mortality	Days to 50% flowering	Plant height	Panicle length	Number of productive tillers/m ²	Total number of grains/panicle	Number of unfilled grains/panicle	Spikelet sterility	1000 grain weight	Seed yield/plant
Replication	2	5.88*	18.07	5.62	5.06	3818.87	66.66	982.26**	189.30*	1.351	8.36
Treatments	33	252.67**	47.19**	270.77**	10.53	58045.84**	9355.17**	994.90**	364.13**	1.197	43.03**
Parents	9	325.65**	35.50*	520.96**	7.50	29657.95**	10955.00**	454.90*	99.10*	1.344	2.69
Parents (Lines)	5	419.25**	42.76*	926.49**	9.67	41173.88**	6498.93**	281.39	90.94	1.281	1.39
Parents (Testers)	3	278.07**	32.97	12.55	5.98	19179.40*	21663.42**	795.19**	113.50	1.879	4.81
Parents vs Crosses	1	1559.52**	122.26**	178.16**	7.35	531083.55**	32753.10**	342.13	643.89**	0.316	214.78**
Crosses	23	167.29**	48.51**	176.89**	11.86	48587.29**	7711.85**	1234.58**	455.68**	1.177	51.35**
Line x Tester effect	15	171.50**	37.14**	156.01**	11.95	17713.35**	2220.92**	618.56**	178.58**	1.093	29.11**
Error	66	1.57	14.01	19.39	7.01	6120.73	424.48	178.07	47.47	2.05	6.07
σ^2_{gca}		8.78	3.29	13.72	0.27	5356.86	949.30	117.67	50.25	0.06	5.21
σ^2_{sca}		56.64	7.71	45.54	1.64	3864.21	598.82	146.82	43.70	0.32	7.68
$\sigma^2_{gca}/\sigma^2_{sca}$		0.16	0.43	0.30	0.16	1.39	1.59	0.80	1.15	0.19	0.68

* significant at 5 per cent level

** significant at 1 per cent level

Table 5. General combining ability (gca) for yield and its components

Parents	Mortality	Days to 50% flowering	Plant height	Panicle length	Number of productive tillers/m ²	Total number of grains/panicle	Number of unfilled grains/panicle	Spikelet sterility	1000 grain weight	Seed yield/plant
LINES										
KPS 10628	4.257**	2.764 *	2.822*	-1.080	-123.567**	-41.806**	18.264 **	13.929**	-0.306	-5.282**
KPS 10631	-2.181**	-0.236	-1.103	-1.470	-122.192 **	-33.389**	16.014 **	10.838**	-0.522	-1.782*
KPS 10633	0.541	3.847**	5.256**	0.590	-22.642	-26.639**	4.347	3.529	0.569	0.318
KPS 10640	-0.496	-1.486	-5.769**	0.438	53.258 *	20.611**	-13.069 **	-8.396**	-0.039	2.460**
KPS 10642	4.999**	-1.903	-2.586 *	1.363	27.958	-6.222	-27.736 **	-13.913**	-0.114	0.835
KPS 10651	-7.120**	-2.986**	1.381	0.163	187.183 **	87.444**	2.181	-5.988**	0.411	3.451**
TESTERS										
CSR 23	-0.598*	1.986 *	-1.214	0.360	8.250	-0.806	-1.097	-1.004	-0.089	-1.076
CSR 36	-1.366**	-1.236	4.875 **	-0.918	-27.867	7.528	0.625	1.057	0.050	-1.576 **
KPS 2874	1.536**	-0.847	0.581	0.626	5.317	-11.583 *	3.736	2.751	0.011	2.024 **
RNR 11718	0.429	0.097	-4.242**	-0.068	14.300	4.861	-3.264	-2.804	0.028	0.629
SE (Line)	0.362	1.080	1.271	0.764	22.585	5.948	3.852	1.989	0.413	0.711
SE (Tester)	0.296	0.882	1.038	0.624	18.440	4.856	3.145	1.623	0.338	0.581

* - significant at 5 per cent level

** - significant at 1 per cent level

with the highest significant negative value followed by KPS 10640. The findings of Saravanan *et al.* (2018), Sanjay singh *et al.* (2008), Sudharani *et al.* (2013) and Nanditha *et al.* (2021) reported similar results in rice.

Parents exhibiting good *gca* were utilized to develop better performing hybrids as these genotypes possess good inherent potential. The lines KPS 10640, KPS 10651

and the tester RNR 11718 and CSR 36 were determined to be good combiners. Hence, genotypes showing high *gca* are exploited for pedigree breeding to obtain superior recombinants. *sca* is most often linked to non-additive gene action caused by dominance, over-dominance, or epistatic effects. There was no hybrid cross that simultaneously achieved beneficial *sca* effects for all of the examined traits, similar to the results shown for *gca*

effects of parents. The estimates of the *sca* of 24 hybrids for ten characters are represented in **Table 6**. The specific combining ability is due to non-additive gene action and epistatic gene action (Sprague and Tatum, 1942). The usefulness of a particular cross in the exploitation of heterosis is judged by the *sca* effects.

The cross combinations which recorded less mortality per cent are KPS 10631 x KPS 2874 followed by KPS 10651 x RNR 11718 with negative significant *sca* effects. It indicates a high probability to identify the low per cent of mortality under stress conditions in these combinations. Both the crosses involved low x low combining parents indicating over dominance or epistatic interactions. Among the crosses, KPS 10633 x KPS 2874 followed by KPS 10640 x CSR 23 showed the highest positive

significant *sca* effect. The *gca* effects were low x low in both the crosses, indicating that beneficial genes given by parents were interacting. The highest positive significance was observed in the cross KPS 10640 x CSR 23 with high x low combiner effects reporting the likely hood of interaction between beneficial and negative alleles was highly desirable for the trait number of productive tillers followed by KPS 10640 x CSR 36 with high x high combiner effects preponderance additive x additive gene action. These estimates were collinear with the findings of Khute *et al.* (2015), Waza *et al.* (2015), Prajapati and Kathiria (2018) in rice.

The highest negative significant *sca* effect was observed for the cross KPS 10633 x KPS 2874 followed by cross KPS 10651 x CSR 36 which were negative non-significant

Table 6. Specific combining ability (*sca*) of crosses for yield and its components

Crosses	Mortality	Days to 50% flowering	Plant height	Panicle length	Number of productive tillers/m ²	Total number of grains/panicle	Number of unfilled grains/panicle	Spikelet sterility	1000 grain weight	Seed yield/plant
KPS 10628 x CSR 23	-3.101**	4.014	4.222	0.357	-24.750	10.639	-2.653	-3.529	0.506	2.943 *
KPS 10628 x CSR 36	3.901 **	-0.764	-5.900 *	-1.099	54.267	-9.028	-2.042	-1.524	-0.833	0.710
KPS 10628 x KPS 2874	-3.102**	1.181	-5.439 *	1.857	-17.417	-3.583	14.847	11.649 **	-0.028	-2.224
KPS 10628 x RNR 11718	2.302 **	-4.431 *	7.117 **	-1.115	-12.100	1.972	-10.153	-6.596	0.356	-1.429
KPS 10631 x CSR 23	5.187 **	3.014	8.847 **	0.149	-21.725	4.556	-13.403	-7.371	-0.278	-1.890
KPS 10631 x CSR 36	11.336**	2.569	-0.642	-0.574	27.592	-8.111	14.875	7.735	-0.017	-0.957
KPS 10631 x KPS 2874	-11.667**	-4.819 *	-7.181 **	-0.185	10.908	4.667	-5.569	-2.593	0.456	2.943 *
KPS 10631 x RNR 11718	-4.856**	-0.764	-1.025	0.610	-16.775	-1.111	4.097	2.229	-0.161	-0.096
KPS 10633 x CSR 23	-4.549**	-2.403	5.756 *	-3.976 *	-104.775*	-0.861	17.264 *	9.238 *	-0.403	-4.524 **
KPS 10633 x CSR 36	-6.780**	-2.514	-4.700	-1.165	-30.158	-19.528	15.208	9.076 *	0.392	-2.157
KPS 10633 x KPS 2874	4.994 **	3.097	0.128	1.290	110.458*	21.250	-18.569 *	-11.385 **	0.164	3.776 *
KPS 10633 x RNR 11718	6.335 **	1.819	-1.183	3.851 *	24.475	-0.861	-13.903	-6.929	-0.153	2.904 *
KPS 10640 x CSR 23	-2.491 **	-0.069	-7.919 **	0.407	98.725*	39.556 **	7.014	1.029	-0.394	2.435
KPS 10640 x CSR 36	-6.663**	2.486	2.492	0.918	52.342	37.889 **	-6.042	-5.299	0.967	2.101
KPS 10640 x KPS 2874	2.852 **	-1.236	1.786	-1.260	-28.142	-41.667 **	-1.486	1.607	-0.661	-4.965 **
KPS 10640 x RNR 11718	6.302 **	-1.181	3.642	-0.065	-122.925**	-35.778 **	0.514	2.663	0.089	0.429
KPS 10642 x CSR 23	2.187 **	-3.653	-5.003	2.482	-20.075	-47.278 *	3.014	3.813	0.614	3.293 *
KPS 10642 x CSR 36	3.706 **	0.903	-0.692	1.193	-59.858	4.722	-1.708	-2.115	-0.658	-2.607
KPS 10642 x KPS 2874	-4.233**	-2.486	2.436	-1.451	23.558	28.833 *	-7.486	-5.043	0.647	0.493
KPS 10642 x RNR 11718	-1.659 *	5.236 *	3.258	-2.224	56.375	13.722	6.181	3.346	-0.603	-1.179
KPS 10651 x CSR 23	2.766 **	-0.903	-5.903 *	0.582	72.600	-6.611	-11.236	-3.179	-0.044	-2.257
KPS 10651 x CSR 36	-5.499**	-2.681	9.442 **	0.726	-44.183	-5.944	-20.292 *	-7.874	0.150	2.910 *
KPS 10651 x KPS 2874	11.156**	4.264	8.269 **	-0.251	-99.367*	-9.500	18.264 *	5.765	-0.578	-0.024
KPS 10651 x RNR 11718	-8.424**	-0.681	-11.808 **	-1.057	70.950	22.056	13.264	5.288	0.472	-0.629
SE hybrids	0.724	2.161	2.543	1.529	45.169	11.895	7.704	3.978	0.827	1.423

* significant at 5 per cent level

** significant at 1 per cent level

desirable for the trait mortality percentage. In the above crosses *sca* effect was expressed in a significant direction due to the interaction between the favourable alleles contributed by the parents even though they were poor combiners showing low \times low *gca* effect. These results were in accordance with Bedi and Sharma (2014), and Thorat *et al.* (2017) in rice. The cross KPS 10633 \times KPS 2874 recorded the highest positive significance which is desirable for seed yield and important for the hybrid with low \times high combiner effects reporting the possibility of interaction between negative and beneficial alleles followed by cross KPS 10642 \times CSR 23 having low \times low *gca* effects preponderance the presence of over dominance or epistatic interactions. These results were in line with that of Sala *et al.* (2016), Satheesh kumar and Saravanan, (2012), Thorat *et al.* (2017) and Ambikabathy *et al.* (2019) in rice. Hence, the hybrids obtained from these crosses can be forwarded to further generations for improving desired traits.

Based on *gca* and *sca* effects, KPS 10642 \times KPS 2874, KPS 10640 \times CSR 23, KPS 10651 \times CSR 36 and KPS 10651 \times CSR 23 were found to be the best hybrids. Hence, the above hybrids can be exploited in future breeding programs related to salt stress.

Under salt stress, the experiment investigates the association between the number of productive tillers and the number of grains per panicle and seed yield. The findings cleared the door for additional advancements in salt tolerance in high-salinity environments. The best combiners identified could be utilized as parents for creating a mapping population for QTL mapping. KPS 10640 \times CSR 23, KPS 10651 \times CSR 36 and KPS 10651 \times CSR 23 were the best hybrid combinations. These prospective crossings, which were found as overall high general combiners, might be used to develop synthetic varieties or an elite breeding population by enabling new genetic recombination among them and then subjecting the resultant population to recurrent selection.

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