

Combining Ability Studies for Rice (*Oryza sativa* L.) under Coastal Saline Soil Conditions

M Sudharani, P Raghava Reddy, V Ravindrababu, G Hariprasad Reddy and Ch Surendra Raju Seed Research and Technology Centre, Rajendranagar, Hyderabad-30

ABSTRACT

Combining ability study of yield contributing and salt tolerance related physiological traits from the diallel analysis of eight varieties under saline soil conditions revealed the predominance of *sca* variance than *gca* variance for all the characters studied except yield reduction per cent, suggesting the significant role of non-additive gene action for majority of the parameters. Under saline soils, SR26B was adjudged as the best general combiner coupled with high *per se* performance for twelve traits *viz.*, total and productive tillers, panicle length, panicle weight, number of filled grains panicle⁻¹,1000-grain weight, grain yield, low visual salt injury, harvest index, low Na⁺/ K⁺ ratio, SPAD readings and low yield reduction, while CSRC(S)7-1-4 was the next best general combiner which showed high *gca* and *per se* for six traits *viz.*, number of tillers plant⁻¹, panicle weight, number of filled grains panicle⁻¹, test weight, root/shoot ratio and Na⁺/ K⁺ ratio. Further, CSRC(S) 5-2-2-5 was also found to be promising for six traits *viz.*, number of tillers plant⁻¹, number of filled grains panicle⁻¹, spikelet fertility, test weight, low visual salt injury and low yield reduction. Hence, these parents could be exploited for development of salt tolerant high yielding varieties.

Key words: Combining ability, Rice, Saline soils.

Rice ($Oryza\ sativa\ L$.) is the most important food crop in the world, which accounts for more than 21% of the calorific needs of the world's population (Ma et al., 2007 and Melissa et al., 2009). Though significant improvement in productivity has been achieved over the years, but a series of biotic and abiotic stresses limits its productivity worldwide. Abiotic stresses alone contributes to 50 per cent of the total yield losses. High salt concentration in soil is the major constraint to rice production in Bangladesh and India (Mohammadi-Nejad et al., 2008). Nearly 20 per cent of the world's cultivated area (800 Million ha) and half of the world's irrigated lands are affected by salinity (Zhu et al., 2001 and Maser et al., 2002). In India, nearly 8.5 Million ha are salt affected. Out of which 2.19 Million ha are under coastal saline situation and the yield reduction is estimated to the tune of 30 – 50 per cent (Babu et al., 2005). Salinity and sodicity are gradually becoming constraints to rice production in coastal region of Andhra Pradesh. The salt affected soils in Andhra Pradesh are estimated to be 2.74 lakh ha (NRSC, 2010). Investigation of the effects of salinity on rice have been underway for more than 50 years (McWilliam, 1966) and attempts to enhance the salt tolerance in rice through breeding started from the early 1970s (Akbar *et al.*, 1972). Therefore, increasing the yield of rice in poor soils and in less productive saline soils is essential for feeding the world. Genetic information about the combining ability of parents and hybrids and nature of gene action involved in the inheritance of a trait would be of immense value to plant breeders in the choice of parents and to identify potential crosses of practical use.

MATERIAL AND METHODS

In the present investigation eight genotypes viz., RPBio-226, Swarna, CSR-27, CSR-30, CSRC(S)7-1-4, SR26-B, CST-7-1 and CSRC(S)5-2-2-5 were selected based on their reaction to salinity tolerance and were crossed in half diallel fashion (without reciprocals) and the resulting 28 hybrids along with parents were evaluated during kharif, 2010 under salt affected soils of Agricultural Research Station, Machilipatnam.

Table 1. ANOVA for combining ability of eight parents and 28 F₁ progenies for yield and its components under saline and normal soil conditions.

Genotypes df	f PH(cm)	(cm)	D	DFF	II		PT	r :	PL (cm)	(r	PW (g)	g	NFG/P	Ъ	SF	SF (%)	TW(g)	(g)	GY(g)	(
	S	z	\sim	z	\sim	z	$^{\circ}$		\sigma	z	S	z	S		S	z	\sim	z	S	z
GCA	7 150.89	50.89** 69.03** 75.74** 66.11** 8.34** 12.33** 4.84*	75.74*	* 66.11*;	* 8.34**	12.33**	*	13.54** 19.31** 4.94** 1.56** 1.06** 1	19.31**	4.94**	1.56**	1.06**	1447.20**	1447.20** 2286.41** 93.05** 27.83** 13.75** 10.20** 72.76** 30.36**	* 93.05**	: 27.83**	13.75**	10.20**	72.76**	30.36**
	28 94.06	94.06**33.19** 31.39** 26.48** 2.05** 12.85** 2.26*	: 31.39*	* 26.48**	* 2.05**	12.85**	2.26**	13.78**	13.78** 6.73** 4.37** 0.75** 0.50**	4.37**	0.75**	0.50**	693.37*	582.81**	* 59.86**	: 44.32**	5.14**	2.77**	2.77** 19.55** 14.52**	14.52**
Error 7	0 5.10	7.12	1.93	5.11	0.46	0.55	0.25	0.50	0.74	96:0	0.04	0.03	40.49	86.96 8.53 5.89 0	8.53	5.89	0.25	0.59	1.78	2.27
6^2 gca	14.58	6.19	7.38	6.10	0.79	1.18	0.46	1.30	1.86	0.40				219.95	8.45	2.19	1.35	96.0	7.10	2.81
6^2 sca	88.96		29.46	21.37	1.59	12.29	2.01	13.28	5.99	3.42				495.85	51.33	38.43	4.89	2.18	17.78	12.25
6^2 gca / 6^2 sca	0.16	0.24	0.25	0.29	0.49	0.10	0.23	0.10	0.31	0.12				0.44	0.16	90.0	0.28	0.44	0.40	0.23

* Significant at p=0.05; ** Significant at p=0.01; S (Saline soils); N (Normal soils)

PH (cm): Plant height; DFF: Days to 50% flowering; TT: Number of tillers plant⁻¹; PT: Number of productive tillers plant⁻¹; PL (cm): Panicle length; PW(g): Panicle weight; NFGP⁻¹: Number of filled grains panicle⁻¹; SF (%): Spikelet fertility per cent; TW (g): 1000-grain weight; GY (g): Grain yield (g plant⁻¹).

Table 2. ANOVA for combining ability of eight parents and 28 F₁hybridsfor physiological parameters under saline and normal soil conditions.

Genotypes	df	SES for visual salt injury	sual salt y	Root/Sho	oot ratio	Harves (%	Harvest Index (%)	Na ⁺ /K	Na ⁺ /K ⁺ ratio	SPAD chlorophyll meter reading	rophyll ading	Yield reduction (%)
		S	Z	S	z	S	z	S	z	S	z	S
GCA	7	1.13**	0.10**	0.01**	0.02**	32.96*	7.36*	1.46**	0.03**	43.07**	22.32**	1055.26**
SCA	28	1.18**	0.15**	0.01**	0.01**	20.46	12.23**	0.55**	0.05**	16.86**	2.67	157.30**
Error	70	0.05	0.02	0.00	0.00	12.66	2.58	0.01	0.00	2.11	3.37	96.92
6^2 gca		0.11	0.01	0.01	0.00	2.03	0.48	0.15	0.00	4.10	1.90	97.83
6^2 sca		1.13	0.13	0.07	0.01	7.80	9.65	0.55	0.05	14.75	-0.70	80.34
6^2 gca / 6^2 sca		0.10	90.0	0.07	0.13	0.26	0.05	0.27	90.0	0.28	-2.72	1.22

*Significant at p=0.05; **Significant at p=0.01; S (Saline soils); N (Normal soils)

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Genotypes						Yield cor	ntributing pa	ırameter	s and pl	uting parameters and physiological traits related to salinity tolerance	al traits 1	elated to	salinity to	olerance			
	PH (cm)	DFF	TI	PT	PL (cm)	PW (g)	NFG/P	SF (%)	TW (g)	GY (g)	SES	RSR	(%)	N+/K+ R	SPAD	SES	Total
1.RPBio-226	+	 	0	-	-	0	0	+	-1	0	0	-1	0	+	-1	-1	+2
2.Swarna	7	-1	0	0	0	-1	0	0	-1	-	-1	+	0	0	+	-	-
3.CSR-27	0	Ŧ	0	0	+	0	-	0	0	-1	-	0	0	-	0	-1	. 3
4.CSR-30	0	+	-1	-1	-	-1	<u>-</u>	-	0	-1	0	0	-	-1	-1	0	6-
5.CSRSC(S)7-1-4	4 -1	-1	0	-	0	+1	+	0	-	0	0	+	0	+	0	+	+3
6.SR26-B	7	0	7	+	0	-	0	0	Ŧ	-	Ŧ	-	Ŧ	0	0	+	9+
7.CST-7-1	0	0	+	+	0	0	+	0	0	0	-	+	0	-1	0	0	+2
8. CSRC(S)																	
5-2-2-5	0	-1	+1	+	+	+1	+	0	7	7	0	7	0	0	0	+1	8+

PH (cm): Plant height; DFF: Days to 50% flowering; TT: Number of tillers plant-1; PT: Number of productive tillers plant-1; PL (cm): Panicle length; PW(g): Panicle 0 : Moderate status and -1 : Low status +1: High status,

weight;NFGP-1: Number of filled grainspanicle-1; SF (%): Spikelet fertility per cent; TW (g): 1000-grain weight; GY (g): Grain yield (g plant-1); SES: SES for visual

salt injury;RSR: Root /shoot ratio; HI (%): Harvest index per cent;Na⁺/K⁺ R: Sodium Potassium ratio; SPAD: SPAD chlorophyll meter reading.

A site with appropriate chemical properties was selected after intensive sampling from a salt affected field. 30 days old seedlings were transplanted in the main field following randomized block design with three replications on 23-8-2010. The saline soils were of sandy loam in texture with an average electrical conductivity of 6.3 dS m⁻¹ and pH of 7.9. The parents and F₁s were transplanted in 3 rows of 1.5 meter length. A spacing of 20 cm x 15 cm between and within row was adopted. The recommended agronomic and plant protection measures were adopted in conducting the experiment. The results obtained on gene effects governing the inheritance of physiological parameters and yield components through diallel analysis following model I and method II of Griffing (1956) and discussed trait wise for 10 yield parameters and six physiological traits in eight parents and 28 F, hybrids under saline soil environment.

RESULTS AND DISCUSSION

Mean squares due to general combining ability (gca) for yield components and salt tolerance related physiological components were significant, indicating that all the parents differed significantly for their general combining ability for all the traits studied (Table 1 and 2). Similarly, the mean squares due to specific combining ability (sca) were significant for all characters except SPAD chlorophyll meter reading, which indicated that there was momentous variance among the hybrids for the characters under study.

The sca variances of hybrids were higher than the gca variances of parents for all the characters except for yield reduction per cent suggesting the significant role of non-additive gene action for majority of the parameters (Table 1 and 2). These findings are in agreement with the earlier reports of Thirumeni et al. (2003) and Mahmood et al. (2004) for days to 50 per cent flowering; Thirumeni et al. (2003) and Karthikeyan and Anbuselvam (2006) for the plant height; Thirumeni et al. (2003), Karthikeyan and Anbuselvam (2006), Senguttuvel (2008), Salgotra et al. (2009) and Babu G K et al.(2010) for productive tillers plant⁻¹; Thirumeni et al. (2003), et e --- l

Table 4. Score chart of parents for GCA effects in saline soils.

Genotypes					Yield c	contribu	Yield contributing parameters and physiological traits related to salinity tolerance	eters and	1 physio	logical tı	aits rela	ted to sal	inity tole	erance			
	PH (cm)	DFF	II	PT	PL (cm)	PW (g)	NFG/P	SF (%)	TW (g)	GY (g)	SES	RSR	HI (%)	$N^+\!/K^+$ R	SPAD	SES	Total
1.RPBio-226	 	 	-1	-1	-1	0	-1	-1	-	-1	-1	-1	0	-1	-1	-1	-10
2.Swarna	+	-1	0	0	0	-	0	-1	-	-1	7	-1	0	-	+	-	-5
3.CSR-27	0	Ŧ	-1	0	0	0	0	0	7	-1	0	-1	0	-	0	-1	ς-
4.CSR-30	+	+	-1	-1	-	-	-	-1	-	-1	-1	-1	-	-	-1	0	÷
5.CSRSC(S)7-1-4	7	-	+	+	0	-	+	0	7	+	0	+	0	7	0	+	9+
6.SR26-B	7	0	+	+	+	-	+	0	+	+	-	0	+	7	+	+	+
7.CST-7-1	7	+	0	0	0	0	0	+	0	0	-	0	0	7	0	0	+
8. CSRC(S)5-2-2-5	7	-1	+	+	+	7	+	+	7	+	-	+	0	7	+1	+1	+11

PH (cm): Plant height; DFF: Days to 50% flowering; TT: Number of tillers plant-1; PT: Number of productive tillers plant-1; PL (cm): Panicle length; PW(g): Panicle weight; NFGP-1: Number of filled grainspanicle-1; SF (%): Spikelet fertility per cent; TW (g): 1000-grain weight; GY (g): Grain yield (g plant-1); SES: SES for visual 0 : Moderate status and -1 : Low status +1: High status,

salt injury;RSR: Root /shoot ratio; HI (%): Harvest index per cent;Na⁺/K⁺ R: Sodium Potassium ratio; SPAD: SPAD chlorophyll meter reading.

al. (2007) Shukla and Pandey (2008), Salgotra et al. 2009) and Babu G K et al. (2010) for panicle length.

However, in contrast to the present observations, the non-additive gene effects for test weight were reported by Rogbell and Subbaraman (1997), Sarma et al.(2007), Venkatesan et al. (2007), Shukla and Pandey (2008) and Babu G K et al. (2010). Similarly, non- additive gene effects were for number of filled grains panicle-1 were noticed by Thirumeni et al. (2003), Raju et al. (2006), Sharma and Mani (2008), Senguttuvel (2008), Sanjay Singh et al. (2008), Saidaiah et al. (2010).Likewise, Karthikeyan and Anbuselvam (2006) stated similar type of non additive gene action for panicle weight; Mahmood et al. (2002) for Standard evaluation score (SES) for visual salt injury symptoms, Raju et al. (2006) for harvest index; Mahmood et al. (2002), Mishra et al. (2003) and Senguttuvel (2008) for Na⁺/K⁺ ratio; Malarvizhi et al. (2004) and Senguttuvel (2008) for SPAD chlorophyll meter reading.

The estimates of gca effects (Table 3 and 4) showed that genotypes with high gca effects differed for various traits. A score chart was prepared by allotting +1, 0 and -1 scores to the parents with significant, non-significant and negative significant gca effects respectively.

Under normal conditions CSRC(S)5-2-2-5 scored +8 with high gca effects for grain yield and other traits including number of tillers per plant, productive tillers per plant, panicle length, panicle weight, number of filled grains per panicle, test weight, root shoot ratio and yield reduction per cent. SR26-B was found to be the best combiner for total tillers, productive tillers, panicle weight, test weight, grain yield per plant, SES for visual salt injury, harvest index and yield reduction per cent with a score of +6.

Under saline conditions the same parents CSRC(S)5-2-2-5 scored +11 and had favourable genes for all the yield contributing parameters except for plant height, days to 50% flowering and harvest index. While the parent SR26-B also scored +11 and similarly

contributed positive alleles for number of tillers per plant, number of productive tillers per plant, panicle length, panicle weight, number of filled grains per panicle, test weight, grain yield per plant, SES for visual salt injury, harvest index, Na⁺/K⁺ ratio, SPAD value and yield reduction per cent. Some other good general combiners that had also contributed positive genes for various characters were; CSRC(S)7-1-4 (Scored +6) for number of tillers per plant, number of productive tillers per plant, panicle weight, number of filled grains per panicle, test weight, grain yield per plant, root shoot ratio, Na⁺/K⁺ ratio and yield reduction percent; CST-7-1 (Scored +4) and had favourable alleles to transmit for days to 50% flowering, productive tillers per plant, spikelet fertility per cent, salinity score, Na⁺ / K⁺ ratio.

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