



## Research Article

# GENETIC ANALYSIS TO ASSESS THE PARENTAL LINES FOR BIOMETRICAL TRAITS IN RICE (*Oryza sativa* L.)

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Received: December 03, 2019; Revised: December 26, 2019; Accepted: December 27, 2019; Published: December 30, 2019

**Abstract:** The study was conducted to estimate mean performance and general combining ability effects of parents with an objective to develop highly heterotic heat tolerant rice hybrids. The investigation was carried out by using four diverse CGMS lines and 50 tester parents in the hybridization process and 200 hybrids were developed by following line x tester mating design. Analysis of variance for combining ability revealed significant differences among lines and testers. Among the CGMS lines, TNAU CMS 2A showed significant desirable *gca* effects for earliness, plant height, number of productive tillers per plant, panicle length, spikelet fertility and 100 grain weight and another CGMS line IR 68897A revealed significant desirable *gca* effects for earliness, number of spikelets per panicle, number of filled grains per panicle and grain yield per plant. Eight testers viz., CB00-13-84, CB00-13-55, CB00-13-39, CB00-13-171, CB00-14-65, CB00-13-106, CB00-14-81 and CB00-13-133 were good general combiners for earliness. The genotypes COMS 23A, TNAU CMS 2A, IR 8, CB00-13-113, IR 36, HTL 31, HTL 25, HTL 32 and BALILLA were good general combiners for plant height indicating the presence of favourable alleles for desirable plant height. The CGMS line COMS 24A was found to be a good general combiner for number of productive tillers per plant, number of spikelets per panicle, number of filled grains per panicle, 100 grain weight, grain yield per plant. The tester CB00-14-56 was a good general combiner for number of spikelets per panicle, number of filled grains per panicle, spikelet fertility. The other testers CB00-14-82 and CB00-13-97 were good general combiners for panicle length, spikelet fertility, 100 grain weight. The genotypes COMS 24A, CB00-13-55 and CB00-13-126 were found to be the good general combiners for grain yield. The lines and testers showing significant and desirable combining ability effects were associated with better per se performance for the respective traits.

**Keywords:** Rice hybrids, Parental lines, Per se performance, Combining ability, Yield traits

**Citation:** Gangapur D.R., et al., (2019) Genetic Analysis to Assess the Parental Lines for Biometrical Traits in Rice (*Oryza sativa* L.). International Journal of Agriculture Sciences, ISSN: 0975-3710 & E-ISSN: 0975-9107, Volume 11, Issue 24, pp.- 9313-9319.

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**Academic Editor / Reviewer:** Dr PK Mishra, Dr Namburi Hari Satyanarayana

## Introduction

Rice (*Oryza sativa* L.) being the staple food of Asian countries, is consumed by more than half of the world's population. India secures the top place among the rice growing countries in the world. But, when compared to the world's rice productivity, India has low rice productivity per unit area. It had been used as a major food for over ten thousand years and has been cultivated in 114 countries. Major advances had occurred in rice production during the past four decades due to adoption of hi-tech packages [1].

The success of a plant breeding program greatly depends on the right choice of parents for hybridization and the gene action of different economic traits. Successful development of rice hybrids by utilizing the cytoplasmic genetic male sterility and fertility restoration system mainly depends on the availability of stable male sterile lines. The choice of suitable parents with desirable alleles, which on crossing could produce heterotic hybrids, is also important. Combining ability of the parents provides useful information on their selection for better performance of hybrids besides elucidating the nature and magnitude of gene action in the inheritance of a particular character [2]. The concept of combining ability helps the breeder to determine the nature of gene action involved in the expression of quantitative traits of economic importance [3]. The choice of suitable breeding method for the improvement of traits primarily depends on the relative importance of GCA and SCA variances [4]. Line x tester analysis is one of the important biometrical tools which provide information on the nature of gene action as well as general and specific combining ability of parents and hybrids [5].

The present investigation was carried out with the objective to identify best combining parents for yield and its contributing traits in rice.

## Materials and Methods

The materials for the present study comprised of four cytoplasmic genic male sterile (CGMS) lines and their respective maintainer lines and 50 testers. The raised beds were prepared in the nursery for sowing of seeds of all hybrids and their parents. The main field was puddled thoroughly and prepared for transplantation. The seedlings were uprooted from the nursery after 25 days of seed sowing and transplanted in the main field.

Two hundred hybrids developed through line x tester method and their parents were raised in a randomized block design with two replications during summer 2011 at Paddy Breeding Station, Tamil Nadu Agricultural University, Coimbatore, Tamil Nadu. The hybrid CORH 3 and the variety CO 49 were used as standard checks. For each genotype single seedling per hill was planted at 20 x 20 cm spacing in two rows of 1.2 m length consisting of 28 plants. Recommended management practices were adopted.

The performance of F<sub>1</sub> hybrid combinations and their parents were evaluated by recording observations on the following attributes as per the Standard Evaluation System [6]. Observations were recorded at physiological maturity stage in each replication on five randomly selected competitive plants for the yield and its contributing characters viz., days to 50 percent flowering, plant height, number of

Table-1 Analysis of variance for biometrical characters in rice

Source	D.F	Days to 50 per cent flowering	Plant height (cm)	Number of productive tillers per plant	Panicle length (cm)	Mean Square				
						Number of spikelets per panicle	Number of filled grains per panicle	Spikelet fertility (%)	100 grain weight(g)	Grain yield per plant (g)
Replications	1	0.16	6.96	9.54	0.79	14.65	59.58	52.85	0.00	9.06
Genotypes	253	146.16**	620.57**	13.31**	5.51**	863.80**	768.42**	29.53**	0.10**	38.09**
Parents	53	159.29**	838.95**	10.14**	5.35**	622.07**	556.85**	13.65	0.03**	8.80**
Lines	3	25.79**	41.49	4.16	6.76**	468.21**	379.67**	2.41	0.04**	3.23
Testers	49	159.21**	818.18**	10.53**	4.97**	531.08**	438.97**	10.03	0.03**	7.02**
Line vs Tester	1	563.89**	4249.09**	8.99	19.50**	5542.02**	6864.60**	224.38**	0.01*	112.88**
Parent vs Crosses	1	70.23**	3552.97**	319.29**	4.02**	47902.19**	47170.58**	823.39**	17.03**	1037.83**
Crosses	199	143.04**	547.67**	12.61**	5.56**	691.81**	591.59**	29.77**	0.03**	40.87**
Error	253	1.97	26.4	3.31	0.42	44.21	52.74	28.01	0.00	3.52

productive tillers per plant, panicle length, number of spikelets per panicle, number of filled grains per panicle, spikelet fertility, 100 grain weight and grain yield per plant.

## Results and Discussion

### Combining ability analysis

The variation due to genotypes was highly significant for all biometrical traits. The lines differed significantly among themselves for days to 50 percent flowering, plant height, number of productive tillers, number of spikelets per panicle, number of filled grains per panicle and grain yield per plant. The testers also differed significantly for all the characters except panicle length, spikelet fertility and 100 grain weight. The line x tester interaction was significant for all characters except days to 50 percent flowering [Tables-1]. The estimates inferred the presence of wide genetic variation among lines and testers. The results are in accordance with the earlier reports of [3] and [7].

### Mean performance of parents

The mean values of parents related to different biometrical traits are given in [Table-2].

### Days to 50 percent flowering

Among the four CGMS lines, TNAU CMS 2B was the earliest to flower (92.00 days) and COMS 23B recorded late flowering of 100.5 days. All CGMS lines viz., TNAU CMS 2B (92.00 days), IR 68897B (94.50 days), COMS 24B (96.50 days) and COMS 23B (94.00 days) recorded late flowering when compared to the grand mean (88.10 days). In case of testers, the mean performance ranged from 71.50 days (CB00-13-84) to 107.00 days (IR 8). A total of 16 testers recorded significantly higher values than the grand mean (88.10 days). The earliest to flower was CB00-13-84 (71.50 days) followed by CB00-13-55 (72.00 days) and CB00-13-39 (75.00 days) and the late flowering tester was IR 8 (107.00 days).

### Plant height

The mean performance of lines for plant height ranged from 85.80 cm (COMS 23B) to COMS 24B (95.78 cm). The CGMS lines recorded significantly lower in plant height when compared to grand mean (110.99 cm). Among the testers, the mean performance ranged from 64.07 cm (IR 8) to 136.72 cm (CB00-14-47). The mean performance for 28 testers was found to be significantly higher than the grand mean value (110.99 cm).

### Number of productive tillers per plant

For this trait, the mean performance of lines ranged from 12.50 (COMS 23B) to 15.50 (IR 68897B). All the lines COMS 23B (12.5), TNAU CMS 2B (12.84), COMS 24B (14.67) and IR 68897B (15.50) showed low mean values when compared to grand mean (14.90). Among the testers, the mean performance ranged between 8.34 (IR 8) to 21.17 (CB00 -13-61) when compared to the grand mean value (14.90). Only one tester (CB00 -13-61) recorded significantly higher mean performance for this trait.

### Panicle length

The mean performance of lines for panicle length ranged from 21.69 cm (COMS 23B) to 26.00 cm (COMS 24B). All the lines showed low mean value when compared to grand mean value 25.14 cm for panicle length. In case of testers, the mean performance ranged between 20.03 cm (IR 8) and 28.62 cm (CB00-14-81). When compared to the grand mean (25.14 cm), ten testers recorded higher mean values for panicle length.

### Number of spikelets per panicle

Among the lines, the mean performance for this trait ranged from 141.00 (TNAU CMS 2B) to 174.17 (COMS 24B). Three lines viz., COMS 24B (174.17), COMS 23B (172.50) and IR 68897B (164.84) recorded maximum number of spikelets when compared to the grand mean (138.83). In case of testers, the mean performance ranged from 110.00 (CB00-13-73) to 183.34 (CB00-14-37). When compared to the grand mean (138.83), three testers viz., CB00-14-37 (183.34), HTL 39 (175.00) and CB00-14-136 (170.00) recorded significantly higher mean values.

### Number of filled grains per panicle

The mean performance of lines ranged from 117.50 (TNAU CMS 2B) to 146.83 (COMS 23B). When compared to the grand mean (110.69), the line COMS23 B (146.83) and COMS 24B (145.84) recorded higher mean values. Among the testers, the mean performance ranged from 82.50 (IR 36) to 148.17 (CB00-14-37). Two testers viz., CB00-14-37 (148.17) and HTL 39 (143.00) recorded significantly higher mean values.

### Spikelet fertility

The mean performance of lines for this trait ranged from 83.33 percent (TNAU CMS 2B) to 85.64 percent (IR 68897B). All the lines showed low mean value when compared to grand mean value 79.58 percent. Among the testers, the mean performance ranged from 73.14 percent (IR 36) to 83.89 percent (CB00-13-97). All testers recorded significantly lower mean value when compared to grand mean of 79.58 percent

### Hundred grain weight

For hundred grain weight, the mean performance among lines ranged from 1.53 g (COMS 23B) to 1.82 g (TNAU CMS 2B). In case of testers, the mean performance ranged from 1.44 g (CB00-13-133) to 2.15 g (CB00-13-106). Among the testers, 22 testers recorded higher mean value for hundred grain weight when compared to grand mean (1.75 g).

### Grain yield per plant

For grain yield per plant, the mean performance of lines ranged from 19.19 g (COMS 23B) to 22.03 g (COMS 24B). The lines COMS 23B (19.19 g), IR 68897B (19.52 g), TNAU CMS 2B (20.10 g) and COMS 24B (22.03 g) had the lower mean performance over grand mean (23.89 g). The mean performance for grain yield among the testers ranged from 17.33 g (N 22) to 27.18 g (CB00-13-88). When compared to grand mean (23.89 g), 30 testers recorded higher mean value for grain yield per plant.

Table-2 Mean performance of lines and testers for yield and yield contributing traits in rice

Genotypes	Days to 50 percent flowering	Plant height (cm)	Number of productive tillers per plant	Panicle length (cm)	Number of spikelets per panicle	Number of filled grains per panicle	Spikelet fertility (%)	100 grain weight (g)	Grain yield per plant (g)
<b>Lines</b>									
TNAUCMS2B	92.00**	86.69	12.84	23.95	141.00	117.50	83.33	1.82	20.10
IR68897B	94.50**	90.69	15.50	22.84	164.84	141.17	85.64	1.70	19.52
COMS24B	96.50**	95.78	14.67	26.00	174.17**	145.84*	83.73	1.80	22.03
COMS23B	100.50**	85.80	12.50	21.69	172.50*	146.83*	85.12	1.53	19.19
Mean	95.88	89.74	13.88	23.62	163.13	137.84	84.50	1.71	20.21
<b>Testers</b>									
CB00-13-04	94.50**	123.78**	15.00	24.77	140.34	111.50	79.47	1.72	25.44
CB00-13-18	80.00	109.63	15.50	23.72	125.34	99.50	79.40	1.61	24.85
CB00-13-34	87.00	122.87**	15.50	23.15	117.00	90.67	77.48	1.76	21.14
CB00-13-39	75.00	134.75**	17.00	26.59*	135.00	107.33	79.50	1.70	25.27
CB00-13-52	82.50	107.75	15.50	24.80	119.50	93.83	78.56	1.72	24.62
CB00-13-55	72.00	122.74**	15.00	23.14	128.00	102.34	79.96	1.68	27.04
CB00-13-61	96.00**	121.60**	21.17**	27.19**	135.34	107.34	79.28	1.79	26.58
CB00-13-67	84.00	85.40	13.84	24.22	126.17	101.00	80.08	1.75	23.60
CB00-13-73	95.50**	136.04**	15.00	27.20**	110.00	83.17	75.62	1.72	24.93
CB00-13-79	88.00	122.35**	15.17	24.84	138.17	111.50	80.66	1.80	24.67
CB00-13-84	71.50	125.45**	16.67	23.80	136.34	105.50	77.41	1.70	25.53
CB00-13-88	86.50	117.84*	15.33	26.14	133.50	105.17	78.80	1.81	27.18
CB00-13-97	80.00	126.12**	15.50	27.90**	136.50	114.50	83.89	1.72	24.62
CB00-13-104	80.50	112.02	15.17	23.84	123.17	95.50	77.54	1.78	24.40
CB00-13-106	77.50	131.83**	15.50	24.09	130.84	102.00	77.99	2.15	23.49
CB00-13-113	88.00	73.05	14.00	24.04	127.50	99.84	78.29	1.79	23.12
CB00-13-117	83.50	106.04	9.84	24.94	126.67	98.84	78.03	1.73	25.90
CB00-13-126	90.50*	122.68**	14.17	24.69	129.17	101.17	78.33	1.71	26.30
CB00-13-133	79.00	126.14**	14.17	27.20**	167.34	135.34	80.89	1.44	24.92
CB00-13-145	80.50	112.02	11.83	25.00	127.00	101.50	79.93	1.81	23.50
CB00-13-157	88.50	135.72**	13.67	25.59	141.00	114.67	81.34	2.15	23.67
CB00-13-164	84.50	113.82	15.00	24.19	138.67	112.67	81.27	1.66	21.94
CB00-13-165	86.00	127.44**	17.17	25.02	164.00	133.34	81.29	1.62	25.95
CB00-13-171	77.00	114.27	12.67	25.00	151.67	121.67	80.21	1.69	23.32
CB00-14-09	81.50	114.27	11.17	25.95	119.34	94.00	78.76	1.80	24.05
CB00-14-12	86.00	124.89**	15.00	25.85	114.50	85.34	74.57	1.86	23.30
CB00-14-37	84.00	133.79**	15.67	26.98**	183.34**	148.17**	80.81	1.80	24.75
CB00-14-47	87.50	136.72**	16.00	26.19	139.84	112.84	80.70	1.96	23.47
CB00-14-56	90.00*	130.98**	14.67	24.87	152.17	125.67	82.58	1.85	24.39
CB00-14-65	77.00	134.99**	15.67	25.40	135.84	108.17	79.63	2.01	25.13
CB00-14-81	77.50	134.68**	16.34	28.62**	127.67	97.00	75.98	1.68	23.74
CB00-14-82	83.00	125.00**	14.00	27.83**	126.00	103.67	82.28	1.88	20.08
CB00-14-120	80.50	135.30**	13.34	26.05	143.17	118.67	82.88	1.61	20.24
CB00-14-136	83.50	131.40**	16.00	24.35	170.00*	136.34	80.19	1.61	26.23
CB00-14-144	85.00	128.20**	13.17	25.90	134.00	106.84	79.75	1.69	25.39
HTL2	103.50**	131.79**	14.17	25.17	130.67	100.67	77.04	1.74	23.35
HTL25	95.00**	82.82	15.17	23.35	124.84	96.83	77.57	1.71	20.67
HTL31	101.00**	79.67	17.17	23.62	132.00	106.50	80.70	1.66	25.35
HTL32	93.50**	85.45	17.50	24.90	124.67	95.00	76.20	1.69	24.02
HTL33	107.00**	90.25	18.50	23.95	157.17	120.84	76.88	1.77	23.85
HTL34	91.50**	82.55	14.50	25.87	125.83	94.50	75.05	1.79	24.68
HTL 35	101.50**	84.33	19.50	27.62**	132.50	102.00	76.95	1.66	25.69
HTL39	101.00**	130.30**	15.67	27.74**	175.00**	143.00*	81.71	1.73	22.50
HTL40	95.50**	128.45**	17.50	25.95	126.83	97.50	76.91	1.79	25.68
IR8	107.00**	64.07	8.34	20.03	149.17	117.67	78.87	1.74	24.54
IR36	89.50	79.54	18.84	25.22	112.84	82.50	73.14	1.55	22.38
BALILLA	85.50	88.27	11.00	25.85	162.00	128.67	79.43	1.81	22.02
DULAR	79.50	104.94	14.00	25.02	117.17	89.17	76.11	1.69	25.44
N22	79.50	89.52	13.17	25.87	132.50	105.67	79.73	1.62	17.77
SADARI	103.50**	101.00	13.50	22.88	131.50	102.50	77.92	1.90	24.92
Mean	87.15	113.69	14.98	25.24	135.78	107.39	80.00	1.75	24.11
Parental mean	87.80	111.91	14.90	25.12	137.80	109.65	80.24	1.75	23.82
<b>Checks</b>									
CORH3	90.00*	85.65	15.50	26.23	174.34	148.00	84.70	1.89	28.42
CO49	102.50**	86.10	14.34	25.07	158.83	129.50	86.47	1.92	22.74
Grand mean	88.10	110.99	14.90	25.14	138.83	110.69	79.58	1.75	23.89
S.E.	0.99	3.62	1.28	0.46	4.68	5.15	2.74	0.04	1.33
C.D. (5%)	2.76	10.03	3.57	1.28	13.04	14.24	7.58	0.11	3.70
C.D. (1%)	3.62	14.20	4.70	1.68	17.15	18.74	9.97	0.15	4.84

\* Significant at 5% level, \*\* Significant at 1% level

Table-3 General combining ability effects of parents for different biometrical traits

Parents	Days to 50 percent flowering	Plant height (cm)	Number of productive tillers per plant	Panicle length (cm)	Number of spikelets per panicle	Number of filled grains per panicle	Spikelet fertility (%)	100 grain weight (g)	Grain yield per plant (g)
<b>Lines</b>									
TNAUCMS2B	-1.89**	-10.94**	0.45*	0.08	-2.08**	-2.1**	-0.19	-0.02**	-1.10**
IR68897B	-0.84**	0.48	0.38*	-0.39**	-0.85	-1.13	-0.20	-0.04**	-0.09
COMS24B	1.36**	10.44**	0.47*	-0.03	6.98**	7.32**	0.78	0.13**	1.84**
COMS23B	1.36**	0.01	-1.31**	0.34**	-4.04**	-4.09**	-0.39	-0.07**	-0.65**
S. E. (g)	0.15	0.55	0.19	0.07	0.74	0.79	0.41	0.01	0.20
C.D. (5%)	0.29	1.08	0.37	0.13	1.47	1.56	0.81	0.01	0.40
<b>Testers</b>									
CB00-13-04	6.49**	4.26*	-0.21	-1.37**	6.51*	2.43	-1.72	0.11**	-1.44*
CB00-13-18	-6.39**	6.33**	-1.58*	-0.24	-5.03	-6.07*	-1.20	0.01	-2.81**
CB00-13-34	0.11	15.1**	-0.83	1.01**	1.18	-5.57*	-3.76**	-0.03	-2.19**
CB00-13-39	-11.39**	10.29**	-0.63	-0.07	-4.82	-5.03	-0.59	-0.01	-2.41**
CB00-13-52	-3.76**	3.69	1.58*	-0.01	-5.53*	3.05	4.82**	-0.01	0.95
CB00-13-55	-14.39**	16.79**	3.04**	0.60*	31.18**	32.3**	3.54*	0.08**	8.28**
CB00-13-61	7.99**	-11.73**	-0.50	-0.40	1.30	1.97	0.60	-0.03	0.42
CB00-13-67	-2.64**	-11.55**	-1.00	0.91**	3.88	-0.37	-2.14	0.00	-1.05
CB00-13-73	6.99**	5.84**	-1.08	1.68**	5.97*	4.97	0.25	0.05**	2.56**
CB00-13-79	0.74	9.29**	0.13	-0.60*	1.09	3.97	1.71	0.00	-0.85
CB00-13-84	-14.76**	8.34**	-2.08**	-0.02	-1.99	-8.24**	-4.09**	0.04*	-2.48**
CB00-13-88	-1.51**	2.41	2.04**	-2.24**	-1.66	1.10	1.50	0.02	-0.41
CB00-13-97	-5.89**	2.74	2.63**	0.94**	16.88**	19.22**	2.84	0.10**	6.55**
CB00-13-104	-6.01**	-2.08	-0.12	-0.58*	-0.12	-1.65	-1.12	0.07**	-2.52**
CB00-13-106	-9.51**	7.48**	-0.83	-2.29**	-6.24*	-2.49	1.93	-0.01	-2.59**
CB00-13-113	-0.26	-25.95**	-1.00	-1.26**	-11.7**	-9.86**	-0.08	-0.02	-4.44**
CB00-13-117	-4.51**	3.63	0.83	0.87**	8.42**	9.85**	1.56	0.02	0.39
CB00-13-126	2.36**	3.86*	1.42*	-0.05	9.26**	8.51**	0.37	0.00	2.57**
CB00-13-133	-8.01**	16.85**	-1.08	0.61*	-1.78	-5.24	-2.34	0.02	-1.90**
CB00-13-145	-6.76**	13.02**	-2.21**	1.21**	-12.99**	-13.36**	-1.65	-0.05**	-0.51
CB00-13-157	1.74**	7.36**	-1.79**	0.27	-4.37	-5.07	-0.81	0.01	-2.15**
CB00-13-164	-3.14**	7.82**	0.21	-0.82**	8.88**	4.85	-1.23	0.00	1.59*
CB00-13-165	-1.39**	-1.63	-0.33	-1.37**	-15.41**	-9.95**	1.98	-0.02	-0.65
CB00-13-171	-8.76**	10.32**	-1.00	-0.8**	6.59*	2.60	-1.75	0.00	1.16
CB00-14-09	-5.39**	5.07**	0.83	0.22	-0.57	-4.45	-2.29	0.05**	-1.04
CB00-14-12	-0.76	4.77*	0.62	0.52*	-5.03	-1.40	1.72	-0.03	1.34
CB00-14-37	-2.51**	6.34**	0.25	0.42	-13.41**	-11.74**	-0.26	0.00	0.00
CB00-14-47	-0.76	3.77	-1.33*	0.69**	11.80**	9.39**	-0.32	0.00	1.67*
CB00-14-56	3.24**	1.45	3.04**	1.88**	27.84**	28.55**	2.90*	0.01	8.76**
CB00-14-65	-8.51**	-2.2	0.54	0.12	6.34*	4.47	-0.52	-0.04*	0.65
CB00-14-81	-8.89**	13.15**	-2.33**	0.06	-17.58**	-14.74**	0.22	-0.02	-0.45
CB00-14-82	-3.89**	6.24**	4.62**	1.88**	24.55**	28.05**	4.19**	0.08**	9.83**
CB00-14-120	-5.51**	17.67**	1.75**	1.36**	-0.82	-4.36	-2.13	0.00	0.14
CB00-14-136	-3.89**	9.68**	-0.71	0.14	-13.53**	-9.61**	1.08	-0.04*	-0.34
CB00-14-144	-1.89**	8.52**	-1.33*	-1.24**	1.34	-2.95	-2.25	-0.01	-2.22**
HTL2	15.49**	-1.42	0.25	-0.14	1.18	2.26	0.70	-0.03	-2.08**
HTL25	9.49**	-20.56**	2.25**	0.34	-3.66	-0.90	1.32	0.00	-0.78
HTL31	12.74**	-17.96**	1.00	0.54*	-4.37	-0.57	1.88	-0.01	0.04
HTL32	6.36**	-12.34**	-0.75	-0.46	-12.2**	-12.53**	-1.64	-0.10**	-0.26
HTL33	17.86**	-20.41**	-0.54	-0.76**	2.67	0.55	-1.2	-0.02	-1.69*
HTL34	4.86**	-11.86**	-0.08	-0.48*	-6.07*	-7.99**	-1.78	-0.06**	-1.08
HTL 35	14.24**	-9.82**	-0.54	-0.72**	11.38**	8.68**	-0.48	0.02	1.10
HTL39	12.61**	-0.19	0.12	-0.08	-0.49	-2.28	-1.07	0.04*	-0.31
HTL40	7.11**	8.76**	-0.79	0.66**	-13.41**	-11.28**	0.17	-0.03	-1.84*
IR8	19.24**	-23.57**	1.92**	-0.27	15.18**	18.47**	3.35*	0.12**	1.45*
IR36	2.74**	-12.88**	-0.50	0.07	-2.49	3.89	3.72*	-0.10**	0.90
BALILLA	-2.26**	-14.9**	-0.79	0.21	-10.41**	-7.53**	0.67	0.00	-1.19
DULAR	-7.26**	-14.41**	0.00	-0.19	-9.7**	-9.78**	-1.21	-0.07**	-2.62**
N22	-6.76**	-14.48**	-1.46*	-0.84**	-8.12**	-10.82**	-2.37	-0.05**	-3.62**
SADARI	14.99**	-10.93**	-1.67*	0.11	-9.91**	-13.24**	-3.02*	-0.08**	-2.44**
S. E. (g)	0.52	1.93	0.66	0.24	2.63	2.80	1.46	0.02	0.72
C.D. (5%)	1.02	3.81	1.31	0.47	5.19	5.52	2.87	0.03	1.41

\* Significant at 5% level, \*\* Significant at 1% level

**General combining ability effects of parents**

The *gca* effects of lines as well as testers for various quantitative traits are presented in [Table-3].

**Days to 50 percent flowering**

The *gca* effects of the lines for days to 50 percent flowering ranged from -1.89 (TNAU CMS 2B) to 1.36 (COMS 23B). Significant negative *gca* effects were

noticed in two lines viz., TNAU CMS 2B (-1.89) and IR 68897B (-0.84). In case of testers, the *gca* effects for days to 50 percent flowering ranged from -14.76 (CB00-13-84) to 19.24 (IR 8). Significant negative *gca* effects were noticed in twenty seven male parents which ranged from -14.76 (CB00-13-84) to -1.39 (CB00-13-165).

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Table-4 Best parents based on per se performance and gca effects

SN	Characters	Per se performance	gca effects	Both per se performance and gca effects
1	Days to 50 per cent flowering	TNAUCMS2A	TNAUCMS2A	TNAUCMS2A
		IR68897A	IR68897A	IR68897A
		CB00-13-84	CB00-13-84	CB00-13-84
		CB00-13-55	CB00-13-55	CB00-13-55
		CB00-13-39	CB00-13-39	CB00-13-39
		CB00-13-171	CB00-13-106	CB00-13-171
		CB00-14-65	CB00-14-81	CB00-14-65
		CB00-13-106	CB00-13-171	CB00-13-106
		CB00-14-81	CB00-14-65	CB00-14-81
		CB00-13-133	CB00-13-133	CB00-13-133
		COMS23A	TNAUCMS2A	TNAUCMS2A
		TNAUCMS2A	COMS23A	COMS23A
2	Plant height (cm)	IR8	CB00-13-113	CB00-13-113
		CB00-13-113	IR8	IR8
		IR36	HTL25	HTL31
		HTL31	HTL33	HTL25
		HTL34	HTL31	IR36
		HTL25	BALILLA	
		HTL35	N 22	
		CB00-13-67	IR36	
		IR68897A	COMS24A	COMS24A
		COMS 24A	TNAUCMS2A	
		CB00-13-61	CB00-14-82	
		HTL 35	CB00-13-55	
3	Number of productive tillers per plant	IR36	CB00-14-56	
		HTL33	CB00-13-97	
		HTL32	HTL25	
		HTL40	CB00-13-88	
		CB00-13-165	IR8	
		HTL31	CB00-14-120	
		COMS24A	COMS23A	TNAUCMS2A
		TNAUCMS2A	TNAUCMS2A	CB00-13-97
		CB00-14-81	CB00-14-56	CB00-14-82
		CB00-13-97	CB00-14-82	CB00-13-73
		CB00-14-82	CB00-13-73	
		HTL39	CB00-14-120	
4	Panicle length (cm)	HTL 35	CB00-13-145	
		CB00-13-73	CB00-13-34	
		CB00-13-133	CB00-13-97	
		CB00-13-61	CB00-13-67	
		COMS24A	COMS24A	COMS24A
		COMS23A	COMS23A	CB00-14-56
		CB00-14-37	CB00-14-37	IR8
		HTL39	HTL39	
		CB00-14-136	CB00-14-136	
		CB00-13-133	CB00-13-133	
		CB00-13-165	CB00-13-165	
		BALILLA	BALILLA	
5	Number of spikelets per panicle	HTL33	HTL33	
		CB00-14-56	CB00-14-56	
		COMS23A	COMS24A	COMS24A
		COMS24A	IR68897A	CB00-14-56
		CB00-14-37	CB00-13-55	
		HTL39	CB00-14-56	
		CB00-14-136	CB00-14-82	
		CB00-13-133	CB00-13-97	
		CB00-13-165	IR8	
		BALILLA	CB00-13-117	
		CB00-14-56	CB00-14-47	
		CB00-13-171	HTL 35	
6	Number of filled grains per panicle	IR68897A	COMS24A	CB00-13-97
		COMS23A	TNAUCMS2A	CB00-14-56
		CB00-13-97	CB00-13-52	CB00-14-82
		CB00-14-120	CB00-14-82	CB00-13-165
		CB00-14-56	IR36	
		CB00-14-82	CB00-13-55	
		HTL39	IR8	
		CB00-13-157	CB00-14-56	
		CB00-13-165	CB00-13-97	
		CB00-13-164	CB00-13-165	
		TNAUCMS2A	COMS24A	COMS24A
		COMS24A	TNAUCMS2A	TNAUCMS2A
7	Spikelet fertility (%)	CB00-13-106	IR8	CB00-14-82
		CB00-13-157	CB00-13-04	
		CB00-14-65	CB00-13-97	
		CB00-14-47	CB00-13-55	
		SADARI	CB00-14-82	
		CB00-14-82	CB00-13-104	
		CB00-14-12	CB00-13-73	
		CB00-14-56	CB00-14-09	
		COMS24A	COMS24A	COMS24A
		TNAUCMS2A	IR68897A	CB00-13-55
		CB00-13-88	CB00-14-82	CB00-13-126
		CB00-13-55	CB00-14-56	
8	100 grain weight (g)	CB00-13-61	CB00-13-55	
		CB00-13-126	CB00-13-97	
		CB00-14-136	CB00-13-126	
		CB00-13-165	CB00-13-73	
		CB00-13-117	CB00-14-47	
		HTL 35	CB00-13-164	
		COMS24A	COMS24A	COMS24A
		TNAUCMS2A	IR68897A	CB00-13-55
		CB00-13-88	CB00-14-82	CB00-13-126
		CB00-13-55	CB00-14-56	
		CB00-13-61	CB00-13-55	
		CB00-13-126	CB00-13-97	
9	Grain yield per plant (g)	CB00-14-136	CB00-13-126	
		CB00-13-165	CB00-13-73	
		CB00-13-117	CB00-14-47	
		HTL 35	CB00-13-164	
		COMS24A	COMS24A	COMS24A
		TNAUCMS2A	IR68897A	CB00-13-55
		CB00-13-88	CB00-14-82	CB00-13-126
		CB00-13-55	CB00-14-56	
		CB00-13-61	CB00-13-55	
		CB00-13-126	CB00-13-97	
		CB00-14-136	CB00-13-126	
		CB00-13-165	CB00-13-73	



**Plant height**

The *gca* effects of lines for this trait varied from -10.94 (TNAU CMS 2B) to 10.44 (COMS 24B). The line TNAU CMS 2B recorded significant negative effects (-10.94) and the line COMS 24B (10.44) recorded significant positive effects. In case of testers, the *gca* effects ranged from -25.95 (CB00-13-113) to 17.67 (CB00-14-120). Significant negative effects were noticed in 15 testers which ranged from -25.95 (CB00-13-113) to -9.82 (HTL 35).

**Number of productive tillers per plant**

Among the lines, the range of *gca* effects was from -1.31 (COMS 23B) to 0.47 (COMS 24B). Positive and significant *gca* effects was observed in CGMS lines IR 68897B (0.38), TNAU CMS 2B (0.45) and COMS 24B (0.47). In case of testers, the range of *gca* effects was from -2.33 (CB00-14-81) to 4.62 (CB00-14-82). Significant and positive *gca* effects were observed in 10 testers which ranged from 1.42 (CB00-13-126) to 4.62 (CB00-14-82).

**Panicle length**

The *gca* effect for panicle length among lines ranged from -0.39 (IR 68897B) to 0.34 (COMS 23B). Significant positive *gca* effects for panicle length was recorded by the CGMS line COMS 23B (0.34). In case of testers, the range of *gca* effects was from -2.29 (CB00-13-106) to 1.88 (CB00-14-56). Significant and positive *gca* effects were observed in 15 testers and the highest being CB00-14-56 (1.88).

**Number of spikelets per panicle**

The *gca* effects for number of spikelets per panicle in case of CGMS lines ranged from -4.04 (COMS 23B) to 6.98 (COMS 24B). Positive and significant *gca* effect for this trait was recorded by the CGMS line COMS 24B (6.98). In case of testers, minimum *gca* effects was recorded by the male parent -17.58 (CB00-14-81) and the maximum *gca* effect was recorded by CB00-13-55 (31.58). Significant positive *gca* effects were recorded by 14 testers.

**Number of filled grains per panicle**

For the lines the *gca* effects ranged from -4.09 (COMS 23B) to 7.32 (COMS 24B). The CGMS line COMS 24B recorded the highest *gca* effects for number of filled grains per panicle. In case of testers, the *gca* effects ranged from -14.74 (CB00-14-81) to 32.30 (CB00-13-55). Significant positive *gca* effects were recorded by nine testers the lowest being 8.51 (CB00-13-126) and the highest being 32.30 (CB00-13-55).

**Spikelet fertility**

Among the lines, COMS 24A recorded positive and non-significant *gca* effects of 0.70. Among the testers, highest *gca* effect for spikelet fertility was recorded by CB00-13-52 (4.82) and the lowest by CB00-13-84 (-4.09). Six testers recorded significant and positive *gca* effects.

**Hundred grain weight**

The *gca* effects for this trait ranged from -0.07 (COMS 23B) to 0.13 (COMS 24B). Desirable negative significance for this trait was recorded by the lines COMS 23B (-0.07), IR 68897B (-0.04) and TNAU CMS 2B (-0.02). Among the testers, the *gca* effects ranged from -0.10 (IR 36) to 0.12 (IR 8). Significant and negative *gca* effects was recorded by nine testers ranging from -0.1 (IR 36) to -0.04 (CB00-14-65).

**Grain yield per plant**

Among the lines, highest *gca* effect (1.84) was observed in COMS 24B, while TNAU CMS 2B (-1.10) recorded the lowest value. Among testers the *gca* effects ranged from -4.44 (CB00-13-133) to 9.83 (CB00-14-82). Significant positive *gca* effect was recorded by nine testers. The tester CB00-14-82 (9.83) recorded maximum positive *gca* effect followed by CB00-14-56 (8.76), CB00-13-55 (8.28), CB00-13-97 (6.55) and CB00-13-126 (2.57).

**Per se performance and *gca* effects of parents**

Selection of parents based on per se performance and *gca* effects is of great

importance in breeding programmes, as it provides useful information on the choice of parents in terms of expected performance of hybrids and progenies [8]. Evaluation of parents based on per se performance and *gca* effects separately might lead to contradiction in selection of promising parents since per se performance of parents was not always associated with high *gca* effects [9]. Combination of both per se performance and *gca* effects will result in the selection of parents with good reservoir of superior genes [2]. Therefore, the parents were evaluated for high per se performance coupled with high *gca* effects [Table-4].

In the present study, the parents CB00-13-84, CB00-13-55 and CB00-13-39 had high mean performance combined with high *gca* effects, for earliness. Contribution of desirable alleles for earliness by these genotypes can be utilized for developing short duration hybrids. Good general combiners for earliness were earlier reported by [10] and [11].

The parental lines TNAU CMS 2A and CB00-13-113 were considered as good general combiners for plant height as they showed highly significant negative *gca* effects combined with high per se performance. In addition, the CGMS lines COMS 23A, IR 68897A and COMS 24A and the testers viz., IR 8, IR 36 and HTL 31 were identified as good general combiners for plant height indicating the presence of favourable alleles for semi dwarf plant type. The tester IR 36 was reported as a good general combiner for desirable plant height by [12] and [11]. Further, [13] and [14] also reported that intermediate plant height would be favourable when compared to tall plant.

More number of productive tillers per plant is one of the important traits to increase the yield in rice. High per se performance combined with positive significant *gca* effects were observed in the line COMS 24A for number of productive tillers per plant. Therefore, this genotype possessing desirable alleles can be used as potential donor for improvement of number of productive tillers. Similar results were obtained by [15].

Lengthy panicles are generally associated with higher number of spikelets per panicle resulting in higher productivity. The parental lines TNAU CMS 2A, CB00-13-97, CB00-14-82 and CB00-13-73 were identified as good general combiners with high mean performance indicating the presence of desirable genes for the expression of longer panicles. Hence, these testers can be used in the breeding programme for improving panicle length. Similar findings were reported by [16].

Number of spikelets per panicle is one of the most important yield components that improve yield. For this trait, the CGMS line COMS 24A and two testers viz., CB00-14-56 and IR 8 were found to be good general combiners with high mean performance. Expression of desirable genes for this trait decides the grain filling percent in hybrids which is due to the restoration ability of the male parents [17]. The results indicate that the genotypes COMS 24A and CB00-14-56 can be used as male parents to improve the number of filled grains in the hybrids. Similar results were obtained by [18]. With respect to spikelet fertility, the testers CB00-13-97, CB00-14-56, CB00-14-82 and CB00-13-165 were identified as good general combiners. These results are in conformity with the findings of [19] and [20]. These general combiners with desirable genes for spikelet fertility can be used as potential donors.

Hundred grain weights is one of the important characters that influence grain yield. The genotypes COMS 24A, TNAU CMS 2A and CB00-14-82, were found to be good general combiners for this trait. These genotypes can be utilized for developing good grain quality rice hybrids. Good general combiners with desirable alleles for 100 grain weight were reported by [21]. The genotypes COMS 24A, CB00-13-55, and CB00-13-126 were found to have desirable genes for expression of high grain yield per plant and were identified as good general combiners for this trait. The results are in conformity with reports of [14].

**Conclusion**

The genotypes showing high per se performance and significantly higher *gca* effects can be used as potential donors in the rice breeding programme for developing high yielding hybrids.

**Application of research:** The superior genotypes identified in the present study may be used as donors in the future rice breeding programme.

**Research Category:** Hybrid rice breeding

**Abbreviations:**

CGMS lines-Cytoplasmic Genic Male Sterile lines

cm- Centimetres, g- Grams

gca- General Combining Ability

sca- Specific Combining Ability

**Acknowledgement / Funding:** Authors are thankful to Centre for Plant Breeding and Genetics, Tamil Nadu Agricultural University, Coimbatore, 641003, Tamil Nadu, India.

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Research project name or number: Ph.D. Thesis

**Author Contributions:** All authors equally contributed

**Author statement:** All authors read, reviewed, agreed and approved the final manuscript. Note-All authors agreed that- Written informed consent was obtained from all participants prior to publish / enrolment

**Study area / Sample collection:** Centre for Plant Breeding and Genetics, Tamil Nadu Agricultural University, Coimbatore, 641003, Tamil Nadu, India.

**Cultivar / Variety / Breed name:** Rice (*Oryza sativa* L.)

**Conflict of Interest:** None declared

**Ethical approval:** This article does not contain any studies with human participants or animals performed by any of the authors.

Ethical Committee Approval Number: Nil

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