



Combining ability and heterosis studies for grain yield in rice (*Oryza sativa* L.)

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ABSTRACT

Thirty six F_1 s along with the parents (B and R lines) and standard checks viz., RNR 15048 and PA 6444 were evaluated for grain yield and related yield attributing traits to assess combining ability and heterotic estimates in rice. The analysis of variance divulges that for parents, hybrids and parent vs hybrids were highly significant in all the traits barring spikelet fertility for parents, effective bearing tillers and number of grains per panicle for crosses. Predictability ratio and average degree of dominance values derived from *gca* and *sca* variances clearly mention that all the traits studied except effective bearing tillers were under control of genes having additive effects. The *gca* effects revealed that among the lines, RNR 17441, TP 29631 and TP 30011 whereas in testers, CMS 59A were recognized as good general combiner with respect to grain yield and spikelet fertility. Similarly, the hybrids CMS 11A \times CB 12593, CMS 59A \times RNR 25843, CMS 23A \times TP 29631, CMS 23A \times IR 11A 334 and CMS 59A \times RNR 25842 were found to be good specific combiner for grain yield. Significant positive standard heterosis over variety and hybrid check was recorded in seven and six hybrids, respectively. Overall data disclose that hybrids viz., CMS 59A \times RNR 25842, CMS 59A \times RNR 25843 and CMS 23A \times TP 29631 were identified as superior based on their *sca*, heterosis estimates and their parental *gca* effects besides good *per se* performance.

Keywords: Heterosis, combining ability, gene action, hybrid rice

Rice is one of the most predominant food crops on the earth, particularly in Asian continent. Human consumption in 2009 accounted for 78% of total production for rice, compared with 64% for wheat and 14% for maize (GRiSP, 2013). Of these, for low and lower middle income countries rice is the most important food crop. According to the USDA, approximately 500 million tonnes of milled rice has been produced globally during 2019-20 marketing year (USDA, 2020). China is the largest producer, accounting for 28% of the production, followed by India (22%), Indonesia (10%), Bangladesh (7%), Vietnam (6%) and Thailand (5%) (Nirmala, 2017). Similarly with respect to consumption pattern, same ranking was observed: China is the largest consumer with 29% of the global consumption followed by India (21%), Bangladesh (7%), Indonesia (7%), Vietnam (4%) and Philippines (3%) (USDA, 2020).

Approximately by 2035, universal insistence for rice would rise upto 555 million tonnes among which 465 million tonnes are required only in Asian countries despite a steady decline in per capita consumption in China and India (GRiSP, 2013). Annual growth of 1.0–1.2% in rice yield beyond 2020 would be needed to feed the ever-growing population with affordable prices (GRiSP, 2013). The expected requirement of rice in India would be 130 and 168 million tonnes with reduced cultivated area of only 42 and 40 million ha by 2030

and 2050, respectively (Gupta *et al.*, 2020). However, documentation revealed that annual yield growth was only by greater than or equal to 1% in the earlier decade (Khush, 2013). In view of restricted resources presently spotted like reducing arable area and irrigation water availability in addition to abundant climatic hindrance, namely biotic and abiotic stress background to escalate rice production left overs an immeasurable challenge (Gramaje *et al.*, 2020). Theoretically there is a great potential to be tapped to raise yields, such as hybrid rice technology, new plant type and application of molecular breeding. Among them, hybrid rice technology offers as the most effective and sustainable option to enhance rice productivity. The economical way to increase productivity is to develop hybrid varieties based on the successful experience of identifying superior hybrids and their large scale adoption in China (Galal *et al.*, 2017). Considering the success of hybrid rice technology in China (Lin and Yuan, 1980) as leading producer of hybrid rice among the nations (Swaminathan, 2006) and other countries including India has been witnessed as an important and readily adoptable genetic option for increasing the rice production and could be identified as viable solution to meet the ever-increasing food demand in different countries (Rai, 2009 ; Sanghera and Wani, 2008; Virmani *et al.*, 2003).

Short communication

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The hybrid rice technology revolutionized the rice farming through boosting the yield from 35 to 40 q ha⁻¹ from straight varieties of rice to the tune of 65 to 70 q ha⁻¹ in rice hybrids (Yuan *et al.* 1989). Hybrid rice technology helped the farmers in raising their economic status and helped in changing areas under straight varieties to rice hybrids in China (Yuan *et al.*, 1989). In India, as a result of concerted efforts made over the last three decades, 127 hybrids with high yield potential and better grain quality have been released for commercial cultivation in different rice growing states across the country (ICAR-IIRR, 2021). Immense efforts of rice breeders made during the last ten years have enabled the country to become the second largest in the world to develop and commercialize hybrid and its technology. (Rekah *et al.*, 2020). It's a matter of concern to note that area under hybrid rice remains at 3 million ha since 2016 and it might be due to unfavourable monsoons at the beginning of crop season besides factors like inadequate yield heterosis (ICAR-IIRR, 2020). Breeding strategies for identification of hybrids which have at least 15 % higher yield than high yielding varieties need to be strengthened.

For generating promising hybrids, the first step would be selection of desirable parents. The parental lines are considered as backbone of hybrid rice breeding subsequently the execution of the offspring predominantly rely on the inheritance ability of the parents. Breeders are hence persistently fronting a dispute challenge while hand-pick, breed, improve and develop promising parental lines for production of heterotic hybrids (Gramaje *et al.*, 2020). The selection of parents cannot be established totally on mean performance, however, require information on gene actions. In this context, the purpose of combining ability is to identify the potentiality of different parental lines to inherit genetic material to its offspring's. (Sprague and Tatum, 1942; Aly, 2013). Line × Tester analysis devised by Kempthorne (1957) is an efficient mating design followed to estimate *gca* and *sca* which empower the potent screening of parental lines for further selection. In the current scenario, studies were accomplished on the combining ability and magnitude of heterosis for grain yield and important yield attributes in 36 rice hybrids.

The experiment was conducted at Rice Research Center of Agricultural Research Institute, Hyderabad, Telangana, India. During *rabi*, 2017-18, 12 restorer lines and 3 stable CMS lines *viz.*, CMS 11A, CMS 23A and CMS 59A were sown and planted in three different staggered sowings and crosses were made in line × tester mating design to obtain 36 hybrids. These 36 hybrids along with their 15 parents and four checks (US 314, PA 6444, MTU 1010 and RNR 15048) were grown in

5.67 m² plot with two replications in randomized complete block design (RBD) by adopting a spacing of row to row 20 cm and plant to plant 15cm during *khariif*, 2018. For CMS lines, corresponding maintainer lines were raised to record yield and its contributing traits. Standard agronomic package of practices was followed to raise healthy crop. Recommended dose of fertilizers *viz.*, 40 N: 20 P₂O₅: 16 K kg per acre were applied under irrigated ecosystem.

Five plants were selected at random in each plot and observations were recorded on different traits *viz.*, plant height (cm), effective bearing tillers, panicle length (cm), spikelet fertility (%) and number of grains per panicle. Days to 50% flowering and grain yield (kg/plot) were noted on entire plot basis, however, test weight (g) was recorded on a random sample of 1000 grains taken in each plot. The means of all characters were subjected for variance analysis (Panse and Sukhatme 1985), combining ability (Kempthorne, 1957) and estimated the heterosis (Hayes *et al.*, 1955) using statistical methods. Among checks, PA 6444 and RNR 15048 were identified as promising with high grain yield in hybrid and varieties, respectively and hence considered for estimating standard heterosis over hybrid and variety. Relative significance of *gca* and *sca* was estimated by the predictability ratio $2\sigma^2g/2\sigma^2g + \sigma^2s$ (Baker, 1978) for fixed effect model where, $2\sigma^2g$ and σ^2s is additive and non-additive component of variance, respectively. Average degree of dominance was calculated by the formula $\sqrt{\sigma^2s/2\sigma^2g}$.

The analysis of variance revealed that for parents, hybrids and parent vs hybrids were highly significant in all the traits except spikelet fertility for parents, effective bearing tillers and number of grains per panicle for crosses (Table 1). Mean sum of squares for crosses was partitioned into different components as lines, testers and line × tester. Significant variances were observed among lines for all the traits except spikelet fertility whereas in testers, significant variances were recorded for the characters *viz.*, days to 50 per cent flowering, plant height, effective bearing tillers and panicle length. In lines × testers, significant variances were observed for four traits *viz.*, days to 50% flowering, plant height, panicle length, and spikelet fertility. Parents × hybrids showed significant variance for seven characters indicating the superiority of hybrids and the presence of heterosis for almost all the traits studied. These outcomes accentuate the significance of combining ability analysis in the material and possibility for establishing the promising parents and heterotic cross combinations for yield improvement.

In the present study, GCA variances were higher than SCA variances for all the traits barring effective bearing

Table 1: Analysis of variance, general and specific combining ability variance estimates and proportionate gene action for various traits in rice.

Source of variation	DF	Days to 50% flowering	Plant height (cm)	Effective bearing tillers	Panicle length (cm)	Test weight (g)	Number of grains per panicle	Spikelet fertility (%)	Grain yield per plot (kg)
Treatments	50	46.12**	121.71**	7.71**	5.17**	18.90**	2163.78**	110.18**	3.44**
Parents	14	80.26**	247.53**	10.91**	11.80**	17.05**	2522.70**	28.7	0.56**
Lines	11	76.13**	98.58**	11.69**	10.99**	19.04**	3106.85**	16.35	0.65**
Testers	2	105.50**	216.52**	11.27*	18.84**	9.23	460.5	11.64	0.32
Line × Tester	1	75.20**	1948.10**	1.58	6.62*	10.75	221.4	198.66**	0.1
Parents × hybrids	1	227.51**	769.78**	111.05**	7.09*	49.42**	18217.72**	965.88**	106.66**
Hybrids	35	27.28**	52.86**	3.48	2.46**	18.76**	1561.52	118.33**	1.65**
Error	35	2.11	16.68	2.71	1.09	3.91	537.05	21.2	0.18
Total	71	230.88	69.59	6.1	3.11	11.29	1338.02	65.98	1.8
σ^2_g		15.91	18.81	0.27	0.59	4.31	214.42	38.84	0.50
σ^2_s		4.69	7.22	0.70	0.18	1.39	218.29	22.58	0.28
Predictability ratio ($2\sigma^2_g/2\sigma^2_g + \sigma^2_s$)		0.87	0.84	0.44	0.87	0.86	0.66	0.77	0.78
Average Degree of Dominance ($\sqrt{\sigma^2_s/2\sigma^2_g}$)		0.38	0.44	1.14	0.39	0.40	0.71	0.54	0.53
Nature of gene action		Additive	Additive	Non-Additive	Additive	Additive	Additive	Additive	Additive

*, ** Significant at 5%, 1% probability level, respectively; σ^2 : variance; g: general combining ability; s: specific combining ability

Table 2: Mean, general combining ability effects of lines and testers for yield and its attributes in rice

Parents	Days to 50% flowering			Plant height (cm)			Effective bearing tillers			Panicle length (cm)			Test weight (g)			Number of grains per panicle			Spikelet fertility (%)			Grain yield per plot (kg)		
	MEAN	GCA	MEA	MEAN	GCA	MEA	MEAN	GCA	MEA	MEAN	GCA	MEA	MEAN	GCA	MEA	MEAN	GCA	MEA	MEAN	GCA	MEA	MEAN	GCA	MEA
RNR 17441	91.5	1.72**	103.5	0.76	14.0	0.87	23.81	0.16	25.64	0.48	112	-15.60	93.8	5.89**	4.20	0.84**								
RNR 21571	91.5	1.22*	111.3	2.20	17.0	-0.47	25.25	0.16	25.15	1.92*	92	-7.43	94.8	-7.18**	4.25	0.16								
RNR 25842	95.0	0.72	113.1	1.03	15.7	0.10	24.00	0.46	20.34	-2.37**	180	34.57**	96.8	-5.84**	4.05	0.50**								
RNR 25843	93.5	1.06	111.3	1.30	14.5	2.13**	24.95	0.16	20.90	-2.33**	196	34.24**	96.4	-0.48	3.64	0.01								
NLR 3296	94.5	0.56	100.1	-7.24**	15.1	1.63*	18.95	-1.16	18.60	-2.53**	133	17.90	91.3	4.22*	3.04	0.01								
TP 29651	91.5	-0.28	99.5	-3.07	13.5	1.00	22.75	-0.79	19.45	-0.68	115	-1.10	95.1	-0.26	3.30	0.18								
TP 29631	93.5	-1.94**	102.6	-0.74	14.5	-0.53	24.70	0.41	20.24	0.76	217	11.90	91.7	4.66*	4.14	0.71**								
TP 30011	101.5	2.72**	106.0	1.75	21.4	-1.20	25.10	0.84	26.99	1.14	139	-1.26	92.2	4.12*	2.88	0.62**								
TP 30173	82.5	-0.44	102.1	0.20	14.2	-1.47**	19.65	-0.77	21.82	-1.74*	154	-24.10*	96.0	-7.41**	3.84	-1.12**								
IR 11A 334	94.5	1.56*	100.0	3.93*	15.7	-1.30	25.50	1.24**	21.30	0.07	146	-10.26	96.6	4.46*	4.82	0.29								
P 1509	82.5	-3.61**	113.6	3.10	11.3	-0.53	25.55	0.29	27.15	6.73**	94	-34.43**	87.5	3.22	3.76	-0.53**								
CB 12593	80.5	-3.28**	89.8	-3.20	14.2	-0.23	20.90	-1.02*	19.66	-1.45	121	-4.43	91.4	-5.41**	3.23	-1.30**								
Testers																								
CMS 11B	95.5	-0.57	77.0	-1.79*	14.9	0.19	21.70	-0.30	19.39	-0.96*	127	-4.35	86.6	-4.67**	3.70	-0.32**								
CMS 23B	87.5	-2.69**	79.7	-1.98*	13.8	0.08	24.23	-0.35	23.25	1.28**	152	-4.93	89.9	0.59	3.18	-0.20*								
CMS 59B	102.0	3.26**	96.2	3.77**	18.3	-0.27	27.86	0.65**	19.68	-0.32	125	9.28	85.2	4.08**	3.97	0.52**								

*, ** Significant at 5%, 1% probability level, respectively

Table 3: Specific combining ability estimates in crosses for yield and yield contributing characters in rice

Cross	Days to 50% flowering	Plant height (cm)	Effective bearing tillers	Panicle length (cm)	Test weight (g)	Number of grains per panicle	Spikelet fertility (%)	Grain yield per plot (kg)
CMS 11A × RNR 17441	1.73	0.35	0.51	-0.15	-0.03	20.18	1.26	0.11
CMS 23A × RNR 17441	-0.64	-0.75	0.27	0.60	0.23	3.26	-0.11	0.05
CMS 59A × RNR 17441	-1.10	0.39	0.84	-0.45	0.06	-23.44	-1.15	-0.16
CMS 11A × RNR 21571	0.24	-2.47	-0.74	0.05	1.40	-3.49	2.52	0.26
CMS 23A × RNR 21571	-0.14	1.61	-0.10	0.40	0.53	11.60	3.81	0.11
CMS 59A × RNR 21571	-0.10	0.86	-0.03	-0.45	-1.94	-8.11	-6.33	-0.37
CMS 11A × RNR 25842	-2.76*	-0.51	-0.31	-0.70	-2.17	15.01	-1.56	-0.24
CMS 23A × RNR 25842	-0.64	-1.42	0.33	0.15	0.26	-21.90	-10.52	-0.40
CMS 59A × RNR 25842	3.40**	1.92	-0.26	0.55	1.91	6.89	12.09	0.64*
CMS 11A × RNR 25843	-3.10**	-3.77	0.66	0.95	-1.94	11.35	-10.68	-1.03**
CMS 23A × RNR 25843	-0.47	-0.19	-0.40	-0.80	0.27	-0.07	5.01	0.11
CMS 59A × RNR 25843	3.57**	3.96	0.84	-0.15	1.67	-11.28	5.67	0.92**
CMS 11A × NLR 3296	1.40	1.35	-0.14	0.07	0.55	-20.82	4.67	-0.07
CMS 23A × NLR 3296	2.03	0.04	-0.70	-0.28	-0.24	10.76	0.56	0.18
CMS 59A × NLR 3296	-3.43**	-1.40	0.58	0.21	-0.31	10.06	-5.23	-0.11
CMS 11A × TP 29651	0.74	3.09	0.79	0.90	0.20	-47.32**	-6.09	0.07
CMS 23A × TP 29651	-0.64	-0.02	-1.37	-1.50	-1.14	23.26	4.99	-0.16
CMS 59A × TP 29651	-0.10	-3.07	0.51	0.60	0.94	24.06	1.10	0.09
CMS 11A × TP 29631	-2.10*	-0.94	-0.28	-0.35	0.81	-8.32	-3.16	-0.92**
CMS 23A × TP 29631	-1.47	2.05	-0.23	-0.10	0.34	-9.74	3.83	0.83**
CMS 59A × TP 29631	3.57**	-1.10	-0.73	0.45	-1.15	18.06	-0.67	0.09
CMS 11A × TP 30011	1.24	-3.78	0.39	-0.98	0.95	-14.15	-0.18	-0.22
CMS 23A × TP 30011	0.36	1.86	0.33	1.07	-0.77	9.93	1.71	0.11
CMS 59A × TP 30011	-1.59	1.91	-0.96	-0.09	-0.18	4.22	-1.53	0.11
CMS 11A × TP 30173	1.40	-1.68	-0.44	-0.97	2.95*	8.18	4.81	0.40
CMS 23A × TP 30173	0.52	1.01	1.40	0.99	1.33	3.76	-1.26	-0.50
CMS 59A × TP 30173	-1.93	0.66	-0.13	-0.02	-4.28**	-11.94	-3.55	0.10
CMS 11A × IR 11A 334	0.40	-1.21	-0.51	-0.38	0.29	-14.65	2.39	-0.09
CMS 23A × IR 11A 334	0.52	1.18	0.63	0.57	0.19	11.43	-0.77	0.64*
CMS 59A × IR 11A 334	-0.93	0.03	-0.89	-0.19	-0.48	3.22	-1.62	-0.55
CMS 11A × P 1509	-1.93	3.23	1.13	0.57	-1.31	20.51	3.62	0.79*
CMS 23A × P 1509	-0.30	-8.29**	-0.23	-1.23	-1.74	-29.90	-3.84	-0.72*
CMS 59A × P 1509	2.23*	5.06	-0.29	0.66	3.04*	9.39	0.22	-0.08
CMS 11A × CB 12593	2.73*	6.33*	0.23	0.99	-1.46	33.51*	2.41	0.93**
CMS 23A × CB 12593	0.86	2.91	0.07	0.14	0.73	-12.40	-3.41	-0.26
CMS 59A × CB 12593	-3.59**	-9.24**	2.37	-1.12	0.73	-21.11	1.00	-0.67*

*, ** Significant at 5%, 1% probability level, respectively

Table 4: Heterobeltiosis (HB) and standard heterosis over variety (SHV), standard heterosis over hybrid (SHH) for yield and yield contributing traits in rice

Cross	Days to 50% Flowering				Plant Height				Effective Bearing Tillers				Panicle Length			
	HB	SHV	SHH	HB	SHV	SHH	HB	SHV	SHH	HB	SHV	SHH	HB	SHV	SHH	
CMS 11A × RNR 17441	2.62	-6.67**	-7.98**	-9.47*	-12.51**	-8.05	-2.68	42.16*	81.25**	0.63	-3.04	41.30**				
CMS 23A × RNR 17441	2.19	-10.97**	-12.21**	-10.72*	-13.73**	-9.32*	-6.43	28.43	63.75**	1.86	-0.20	45.43**				
CMS 59A × RNR 17441	-2.94	-5.71**	-7.04**	-4.06	-7.28	-2.55	-24.80**	35.29*	72.50**	-11.67**	-0.40	45.13**				
CMS 11A × RNR 21571	0.52	-8.57**	-9.86**	-17.07**	-13.82**	-9.42*	-20.59**	32.35	68.75**	-4.36	-2.23	42.48**				
CMS 23A × RNR 21571	2.19	-10.95**	-12.21**	-13.57**	-10.18*	-5.59	-30.59**	15.69	47.50*	-3.17	-1.01	44.25**				
CMS 59A × RNR 21571	-2.45	-5.24**	-6.57**	-9.07*	-5051	-0.69	-34.06**	18.63	51.25*	-11.67**	-0.40	45.13**				
CMS 11A × RNR 25842	-3.14*	-11.90**	-13.15**	-17.72**	-13.07**	-8.64*	-16.19	29.41	65.00**	-1.25	-4.05	39.82**				
CMS 23A × RNR 25842	-2.63	-11.90**	-13.15**	-18.69**	-14.10**	-9.72*	-18.73	25.49	60.00**	1.24	-0.81	44.54**				
CMS 59A × RNR 25842	0.49	-2.38**	-3.76**	-10.65**	-5.6	-0.79	-28.61**	28.43	63.75**	-7.00	4.86	52.80**				
CMS 11A × RNR 25843	-3.14*	-11.30**	-13.15**	-19.05**	-15.87**	-11.58**	0.67	47.06**	87.50**	0.40	1.42	47.79**				
CMS 23A × RNR 25843	-0.53	-11.43**	-12.68**	-15.99**	-12.70**	-8.24*	8.97	54.90**	97.50**	-6.81	-5.87	37.17**				
CMS 59A × RNR 25843	0.98	-1.90**	-3.29*	-7.1	-3.45	1.47	-21.53*	41.18*	80.00**	-10.59**	0.81	46.90**				
CMS 11A × NLR 3296	1.05	-8.10**	-9.39**	-13.43**	-19.05**	-14.92**	2.97	52.94**	95.00**	5.06	-7.49	34.81**				
CMS 23A × NLR 3296	0.53	-9.52**	-10.80**	-14.93**	-20.45**	-16.39**	-4.29	42.16*	81.25**	-7.23	-9.11*	32.45**				
CMS 59A × NLR 3296	-6.37**	-9.05**	-10.33**	-10.63*	-16.43**	-12.17**	-25.89**	33.33*	70.00**	-14.00**	-3.04	41.30**				
CMS 11A × TP 29651	-0.52	-9.52**	-10.80**	-6.93	-13.54**	-9.13*	-1.34	44.12**	83.75**	5.71	-2.63	41.89**				
CMS 23A × TP 29651	0	-12.86**	-14.08**	-10.25*	-16.62**	-12.37**	7.25	45.10**	85.00**	-10.74*	-12.55**	27.43**				
CMS 59A × TP 29651	-3.92**	-6.67**	-7.98**	-7.54	-14.10**	-9.72*	-32.97**	20.59	53.75*	-11.31**	0.00	45.72**				
CMS 11A × TP 29631	-5.24**	-13.81**	-15.02**	-11.45**	-15.13**	-10.79*	-12.08	28.43	63.75**	-2.83	-2.83	41.59**				
CMS 23A × TP 29631	-4.81**	-15.24**	-16.43**	-8.72*	-12.51**	-8.05	-15.86	19.61	52.50*	-2.02	-2.02	42.77**				
CMS 59A × TP 29631	-1.96	-4.76**	-6.10**	-6.19	-10.08*	-5.50	-35.15**	16.67	48.75*	-7.54	4.25	51.92**				
CMS 11A × TP 30011	-2.96*	-6.19**	-7.51**	-14.58**	-15.45**	-11.14**	-47.66**	9.80	40.00	-5.18	-3.64	40.41**				
CMS 23A × TP 30011	-5.91**	-9.05**	-10.33**	-9.43*	-10.36*	-5.79	-42.99**	19.61	52.50*	2.79	4.45	52.51**				
CMS 59A × TP 30011	-2.45	-5.24**	-6.57**	-3.96	-4.95	-0.10	-44.86**	15.69	47.50*	-7.90*	3.85	51.33**				
CMS 11A × TP 30173	0	-9.05**	-10.33**	-10.77*	-14.94**	-10.60*	-28.19*	4.90	33.75	2.07	-10.12*	30.97**				
CMS 23A × TP 30173	5.71**	-11.90**	-13.15**	-8.33*	-12.61**	-8.15*	-21.83	8.82	38.75	-0.41	-2.43	42.18**				
CMS 59A × TP 30173	-5.88**	-8.57**	-9.86**	-3.04	-7.56	-2.85	-31.34**	23.53	57.50**	-13.46**	-2.43	42.18**				
CMS 11A × IR 11A 334	1.05	-8.10**	-9.39**	-4.7	-11.02**	-6.48	-25.71*	14.71	46.25*	-2.75	0.40	46.31**				
CMS 23A × IR 11A 334	0	-10.00**	-11.27**	-2.5	-8.96*	-4.32	-28.89**	9.80	40.00	0.78	4.05	51.62**				
CMS 59A × IR 11A 334	-2.94*	-5.71**	-7.04**	2.1	-4.67	0.20	-34.60**	17.65	50.00*	-6.82	5.06	53.10**				
CMS 11A × P 1509	-6.81**	-15.24**	-16.43**	-12.98**	-7.66	-2.94	-21.48	14.71	46.25*	-2.94	0.40	46.31**				
CMS 23A × P 1509	1.14	-15.71**	-16.90**	-23.27**	18.58**	-14.43**	-1.45	33.33*	70.00**	-10.18*	-7.09	35.40**				
CMS 59A × P 1509	-4.90**	-7.62**	-8.92**	-6.47	-0.75	4.32	-35.15**	16.67	48.75*	-7.18	4.66	52.51**				
CMS 11A × CB 12593	-1.57	-10.48**	-11.74**	6.51	-10.64**	-6.08	-15.44	23.53	57.50**	9.89*	-3.24	41.00**				
CMS 23A × CB 12593	2.86	-14.29**	-15.49**	2.5	-14.01**	-9.62*	-8.45	27.45	62.50**	-4.96	-6.88	35.69**				
CMS 59A × CB 12593	-10.29**	-12.86**	-14.08	-10.91*	-19.98**	-15.90**	-31.88**	22.55	56.25**	-18.31**	-7.89	34.22**				

*, ** Significant at 5%, 1% probability level, respectively

Table Contd...

Contd.

Table 4 Contd.

Cross	Test Weight			Number of grains per panicle			Spikelet Fertility %			Grain yield per plot		
	HB	SHV	SHH	HB	SHV	SHH	HB	SHV	SHH	HB	SHV	SHH
CMS 11A × RNR 17441	-11.37	87.58**	2.69	33.86	-53.93**	-27.51**	-6.13	-9.83*	-7.41	57.45**	14.08	12.43
CMS 23A × RNR 17441	-0.59	110.40**	15.18	0.00	-58.67**	-34.97**	-1.97	-5.83	-3.31	59.00**	15.20	13.53
CMS 59A × RNR 17441	-7.53	95.71**	7.14	11.55	-62.06**	-40.30**	0.64	-3.33	-0.74	71.39**	24.18**	22.38**
CMS 11A × RNR 21571	2.84	113.50**	16.88	21.65	-58.13**	-34.12**	-19.51**	-21.90**	-19.81**	42.94**	4.92	3.40
CMS 23A × RNR 21571	8.31	124.85**	26.09*	10.82	-54.20**	-27.93**	-12.61*	-15.20**	-12.93*	48.00**	4.23	2.72
CMS 59A × RNR 21571	-7.89	91.21**	4.68	30.28	-55.69**	-30.28**	-19.62**	-22.01**	-19.92**	48.00**	8.64	7.06
CMS 11A × RNR 25842	-11.50	48.62**	-18.64*	19.44	-41.73**	-8.32	-24.06**	-24.72**	-22.70**	45.75**	2.07	0.60
CMS 23A × RNR 25842	-2.49	87.12**	2.44	-1.39	-51.90**	-24.31*	-27.88**	-28.51**	-26.59**	44.88**	1.47	0.00
CMS 59A × RNR 25842	11.65	87.49**	2.64	22.50	-40.24**	-5.97	-0.93	-1.79	0.84	88.29**	31.87**	29.96**
CMS 11A × RNR 25843	-12.56	50.85**	-17.42	7.65	-42.82**	-10.02	-27.63**	-28.56**	-26.64**	25.44**	-19.95	-21.11**
CMS 23A × RNR 25843	-2.26	87.58**	2.69	1.53	-46.07**	-15.14	-5.91	-7.11	-4.62	61.59**	1.73	0.26
CMS 59A × RNR 25843	7.75	85.89**	1.76	3.06	-45.26**	-13.86	-1.61	-2.87	-0.26	87.03**	28.24**	26.38**
CMS 11A × NLR 3296	6.03	69.71**	-7.09	22.18	-55.96**	-30.70**	-1.64	-8.03	-5.57	51.56**	-3.28	-4.68
CMS 23A × NLR 3296	-5.33	81.68**	-0.54	26.89	-47.56**	-17.48	-0.38	-6.86	-4.36	87.87**	3.02	1.53
CMS 59A × NLR 3296	3.28	67.81**	-8.13	55.64**	-43.90**	-11.73	-2.90	-9.21	-6.78	61.21**	10.54	8.94
CMS 11A × TP 29651	13.42	82.09**	-0.32	-7.87	-68.29**	-50.11**	-21.56**	-23.64**	-21.60**	50.07**	-4.23	-5.62
CMS 23A × TP 29651	-1.20	89.60**	3.80	22.62	-49.32**	-20.26*	-4.36	-6.91	-4.41	64.85**	-6.04	-7.40
CMS 59A × TP 29651	19.08	93.48**	5.92	60.96	-45.26**	-13.86	-4.78	-7.32	-4.83	61.71**	10.88	9.28
CMS 11A × TP 29631	19.12	99.01**	8.95	-22.30*	-54.20**	-27.93**	-10.14	-15.61**	-13.35**	31.36**	-5.96	-7.32
CMS 23A × TP 29631	11.35	113.70**	16.99	-23.22*	-54.74**	-28.78**	3.22	-3.07	-0.47	76.60**	26.42**	24.60**
CMS 59A × TP 29631	12.60	88.11**	2.98	3.91	-43.36**	-10.87	2.13	-4.09	-1.52	76.36**	26.25**	24.43**
CMS 11A × TP 30011	-8.74	103.30**	11.30	7.53	-59.35**	-36.03**	-7.92	-13.10**	-10.77*	63.87**	4.58	3.06
CMS 23A × TP 30011	-6.82	107.59**	13.65	13.77	-52.98**	-26.01*	-0.16	-5.78	-3.26	104.72**	12.26	10.64
CMS 59A × TP 30011	-10.60	99.17**	9.04	30.47	-50.68**	-22.39*	0.11	-5.53	-3.00	81.99**	24.78**	22.98**
CMS 11A × TP 30173	8.85	96.04**	7.32	-2.92	-59.49**	-36.25**	-18.43**	-19.81**	-17.66	28.52*	-14.77	-16.00
CMS 23A × TP 30173	4.82	101.16**	10.12	-6.17	-60.84**	-38.38**	-19.26**	-20.62**	-18.50**	8.07	-28.32**	-29.36**
CMS 59A × TP 30173	-21.40*	41.56*	-22.50*	-7.14	-61.25**	-39.03**	-18.01**	-19.40**	-17.24**	38.16**	-5.27	-6.64
CMS 11A × IR 11A 334	7.51	89.06**	3.50	-4.10	-61.92**	-40.09**	-9.16	-10.13*	-7.72	21.58*	1.21	-0.26
CMS 23A × IR 11A 334	7.70	106.69**	13.15	8.85	-55.01**	-29.21**	-6.98	-7.98	-5.52	39.21**	15.89*	14.21
CMS 59A × IR 11A 334	6.88	87.95**	2.89	17.41	-53.39**	-26.65*	-4.24	-5.27	-2.73	29.56**	7.86	6.30
CMS 11A × P 1509	3.00	130.83**	26.37**	19.29	-58.94**	-35.39**	0.34	-10.13*	-7.72	57.31**	2.16	0.68
CMS 23A × P 1509	9.69	145.81**	34.57**	-34.10**	-72.76**	-57.14**	-4.78	-12.38*	-10.04*	20.35	-21.85**	-22.98**
CMS 59A × P 1509	21.38**	172.02**	48.92**	22.71	-58.27**	-34.33**	6.46	-4.66	-2.10	48.36**	1.73	0.26
CMS 11A × CB 12593	-0.18	62.03**	-11.30	53.15**	-47.29**	-17.06	-14.76**	-20.21**	-18.08**	43.03**	-8.72	-10.04
CMS 23A × CB 12593	3.46	98.56**	8.70	2.95	-59.89**	-36.89**	-15.36**	-20.78**	-18.65**	30.34*	-27.29**	-28.34**
CMS 59A × CB 12593	14.07	85.35**	1.47	22.31	-58.40**	-34.54**	-6.72	-12.69*	-10.35*	13.98	-21.85**	-22.98**

*, ** Significant at 5%, 1% probability level, respectively

tillers and number of grains per panicle (Table 1). The predictability ratio was near to unity for most of the traits *viz.*, panicle length (0.87), days to 50 per cent flowering (0.87), test weight (0.86), plant height (0.84), grain yield per plot (0.78), spikelet fertility (0.77) and number of grains per panicle (0.66) and revealing the preponderance of additive gene action in commanding these traits whereas for effective bearing tillers the value (0.44) was far from unity inferring the predominant role of dominance effects. Similarly, average degree of dominance was also found to be greater than one for effective bearing tillers (1.14) suggesting the predominant role of dominance variance and for left over traits influence of additive gene action was confirmed with less than one values. Similarly, certain researchers earlier mentioned the predominance of additive genetic components in rice for days to 50% flowering (Parimala *et al.*, 2018), plant height (Ramesh *et al.*, 2017), panicle length (Rukmini Devi *et al.*, 2018), 1000 grain weight and grain yield per plant (Sanjeev Kumar *et al.*, 2007).

Among lines, RNR 17441(0.84), TP 29631 (0.71), TP 30011 (0.62), RNR 25842 (0.50) and in testers CMS 59B (0.52) had exhibited positive and significant *gca* effect for grain yield per plot (Table 2). Among the lines, RNR 17441 and TP 30011 had significant *gca* effects in the desired direction for important traits *viz.*, grain yield per plot and spikelet fertility, whereas the line TP 29631 had significant *gca* effects for grain yield per plot, spikelet fertility and days to flowering. While among the testers, CMS 59B was good general combiners for the characters *viz.*, grain yield per plot, spikelet fertility and panicle length. However, the lines, CB12593, TP 30011 and the tester, CMS 11B had recorded significant negative *gca* effects for grain yield per plot, test weight and plant height. For higher test weight and earliness, P 1509 and CMS 23B were identified as good general combiners among lines and testers, respectively. In the present study, it was clearly observed in some cases that the lines and testers with good mean performance would not be good general combiners and *vice versa* and hence the potency of choice of parents based on mean performance alone was not relevant for speculate the combining ability of the parents, thus the relationship between mean performance and GCA effects was clear (Manjunath *et al.*, 2020).

The *sca* effects revealed that among thirty-six hybrids, highest positive significant *sca* effect was noticed in CMS 11B × CB 12593 (0.93) for grain yield per plot followed by CMS 59A × RNR 25843 (0.92), CMS 23A × TP 29631 (0.83), CMS 11A × P 1509 (0.79), CMS 59A × RNR 25842 (0.64) and CMS 23B × IR 11A 334 (0.64) and were considered as desirable (Table 3). Five hybrids exhibited negative and significant

sca effects for days to flowering *viz.*, CMS 59A × CB 12593 (-3.59), CMS 59A × NLR 3296 (-3.43), CMS 11A × RNR 25843 (-3.10), CMS 11A × RNR 25842 (-2.76) and CMS 11A × TP 29631 (-2.10) and were considered to be highly desirable for earliness. Two hybrids, CMS 59A × P 1509 (3.04) and CMS 11A × TP 30173 (2.95) exhibited positive significant *sca* effects for test weight. For number of grains per panicle significant positive *sca* effect was recorded in hybrid, CMS 11A × CB 12593 (33.51). CMS 11A × CB 12593 was identified as good specific combiner for characters *viz.*, grain yield per plot and number of grains per panicle. The values of *sca* effects of hybrids and the *gca* of corresponding parents clearly depict that higher *sca* values need not necessarily be from parents having higher *gca* values. Higher or lower *sca* effects are possible with parents having either higher or lower *gca* effects realizing the presence of dominance × dominance, additive × additive and additive × dominance gene interactions. However, parents with high × low, low × high or high × high *gca* effects were also reported by Salgotra *et al.* (2009).

Marked variation in the expression of standard heterosis and heterobeltiosis for yield and its related attributes was observed for all cross combinations. Mid-parent heterosis and heterobeltiosis should be considered for genetic heterosis whereas standard heterosis needs to be more pertinent to obtain superior hybrids for commercial adoption (Sreewongchai *et al.*, 2021). Heterosis studies showed that the heterobeltiosis ranged from 8.07 to 104.72 % for grain yield per plot (Table 4). Thirty three hybrids had shown positive significant heterosis for grain yield. Highest positive significant heterobeltiosis was recorded by CMS 23A × TP 30011, CMS 59A × RNR 25842, CMS 23A × NLR 3296, CMS 59A × RNR 25843 and CMS 59A × TP 30011.

Six hybrids *viz.*, CMS 59A × RNR 25842, CMS 59A × RNR 25843, CMS 23A × TP 29631, CMS 59A × TP 29631, CMS × TP 30011 and CMS 59A × RNR 17441 were recorded significant positive standard heterosis over hybrid check (PA 6444) for grain yield per plot. However, in addition to these six hybrids, CMS 23A × IR 11A 334 also exhibited positive significant standard heterosis over variety (RNR 15048) for grain yield per plot.

Standard heterosis over variety (RNR 15048) was highly significant positively and negatively for test weight and number of grains per panicle, respectively for all the hybrids indicating that RNR 15048 had very slender grain with dense panicle when compared to test hybrids. Further, none of the hybrids had been observed positive standard heterosis for spikelet fertility inferring that the restoration ability of lines was not superior compared to check hybrid, PA 6444. All the hybrids

registered significant negative standard heterosis over both varietal and hybrid checks for days to flowering indicating the earliness in maturity. Similarly, negative heterosis was highlighted by earlier workers in rice (Srijan *et al.*, 2016). These findings are in consistent for significant positive heterosis with the earlier workers viz. Saravanan *et al.* (2008) for panicle length and number of grains per panicle, Singh *et al.* (2013), Bhati *et al.* (2015), Yogita *et al.* (2016), Manjunath *et al.* (2020) and Singh *et al.* (2020) for effective bearing tillers, panicle length, test weight, yield per plant, Pratap *et al.* (2013), Satheesh Kumar *et al.* (2016), Galal *et al.* (2017) for yield per plant, Begum *et al.* (2020) for days to 50% flowering and plant height with negative significant standard heterosis and for effective bearing tillers, panicle length, test weight, yield per plant showing positive significant standard heterosis.

The present investigation acknowledged the predominance of additive gene action for majority of the attributes studied. Among lines, RNR 17441, TP 29631, TP 30011, RNR 25842 and a tester, CMS 59A were identified as good parents for grain yield. Based on *per se* performance, *sca* effects and standard heterosis, three hybrids viz., CMS 59A × RNR 25842, CMS 59A × RNR 25843 and CMS 23A × TP 29631 were identified as superior hybrids with more than 20 per cent standard heterosis over hybrid check and need to be evaluated in multilocation to ascertain the stability in grain yield.

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