

Combining Ability and Gene Action for Productivity Traits in Rice (*Oryza sativa* L.) under Saline Conditions

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ABSTRACT

Salinity is a major abiotic constraint in majority of the rice cultivation areas of the world and improving grain yield in rice under such circumstances is one of the important breeding objectives. In the current study, combining ability estimates for twenty-four hybrids developed by crossing six lines with four testers were used to determine the genetic make up of 11 morphological traits under coastal-saline conditions. The aim of this study was to determine the combining ability, gene action and proportional contribution of cross components in rice genotypes. The experiment was conducted in the experimental farm, Department of Genetic and Plant Breeding, Faculty of Agriculture, Annamalai University. The analysis of variance for combining ability showed that specific combining ability (SCA) variances were larger than the corresponding general combining ability (GCA) variances for all the characters studied, which suggested that predominance of nonadditive gene action for the target traits. The proportional contribution of testers was observed to be higher than that of the lines and interactions of line x tester, revealing the higher estimates of GCA variance due to presence of additive gene action among the testers used. The best general combining parents for grain yield and its component characters were found to be ADT 37, ADT 43 and ADT 38 among the lines and CSR 36 and FL 478 among the testers based on *per se* and *gca* effects. The hybrids ADT 43 x CSR 36, ADT 42 x CSR 36 and ADT 37 x CSR 36 were considered to be superior crosses due to the superior performance for the majority of the economic characteristics examined along with early maturity and low stature plants. Highly significant *sca* effects for grain yield and its component traits were found to be suitable for heterosis breeding. The crosses *viz.*, ADT 46 x CSR 36 and ADT 45 x CSR 36 were identified with high mean and negatively significant *sca* effects for yield and could be exploited for recombination breeding.

Keywords : Combining ability, GCA, LxT, Rice, SCA

RICE (*Oryza sativa* L.) belongs to the family Poaceae (Gramineae) and is one of the most important food crops in the world, providing food for more than half of the world's population (Baroudy *et al.*, 2020). The demand for rice will be 121.2 million metric tonnes by 2030, 129.6 million metric tonnes by 2040 and 137.3 million metric tonnes by 2050. If the cultivated area under plough remains at the current level, rice production should increase to 3.4 metric

tons per ha from the current 2.4 metric tons per ha (Anonymous, 2013). Rice is sensitive to salinity in the seedling and flowering stages, especially in coastal farms. The yield of the rice crop, which ultimately depends on how many seedlings can withstand saline water at the stage of transplantation (Tiwari *et al.*, 2022). The salt affected area is increasing due to the irrigation with water, high intensity of cropping pattern and increased application of chemical fertilizers.

Unfortunately, rice, being the most salt-sensitivity cereal crops the use of some management options can ameliorate yield reduction under salinity stress. However, implementation of such practice is often limited because of high cost and scarcity of good quality water. As a result, the need for genetically enhancing salt tolerance in rice crops through an integrated strategy that uses molecular physiological, biochemical and proteomics approaches for identifying salt tolerance genes for the genetic improvement of rice varieties is of the utmost importance (Reddy *et al.*, 2017). This is the practical means of addressing the constantly increasing demand for food from the world's expanding population (Reddy *et al.*, 2017) as it is the practical means of addressing the ever-increasing demand for food from the world's expanding population.

To meet the growing food demand, development of high yielding varieties with multiple stress resilience is need of the hour, more so with tolerance to salinity in rice. The combining ability is a potent tool for selecting the best combining parents that can be used in hybridization programme to produce desired segregates and take advantage of heterosis or accumulate the fixable genes in crosses. It helps to understand the genetic architecture of various characters that enable the breeder to design an effective breeding plan. This information may also be useful to breeders for genetic improvement of the existing genotypes based on the performance in various hybrid combinations. The line x tester analysis in rice is used principally to determine the general and specific combining ability of the quantitative properties (Rahaman, 2016). Griffing (1956) and Koze (2017) stated that SCA includes the non-additive genetic portion while, GCA includes the additive genetic portion of the total variation. The presence of non-additive genetic variance is the primary justification for initiating the hybrid programme (Cockerham, 1961 and Pradhan & Singh *et al.*, 2008). Line x tester design is the best analysis for estimating GCA, SCA and various types of gene actions (Fahmi *et al.*, 2017). Combining ability aids in defining the pattern of gene effects in the expression of quantitative traits by identifying potentially superior parents and

hybrids (Zhang *et al.*, 2015). In this study, an attempt has been made to evaluate GCA and SCA in rice cultivars for different traits to identify good combiners in the selection of parents and to assist in the choice of breeding strategies for the improvement of salinity tolerance in rice.

MATERIAL AND METHODS

The experiment was conducted in coastal saline condition. Ten selected genotypes of which six (ADT 37, ADT 43, ADT 38, ADT 46, ADT 42 and ADT 45) were used as lines and four (CSR 10, CSR 36, FL 478 and POKKALI) as testers (Table 1). These parents were crossed using line x tester mating design to produce twenty-four hybrids to study the combining ability as well as gene action on yield and yield components. This study was conducted during (Thaladi) October 2020 in the Department of Genetics and Plant Breeding experimental farm, Faculty of Agriculture, Annamalai University, Chidambaram, Tamil Nadu. Located at 11°. 39' N latitude, 79.71' E longitude and height + 5.79 m from mean sea level in coastal saline soil condition having the EC of 4.01 ± 0.13 ds/m. One seedling per hill was transplanted at a spacing of 30 cm between rows and 20 cm. Recommended package of practices and need-based plant protection measures were adopted to raise the good crop. Observations were recorded on ten competitive plants both in parents and hybrids in each

TABLE 1
Source of parents

		Genotypes details	
Lines	L1	ADT 37	
	L2	ADT 43	
	L3	ADT 38	
	L4	ADT 46	
	L5	ADT 42	
	L6	ADT 45	
Tester	T1	CSR 10	
	T2	CSR 36	
	T3	FL 478	
	T4	POKKALI	

replication for the eleven traits viz., days to 50 per cent flowering, plant height at maturity, number of tillers plant⁻¹, number of productive tillers plant⁻¹, panicle length, number of grains panicle⁻¹, thousand seed weight, grain length, grain width, L/B ratio and grain yield plant⁻¹. The statistical analysis was performed using Line x Tester analysis given by Kempthorne (1957) and genetic components of each parameter as suggested by Singh and Chaudhary (1977).

RESULTS AND DISCUSSION

Analysis of Variance

The analysis of variance showed significant variations for the yield and yield contributing characters among the lines, testers and line x tester interactions (Table 2).

The lines, testers and cross combinations showed significant difference indicating the wide genetic diversity for days to 50 per cent flowering, plant height at maturity, number of tillers plant⁻¹, number of productive tillers plant⁻¹, panicle length, number of grains panicle⁻¹, thousand seed weight, grain length, grain width, L/B ratio and grain yield plant⁻¹. In combining ability: significant variances for lines and testers were observed for all eleven characters. In the case of lines x testers also significant positive variance was observed for all the characters.

The estimates of GCA and SCA variances revealed that the SCA variances had greater magnitude than GCA variance for all the characters studied, indicating the predominance of non-additive gene action (Table 2). The significant differences between line x testers interaction indicated that SCA attributed significantly over GCA in the expression of the traits demonstrating the importance of dominance or non-additive variances for all the traits (Sanghera and Hussain, 2012). It provides an opportunity for utilizing hybrid vigour through heterosis breeding and the selection process in late or advanced generations to improve these traits. The preponderance of non-additive variances in the expression of yield-attributing traits has also been reported by

TABLE 2
ANOVA for combining ability analysis in rice (*Oryza sativa* L.) for eleven characters

Source of variation	df	Mean sum of Square										
		Days to 50 per cent flowering	Plant height at maturity	Number of tillers plant ⁻¹	Number of productive tillers plant ⁻¹	Panicle length	Number of grains panicle ⁻¹	Thousand seed weight	Grain length	Grain width	L/B ratio	Grain yield plant ⁻¹
Replication	2	0.89	0.10	0.06	0.05	0.0079	3.09	0.01	0.0002	0.0003	0.0004	0.15
Hybrid	23	331.24 **	2086.89 **	91.99 **	82.99 **	43.64 **	3197.00 **	16.69 **	1.3494 **	0.0845 **	0.3340 **	567.61 **
Line	5	195.36 **	131.18 **	12.01 **	10.80 **	8.38 **	172.74 **	26.68 **	0.2520 **	0.1562 **	0.1906 **	31.89 **
Tester	3	2006.48 **	14522.21 **	535.38 **	462.98 **	134.49 **	17861.31 **	64.77 **	5.9038 **	0.0899 **	1.1475 **	3427.00 **
LxT	23	41.48 **	251.73 **	29.97 **	31.06 **	37.22 **	1272.22 **	3.74 **	0.8044 **	0.0595 **	0.2190 **	174.30 **
Error	66	0.32	0.10	0.04	0.02	0.02	3.53	0.01	0.0003	0.0003	0.0005	0.27
GCA		7.31	46.28	1.56	1.31	0.16	48.54	0.33	0.0137	0.0006	0.0029	9.92
SCA		13.72	83.88	9.97	10.35	12.40	423.01	1.25	0.2680	0.0198	0.0729	58.02
GCA/SCA		0.53	0.55	0.16	0.13	0.01	0.11	0.26	0.0511	0.0303	0.0398	0.17

* Significance at 5% level; ** Significance at 1% level

Sharma *et al.* (2013), Suvathipriya *et al.* (2018) and Sundaram *et al.* (2019).

General Combining Ability (*gca*) Effects

The GCA effect is considered as an intrinsic genetic value of the parent for a trait, which is due to additive gene effects and it is fixable (Simmonds, 1989). Important criteria for genotypic evaluation include mean performance and genetic variability of parents and hybrids; however, parents with high mean values might not pass on this trait to their hybrids (Fellahi *et al.*, 2013) always. Among the lines studied, ADT 42 recorded the highest significant mean value for all the traits except days to fifty per cent flowering and plant height followed by ADT 37 which recorded significant mean values for most of the traits except number of productive tillers, thousand seed weight, seed length, grain L/B ratio and grain yield per plant. While the genotype, ADT 37 showed earliness with short plant height. Among the testers, CSR 36 recorded high *per se* performance for all the traits except seed width (Table 3).

The tester, FL 478 recorded significantly high mean performance for plant height, thousand seed weight, seed length, seed width and grain L/B ratio. The lines, ADT 42, ADT 37 and ADT 45 as well as the testers, CSR 36, FL 478 and POKKALI were observed to be good general combiners for most of the trait's study. Thus, based on the *per se* performance the lines, ADT 42, ADT 37, ADT 45 and the testers, CSR 36 and FL 478 have been isolated as superior parents and are useful for the introgression of the respective traits through hybridization programmes (Table 4).

The proportional contribution of lines, testers and line x tester interaction to total variance is presented in Fig. 1. The per cent contribution towards the total variance was maximum due to the testers for the traits, days to 50 per cent flowering (79.01), plant height (90.77), number of tillers per plant (75.92), number of productive tillers plant⁻¹ (72.76), number of grains panicle⁻¹ (72.87), thousand seed weight (50.63) grain length (57.07), L/B ratio (44.82) and grain yield plant⁻¹ (78.75). The proportional contribution of testers was observed to be higher than that of the line and interactions of line x testers, revealing the higher

TABLE 3
General combining effects of parents for yield and its component traits in rice

Parents	Days to 50 per cent flowering	Plant height at maturity	Number of tillers plant ⁻¹	Number of productive tillers plant ⁻¹	Panicle length	Number of grains panicle ⁻¹	Thousand seed weight	Grain length	Grain width	L/Bratio	Grain yield plant ⁻¹
ADT 37	-0.39 *	0.31 **	0.80 **	-0.04	0.31 **	5.70 **	-0.61 **	-0.12 **	0.05 **	-0.11 **	0.64 **
ADT 43	5.03 **	2.06 **	1.35 **	1.25 **	0.42 **	-0.52	-1.91 **	-0.27 **	0.15 **	-0.27 **	0.35 *
ADT 38	1.61 **	-2.22 **	-1.48 **	-1.23 **	-0.89 **	-4.27 **	0.01	-0.10 **	-0.24 **	0.23 **	-1.79 **
ADT 46	-6.97 **	-4.64 **	-0.36 **	-0.16 **	-0.99 **	2.13 **	2.50 **	0.61 **	0.15 **	0.08 **	1.51 **
ADT 42	-1.14 **	-0.39 **	-0.44 **	0.92 **	1.2 **	-3.96 **	0.67 **	-0.13 **	0.03 **	-0.09 **	1.52 **
ADT 45	1.86 **	4.87 **	0.14 *	-0.75 **	-0.05	0.92	-0.65 **	0.01	-0.14 **	0.16 **	-2.23 **
S.E (GCA for effects lines)	0.16	0.09	0.05	0.05	0.03	0.52	0.004	0.0058	0.005	0.005	0.144
CSR 10	-3.83 **	-14.53 **	2.95 **	2.55 **	-0.57 **	17.24 **	-0.53 **	-0.02 **	-0.04 **	0.04 **	4.76 **
CSR 36	-12.94 **	-20.46 **	6.11 **	5.79 **	1.55 **	35.63 **	2.52 **	0.99 **	0.04 **	0.33 **	17.06 **
FL 478	6.00 **	-6.77 **	-3.51 **	-3.08 **	-3.59 **	-28.92 **	0.06 **	-0.43 **	-0.06 **	-0.11 **	-7.79 **
POKKALI	10.78 **	41.77 **	-5.55 **	-5.26 **	2.61 **	-23.95 **	-2.04 **	-0.54 **	0.06 **	-0.26 **	-14.03 **
S.E (GCA for effects testers)	0.13	0.07	0.12	0.04	0.03	0.42	0.003	0.005	0.004	0.004	0.118

* Significance at 5% level; ** Significance at 1% level

TABLE 4
Mean performance of parents for yield and its component traits in rice

Parents	Days to 50 per cent flowering	Plant height at maturity	Number of tillers plant ⁻¹	Number of productive tillers plant ⁻¹	Panicle length	Number of grains panicle ⁻¹	Thousand seed weight	Grain length	Grain width	L/Bratio	Grain yield plant ⁻¹
<i>Lines</i>											
ADT 37	71.67 **	77.59 **	22.79 **	15.35	24.38 **	156.31 **	19.58	6.79	2.82 **	2.41	41.68
ADT 43	78.33	89.51	24.71 **	16.96 **	24.86 **	152.34	15.83	8.02	2.13	3.76 **	41.58
ADT 38	70.67 **	85.42 **	17.15	14.69	21.94	145.95	22.15 **	9.02 **	2.49	3.62 **	38.55
ADT 46	63.67 **	89.62	12.41	10.33	18.64	150.22	24.63 **	9.07 **	2.70 **	3.36 **	32.77
ADT 42	81.67	90.46	21.46 **	17.83 **	24.11 **	166.23 **	23.92 **	9.09 **	2.81 **	3.23 **	45.28 **
ADT 45	80.67	81.58 **	23.78 **	17.35 **	23.48 **	152.69	16.87	8.01	2.82 **	2.84 **	41.38
SE	0.2504	0.1229	0.086	0.064	0.0431	0.7413	0.0055	0.0105	0.0071	0.0293	0.2343
Mean	74.4444	85.6967	21.0506	16.2528	22.9011	153.956	20.4972	8.3339	2.6289	2.4622	42.705
CD (P=0.05)	0.4629	0.2565	0.1729	0.1286	0.0867	1.4669	0.0113	0.0140	0.0130	0.0176	0.4104
CD (P=0.01)	0.6172	0.342	0.2305	0.1715	0.1156	1.9559	0.015	0.0186	0.0173	0.0235	0.5472
<i>Testers</i>											
CSR 10	68.33 **	72.56 **	16.27	13.73	18.58	118.6	20.54	5.53	2.17	2.55	29.88
CSR 36	66.33 **	95.51 **	24.34 **	20.14 **	23.33 **	143.8 **	21.88 **	8.62 **	2.22	3.88 **	45.27 **
FL 478	76.33	76.71 **	13.77	10.37	16.73	96.76	23.41 **	9.65 **	2.75 **	3.51 **	22.71
POKKALI	70.67	149.57	13.37	11.65	27.88 **	129.97 **	18.27	8.14 **	3.33 **	2.44	29.62
SE	0.2045	0.1004	0.0702	0.0523	0.0352	0.6052	0.0045	0.0085	0.0058	0.0239	0.1913
Mean	70.4167	98.5875	16.6883	13.9742	21.6317	122.284	21.0258	7.9875	2.6192	2.7392	31.8692
CD (P=0.05)	0.378	0.2095	0.1412	0.105	0.0708	1.1977	0.0092	0.0114	0.0106	0.0144	0.3351
CD (P=0.01)	0.504	0.2793	0.1882	0.14	0.0944	1.597	0.0123	0.0152	0.0141	0.0192	0.4468

* Significance at 5% level; ** Significance at 1% level

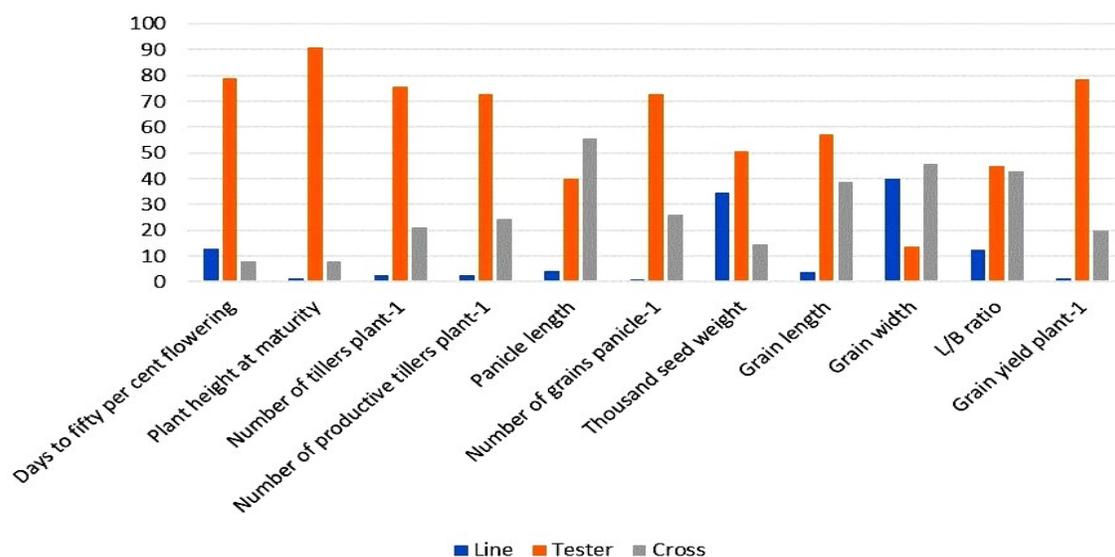


Fig. 1 : Per cent contribution of lines, testers and crosses towards yield and its component traits in rice

TABLE 5
Specific combining ability effects of hybrids for yield and its component traits in rice

Hybrids	DFF	PH	NT	NPT	PL	NGPP	TSW	GL	GB	GL/GB	GYPP
ADT 37x CSR 10	2.17 **	5.00 **	-4.17 **	-3.48 **	0.04	8.28 **	0.31 **	0.08 **	0.06 **	-0.04 **	-2.87 **
ADT 37x CSR 36	-0.72 *	-8.63 **	2.59 **	3.33 **	1.97 **	10.22 **	0.46 **	-0.52 **	0.03 **	-0.22 **	5.05 **
ADT 37x FL 478	-0.67 *	7.18 **	-1.74 **	-1.51 **	-1.58 **	-4.87 **	-1.12 **	0.29 **	-0.01	0.12 **	-3.09 **
ADT 37x POKKALI	-0.78 *	-3.55 **	3.32 **	1.67 **	-0.43 **	-13.63 **	0.35 **	0.16 **	-0.08 **	0.14 **	0.91 **
ADT 43x CSR 10	6.75 **	15.71 **	-2.93 **	-3.72 **	0.34 **	-9.95 **	-1.24 **	0.04 **	0.17 **	-0.16 **	-2.59 **
ADT 43x CSR 36	-3.14 **	-11.40 **	1.67 **	2.26 **	2.45 **	24.53 **	0.85 **	1.09 **	-0.19 **	0.65 **	9.01 **
ADT 43x FL 478	-1.42 **	-4.98 **	0.63 **	0.11	-3.90 **	-17.33 **	0.21 **	-1.19 **	-0.01	-0.47 **	-5.83 **
ADT 43x POKKAL	-2.19 **	0.67 **	0.63 **	1.35 **	1.11 **	2.75 *	0.17 **	0.06 **	0.03 **	-0.02	-0.59 *I
ADT 38x CSR 10	1.17 **	0.89 **	-0.50 **	-1.90 **	-4.49 **	-34.05 **	-1.23 **	0.15 **	-0.11 **	0.19 **	-10.25 **
ADT 38x CSR 36	-2.72 **	-1.88 **	1.31 **	1.49 **	3.04 **	16.47 **	0.64 **	-0.58 **	0.04 **	-0.28 **	4.72 **
ADT 38x FL 478	1.00 **	1.17 **	-0.45 **	-0.51 **	-0.27 **	13.77 **	0.41 **	0.42 **	0.06 **	0.11 **	1.45 **
ADT 38x POKKALI	0.56	-0.18	-0.37 **	0.92 **	1.71 **	3.81 **	0.17 **	0.02	0.01	-0.02	4.09 **
ADT 46x CSR 10	-4.58 **	-10.65 **	-0.05	1.67 **	2.54 **	17.10 **	0.21 **	-0.07 **	-0.10 **	0.07 **	7.10 **
ADT 46x CSR 36	1.86 **	11.73 **	-1.80 **	-4.58 **	-6.50 **	-41.80 **	-0.63 **	0.09 **	-0.15 **	0.18 **	-15.58 **
ADT 46x FL 478	-1.08 **	2.71 **	1.38 **	1.28 **	1.71 **	13.33 **	1.19 **	-0.18 **	-0.04 **	-0.06 **	3.23 **
ADT 46x POKKALI	3.81 **	-3.79 **	0.48 **	1.64 **	2.25 **	11.37 **	-0.77 **	0.15 **	0.29 **	-0.19 **	5.25 **
ADT 42x CSR 10	-3.08 **	-1.87 **	1.15 **	2.13 **	0.31 **	1.23	-0.61 **	-0.04 **	-0.08 **	0.07 **	1.24 **
ADT 42x CSR 36	-1.31 **	-4.77 **	1.94 **	1.49 **	1.37 **	10.69 **	0.17 **	-0.24 **	0.17 **	-0.26 **	5.22 **
ADT 42x FL 478	1.08 **	0.62 **	0.27 *	0.70 **	-1.75 **	-1.30	0.24 **	0.38 **	-0.02	0.17 **	1.25 **
ADT 42x POKKALI	3.31 **	6.02 **	-3.36 **	-4.32 **	0.08	-10.62 **	0.20 **	-0.11 **	-0.07 **	0.02	-7.72 **
ADT 45x CSR 10	-2.42 **	-9.09 **	6.50 **	5.29 **	1.25 **	17.38 **	2.55 **	-0.16 **	0.06 **	-0.13 **	7.37 **
ADT 45x CSR 36	6.03 **	14.95 **	-5.71 **	-3.98 **	-2.33 **	-20.10 **	-1.49 **	0.16 **	0.10 **	-0.06 **	-8.42 **
ADT 45x FL 478	1.08 **	-6.69 **	-0.09	-0.07	5.79 **	-3.61 **	-0.94 **	0.28 **	0.01	0.12 **	2.99 **
ADT 45x POKKALI	-4.69 **	0.83 **	-0.70 **	-1.25 **	-4.71 **	6.32 **	-0.12 **	-0.28 **	-0.17 **	0.07 **	-1.94 **

DFF- Days to fifty per cent flowering, PH- Plant height at maturity, NT- Number of tillers plant⁻¹, NPT- Number of productive tillers plant⁻¹, PL- Panicle length, NGPP- Number of grains panicle⁻¹, TSW- Thousand seed weight, GL- Grain length, GB- Grain width, L/B- Grain Length/Width ratio, GYPP- Grain yield plant⁻¹

* Significance at 5% level; ** Significance at 1% level

estimates of GCA variance due to the presence of additive gene action among the testers used. The similar findings were reported by Bagheri *et al.*, 2010. The maximum contribution of the lines x tester alone towards the total variance was observed for panicle length (55.62) and grain breadth (45.94) exhibiting higher estimates of GCA variances for interaction.

Specific Combining Ability (*sca*) Effects

The cross combination, ADT 43 x CSR 36 had positive and highly significant *sca* effects for all the traits *viz.*, number of tillers plant⁻¹, number of productive tillers plant⁻¹, panicle length, number of grains panicle⁻¹, thousand seed weight, grain length, L/B ratio and grain

TABLE 6
Mean performance of crosses for yield and its component traits in rice

Hybrids	DFF	PH	NT	NPT	PL	NGPP	TSW	GL	GW	L/W	GYPP
ADT 37x CSR 10	73.67 **	96.04 **	18.41	14.32	23.31	168.35 **	19.05	6.98	2.68 **	2.61	38.42 **
ADT 37x CSR 36	61.67 **	76.48 **	28.33 **	24.36 **	27.36 **	188.67 **	22.25 **	7.02	2.73 **	2.57	58.63 **
ADT 37x FL 478	80.67	105.98	14.38	10.66	18.66	109.04	18.21	8.57 **	2.59	3.31 **	25.65
ADT 37xPOKKALI	85.33	143.79	17.4	11.66	26.01 **	105.24	17.58	7.52	2.66 **	2.82	23.41
ADT 43x CSR 10	83.67	108.51	20.2 **	15.37	23.72 *	143.9 **	16.21	6.89	2.77 **	2.49	38.41 **
ADT 43x CSR 36	64.67 **	75.47 **	27.96 **	24.58 **	27.95 **	196.76 **	21.35 **	8.59 **	2.49	3.45 **	62.3 **
ADT 43x FL 478	85.33	95.58 **	17.3	13.57	16.46	90.36	18.25	7.04	2.57	2.74	22.61
ADT 43x POKKALI	89.33	149.77	15.25	12.62	27.66 **	115.40	16.11	7.37	2.75 **	2.68	21.61
ADT 38x CSR 10	74.67 *	89.41 **	19.8 **	14.72	17.59	116.06	18.13	7.25	2.32	3.13 **	28.61
ADT 38x CSR 36	61.67 **	80.70 **	24.77 **	21.33 **	27.23 **	184.96 **	23.05 **	7.15	2.55	2.8	55.87 **
ADT 38x FL 478	84.33	97.44 **	13.39	10.47	18.78	117.71	20.36 **	8.89 **	2.47	3.6 **	27.76
ADT 38x POKKALI	88.67	144.64	11.42	9.72	26.96 **	112.72	18.02	7.57	2.56	2.95 *	24.15
ADT 46x CSR 10	60.33 **	75.45 **	21.36 **	19.35 **	24.52 **	173.6 **	22.06 **	7.06	2.65 *	2.66	49.25 **
ADT 46x CSR 36	57.67 **	91.90 **	22.78 **	16.33 **	17.59	133.09	24.27 **	7.85 **	2.69 **	2.92	38.87 **
ADT 46x FL 478	73.67 **	96.57 **	16.33	13.33	20.66	123.67	23.63 **	8.32 **	2.69 **	3.09 **	32.84
ADT 46x POKKALI	83.33	138.61	13.39	11.5	27.4 **	126.67	19.57	7.73 **	3.17 **	2.44	28.60
ADT 42x CSR 10	67.67 **	88.48 **	22.48 **	20.9 **	24.48 **	151.64 **	19.41	7.14	2.51	2.84	43.41 **
ADT 42x CSR 36	60.33 **	79.64 **	26.44 **	23.49 **	27.65 **	179.48 **	23.24 **	7.59	2.85 **	2.66	59.68 **
ADT 42x FL 478	81.67	98.73 **	15.15	13.83	19.39	102.95	20.85 **	8.95 **	2.56	3.5 **	30.87
ADT 42x POKKALI	88.67	152.67	9.47	6.63	27.42 **	98.60	18.71	7.54	2.66 **	2.84	15.65
ADT 45x CSR 10	71.33 **	86.52 **	28.42 **	22.39 **	24.16 **	172.68 **	21.26 **	6.71	2.53	2.65	45.79 **
ADT 45x CSR 36	70.67 **	104.63 *	19.37 **	16.35 **	22.7	153.58 **	20.26 **	7.67 **	2.66 **	2.88	42.28 **
ADT 45x FL 478	84.67	96.68 **	15.36	11.39	25.68 **	105.52	18.35	8.52 **	2.47	3.45 **	28.85
ADT 45x POKKALI	83.67	152.74	12.72	8.03	21.37	120.42	17.07	7.05	2.43	2.9	17.68
Mean	75.83	105.27	18.83	15.29	23.53	137.13	19.89	7.62	2.63	2.92	35.88
SE	0.32	0.18	0.12	0.09	0.06	1.03	0.0079	0.0098	0.0091	0.0124	0.28
CD (P=0.05)	0.92	0.51	0.34	0.25	0.17	2.93	0.0225	0.0280	0.0259	0.0352	0.82
CD (P=0.01)	1.23	0.68	0.46	0.34	0.23	3.91	0.0301	0.0373	0.0346	0.0470	1.09

DFF - Days to fifty per cent flowering, PH- Plant height at maturity, NT- Number of tillers plant⁻¹, NPT- Number of productive tillers plant⁻¹, PL- Panicle length, NGPP- Number of grains panicle⁻¹, TSW- Thousand seed weight, GL- Grain length, GB- Grain width, L/B- Grain Length/Width ratio, GYPP- Grain yield plant⁻¹; * Significance at 5% level**, Significance at 1% level.

yield plant⁻¹ except grain width while it exhibited negative significant *sca* effects for days to 50 per cent flowering and, plant height at maturity (Table 5). Related results were obtained by Upadhyay and Jaiswal (2015).

The crosses, ADT 42 x CSR 36 and ADT 37 x CSR 36 possessed high *per se* performance for most of the traits except grain length and L/B ratio along with negative significant *sca* effects for the plant height and days to 50 per cent flowering (Table 6).

The parents, ADT 43, ADT 37, ADT 42 and CSR 36 are identified as good general combiners for almost

all the traits studied can be recommended as potential parents for future breeding programme. Out of twenty-four hybrids three cross combinations, ADT 43 x CSR 36, ADT 42 x CSR 36 and ADT 37 x CSR 36 excelled in yield and yield related traits. These three hybrids, ADT 43 x CSR 36, ADT 42 x CSR 36 and ADT 37 x CSR 36 recorded high *per se* performance for yield and highly significant *sca* effects for grain yield and its component traits which were found to be suitable for heterosis breeding. Furthermore, two crosses *viz.*, ADT 46 x CSR 36 and ADT 45 x CSR 36 which recorded high mean and negatively significant *sca* effects for yield could be exploited through recombination breeding.

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