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Combining ability analysis for quality traits in rice (*Oryza sativa* L.)

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Abstract
The present investigation was carried out to study general and specific combining ability of 16 parents and 48 hybrids of rice for their grain quality characters. The 48 hybrids derived from 4 lines and 12 restore parents as testers in L X T matting design. Analysis of variance for combining ability revealed significant for all the characters. Variance due to SCA were greater than GCA for all the traits indicating preponderance of non-additive gene action for these traits except kernal elongation ratio, shows GCA variance higher then SCA variance means predominantly controlled by additive gene action. The GCA effects revealed that among the testers R5, R2, R4 and R6; and among lines CMS 6A and CMS 15A had good genera Quality traits, additive gene action, GCA, SCA and l x t matting design l combining ability for most of the quality traits. On the basis of SCA effects crosses CMS 15A × R5, CMS 15A × R1 and CMS 15A × R2 having positive and desirable SCA effects for quality and some of its component traits merit attention in breeding programme for exploitation of hybrid cultivars.

Keywords: Quality traits, additive gene action, GCA, SCA and l x t matting design

Introduction
Rice is the main cereal crop consumed by more than half of the world's population. In India, rice cultivation is very closely inter woven with livelihood and culture of millions of people and gained the status of major export commodity in the last ten years. In rice research, grain quality was initially overshadowed by the need of higher yield. The importance of rice grain quality is now instrumental and has become a valuable tool for acceptance of varieties and Plant breeders continuously trying to refine and improve genetic traits of new varieties required to produce the most desirable and acceptable Rice hybrids.

After the achievement of self-sufficiency in rice production through high yielding varieties/hybrids, the demand for quality rice is increasing. Rice quality is of great importance for all people involved in producing, processing and consuming rice, because it affects the nutritional and commercial value of grains (Lodh, 2002 and Babu *et al.*, 2013) [3, 12]. The primary components of rice grain quality influencing the commercial value include appearance, milling, cooking and eating quality which are determined by their physical and chemical properties. Generally, the appearance of rice grain is determined by of grain length, grain breadth, grain thickness and grain shape as length: breadth ratio (L/B ratio). The milling quality is assessed by using three principal characters *viz*., hulling, milling yield and head rice recovery. The eating and cooking quality of rice is usually evaluated by three physical and chemical characteristics of the starch as indirect indices: amylose content, gel consistency and gelatinization temperature of these, the amylose content of rice grains is recognized as one of the most important determinants of eating and cooking quality (Jue *et al*., 2009) [10].

The combining ability of the parents in terms of quality should be good so as to obtain crosses with desirable quality attributes. This requires the identification of parents with good general combining ability (GCA) effects and cross combinations with high specific combining ability effects (SCA) for commercial exploitation of heterosis and isolation of pure lines among the progenies of the heterotic hybrids. The Line × Tester design is the effective method of estimation of GCA and SCA which enables screening of large number of parental lines [2]. Recently, Line × Tester analysis was done by Venkatesan *et al*. (2008) [23], Tyagi *et al*. (2010) [22], Priyanka *et al*. (2014) [13, 24], and Showkat *et al*. (2015) [21] for estimation of gene action in rice. Therefore, the present investigation was undertaken to select potential parents and hybrids for rice grain quality traits, besides to elucidate the nature of gene action governing the inheritance of various grain quality traits.

Methods and Material

The present investigation was carried out during two seasons during June 2017 and June 2018 at Raghvendra Joshi Biotech Research Farm, Hyderabad and study comprised of 48 crosses of rice which were generated by crossing the 4 CMS of rice *viz*., CMS 4A, CMS 6A, CMS 14A, CMS15 A; and 12 restorers R1, R2, R3, R4, R5, R6, R7, R8, R9, R10, R11 and R12.

All the parents were raised in a crossing block during June 2017. Sowing and transplanting of parents were done thrice at weekly intervals in order to ensure synchronization in flowering of lines and testers which have duration range of 105 to 135 days. Twenty five days old seedlings of 16 entries were transplanted under irrigated condition in each three rows of three meter row length in the main field adopting a spacing of 30 x 20 cm. A wider spacing of 60cm was maintained between three rows of each entry for ease of hybridization All the recommended agronomical package of practices were well adopted to keep the plants uniformly good throughout the crop growth period. Four testers and 12 lines were grown, and at flowering stage, they were crossed with each other in a line × tester manner as described by Kempthorne (1957) to produce 48 hybrids.

The 48 hybrids along with sixteen parents were raised in a randomized block design with three replications during June, 2018. Twenty five days old seedlings were transplanted in 3m row with 20 x 10cm spacing. The resultant 48 hybrids along with their parents were studied to analyse the *per se* performance and combining ability of 9 grain quality traits *viz.*, milling percentage (MP), head rice recovery percentage (HRR), Grain length (GL), Grain breadth (GB), kernel length (KL), kernel breadth (KB), kernel length/breadth ratio (KLBR), kernel length after cooking (KLAC) and kernel elongation ratio.

To estimate Milling Percentage (MP), **a**fter hulling of well cleaned and dried paddy 12-14% moisture, the brown rice was milled and polished in a Kett polisher for a standard time to find out the milling percentage. Milling percentage was estimated as follows,

$$\text{Milling \%} = \frac{\text{Weight of milled rice (g)}}{\text{Weight of rough rice (g)}} \text{ X } 100$$

To estimate Head Rice Recovery Percentage (HRR), the milled samples were sieved to separate whole grains from the broken ones. Small portion of broken kernels which passed along whole kernels were separated by hand. Head rice recovery, which is the estimate of full size plus three fourth size kernels was expressed in percentage.

$$\text{Head rice recovery \%} = \frac{\text{Weight of head rice (g)}}{\text{Weight of rough rice (g)}} \text{ X } 100$$

Grain length and breadth of ten paddy grains in three sets was measured using graph sheet and the mean was expressed in milli-meters (mm). Kernel length and breadth of ten dehusked rice kernels before milling (brown rice) in three sets was measured using graph sheet and the mean was expressed in milli-meters (mm). Kernel length after cooking was measured by following the method described by Azenz and Shafi (1966) [2]. The ratio of mean length of cooked rice to mean length of milled rice was computed as linear elongation ratio (Juliano and Pe-rez., 1984) [5, 6, 11]. The standard procedure of Juliano (1979) [5, 6, 11] was used for estimating the kernel elongation ratio.

Results and Discussion

The analysis of variance in table 1 revealed that mean squares due to line were highly significant for all the characters except kernel breadth and kernel length after cooking show significant effects, while the variance due to parents, testers and crosses were highly significant for all the characters except kernel length after cooking. The mean squares due to replications, Lines *vs* testers and parents *vs* crosses exhibits highly significant for all the quality traits except kernel length after cooking and kernel elongation ratio exhibited significant variances. The analysis of variance for combining ability in table 2 the nine quality characters presented the mean squares due to line × tester interactions were highly significant for all the nine characters while L:B ratio showed significant variance under study. The mean squares due to testers emerged highly significant for all the characters except significant mean squares recorded for kernel length. The variance due to lines was found to be highly significant for all traits, while non-significant mean squares exhibited by kernel elongation ratio. The mean squares due to replications appeared highly significant for grain breadth, head rice recovery, L:B ratio, milling percentage, kernel length after cooking, kernel length and grain length, and significant for kernel breadth while non-significant for kernel length elongation ratio.

The estimates of components of variance have been presented in table 3. In the present study variance due to GCA was higher than SCA variance for kernel elongation ratio which was predominantly controlled by additive gene action, means transgressive breeding may be useful for this character (Sharma *et al*., 2007, Kumar *et al*., 2007 and Asfaliza *et al*., 2012) [3, 14, 17, 19, 21]. Estimates of SCA variance were higher than the corresponding estimates of GCA variance for all the traits except kernel elongation ratio. This means significant role of non-additive gene action therefore, heterosis breeding is better choice for such character, results was conformity with earlier findings by Gnanamalar R.P. and Vivekanandan P., 2013 [8] and Shivani *et al*., 2009 [20]. The values of average degree of dominance were more than unity (>1) revealing over dominance for milling percentage (9.53), head rice recovery (7.37), L:B ratio (5.70), grain length (4.12) and grain length (3.06). Kernal breadth (0.91) and Kernal length after cooking (0.86) exhibited the average degree of dominance nearly equal to unity to suggest existence of complete dominance, while lesser than unity (<1) estimates of this parameter recorded for kernel length (0.55) and kernel elongation ratio (0.49) indicated partial dominance. The estimates of heritability in narrow sense (h^2n) have been classified by Robinson (1966) into three categories *viz.*, high (> 30%), medium (10-30%) and low (<10%). High estimates of heritability in narrow sense were recorded for kernel length (65.73%) and L:B ratio (40.37%). Four quality characters *viz.*, kernel length after cooking (23.54%), grain breadth (19.79%), kernel breadth (18.82%) and milling percentage (10.85%) exhibited moderate heritability while low estimate of h^2n was recorded for kernel elongation ratio (3.43%), head rice recovery (2.42%) and grain length (1.21%). The high estimates of genetic advance in per cent of mean (>20%) using narrow sense heritability were recorded for kernel length (22.37%). L:B ratio (16.99%), grain breadth (10.73%) and milling percentage (10.05%) exhibited moderate genetic advance. Low estimates of genetic advance were recorded for head rice recovery (5.26%), kernel length after cooking (4.56%), kernel length elongation (1.90%) and grain length (0.16%).

The present investigation done for both general combining ability (GCA) effects and specific combining ability effects for quality characters (table 4). The parents R5 and R4 exhibited good desirable combining ability for all the quality characters. Parent R2 shows good GCA effects for grain length, grain breadth, kernel breadth, KLAC and HRR, while R6 grain length, grain breadth, kernel breadth and L/B ratio. This indicated that these parents were good general combiner for long, cylindrical, fine grain quality. High SCA effect results from dominance and interaction effects existed between the hybridizing parents. The significant SCA effect in desirable direction for grain length, grain breadth, kernel length, kernel breadth and L/B ratio recorded for CMS 15A ×R5. For good cooking quality and elongation after cooking and head rice recovery cross found suitable among the 48 crosses. Thus, in the present study the combining ability effects (both GCA and SCA) was estimated for quality traits. The estimates of combining ability effects aidin selecting desirable parents, crosses as well as breeding procedure for further improvement (Bano and Singh, 2019, Sarkar *et al*., 2002, Rashid *et al*. 2007, Salgotra *et al*., 2009, Raju *et al*, 2014 and Waza *et al*., 2015) [7, 13-16, 18, 21].

The present study showed that among the parents R5, R2, R4 and R6 as well as CMS 15A, CMS 4A and CMS 6A showed good combining ability for maximum quality traits but among the crosses few crosses like CMS 15A × R5, CMS 15A × R1, CMS 14A × R1 and CMS 15A × R2 showed good GCA effects for some characters (table 5 & 6). The SCA value is useful to determine the cross combinations for exploitation of heterosis. The crosses involved high × high general combiner for quality traits, so it can be used for obtaining superior recombinants in advance generation. The crosses involved low × low general combiner for the traits showed scope of obtaining superior quality hybrids (Bansal *et al*., 2006) [4].

Conclusion

From the study of quality characters, it revealed that the importance of H × H general combiners exhibiting high SCA effects can be utilized for improvement through single plant selection in segregating generations. But in crosses having high SCA effects due to H × L general combiners have to be improved through population improvement. The crosses showing high SCA effects involving L × L general combiners may be exploited for heterosis breeding program.

In the present study it was found that only one cross CMS 15A × R5 out of 48 crosses showed good SCA effects for majority the characters. Thus the cross with good *per se* performance and significant SCA effect were also found superior for grain length, grain L/B ratio, kernel length, kernel L/B ratio may be exploited for better grain quality either by exploiting them through heterosis breeding or multiple cross breeding programme for obtaining transgressive segregants for improvement in quality rice.

Table 1: Analysis of variance for 9 quality characters of line × tester set of crosses and their parents in rice

Characters df:	Sources of variation							
	Replications	**Parents**	**Lines**	**Testers**	**Lines *vs* Testers**	**Crosses**	**Parents *vs* Crosses**	**Error**
	2	**15**	**3**	**11**	**1**	**47**	**1**	**126**
Grain Length	17.34**	21.42**	11.92**	22.26**	29.73**	9.07**	18.06**	1.38
Grain Breadth	8.32**	16.28**	10.89**	14.78**	10.50**	19.32**	16.25**	4.70
Kernal Length	7.036**	12.56**	11.58**	24.34**	65.20**	23.14**	32.18**	2.26
Kernal Breadth	9.34**	20.20**	8.56**	29.67**	14.27**	11.29**	16.32**	0.35
L/B Ratio	55.39**	12.89**	31.09**	11.72**	14.53**	19.76**	28.26**	14.00
KLAC	0.38*	4.77*	2.63*	0.87*	1.97*	1.56*	0.81*	2.26
Milling %	35.72**	39.33**	22.70**	26.55**	45.44**	43.40**	29.76**	6.30
HRR	20.07*	31.25**	35.43**	49.06**	10.23**	15.66**	13.78**	3.65
Kernal Elongation Ratio	1.28*	45.98**	11.87**	56.22**	0.88*	6.48**	3.44*	20.11

*, ** Significant at 5% and 1% probability levels, respectively

Table 2: Analysis of variance for combining ability following line × tester mating design for 9 quality characters in rice

Characters df.	Sources of variation				
	Replications	**Lines**	**Testers**	**Lines × Testers**	**Error**
	2	**3**	**11**	**33**	**94**
Grain Length	2.54**	32.50**	52.94**	2.59**	5.60
Grain Breadth	87.91**	76.07**	26.30**	33.71**	58.41
Kernal Length	9.84**	4.31**	0.88*	2.25**	0.51
Kernal Breadth	1.90*	16.32**	8.48**	2.28**	0.27
L/B Ratio	12.86**	10.29**	8.51**	1.08*	9.83
KLAC	10.43**	3.26**	9.82**	5.76**	0.62
Milling %	12.08**	7.42**	27.18**	12.52**	14.17
HRR	23.87**	2.97**	20.24**	10.54**	12.44
Kernal Elongation Ratio	0.21	0.22	17.54**	9.55**	8.31

*, ** Significant at 5% and 1% probability levels, respectively

Table 3: Components of genetic variance, average degree of dominance, predictability ratio and heritability in broad sense for 9 characters in rice

Characters	GCA variance (σ^2g)	SCA variance (σ^2s)	Average degree of dominance $\sqrt{\sigma^2 s/2\sigma^2 g}$	Predictability ratio $2\sigma^2 g/(2\sigma^2 g+\sigma^2 s)$	σ^2A	σ^2D	Heritability (h^2n %)	Genetic advance (%)
Grain Length	2.46	6.23	4.12	0.60	8.29	5.23	1.21	0.16
Grain Breadth	1.72	9.53	3.06	0.79	28.10	9.25	19.79	10.73
Kernal Length	0.48	1.01	0.55	0.30	0.86	1.90	65.73	22.37
Kernal Breadth	0.23	1.74	0.91	0.11	0.91	3.94	18.82	2.82
L/B Ratio	31.76	39.67	5.70	0.61	36.31	31.67	40.37	16.99
KLAC	0.15	1.88	0.86	0.33	0.30	0.61	23.54	4.56
Milling %	15.41	27.84	9.53	0.71	54.65	11.84	10.85	10.05
HRR	2.52	3.68	7.37	0.66	6.11	0.46	2.42	5.26
Kernal Elongation Ratio	5.32	3.08	0.49	0.31	10.05	3.83	3.43	1.90

Table 4: Estimates of general combining ability (GCA) effects of parents (lines and testers) for 9 quality characters in rice

S. No.	Testers	Grain length	Grain breadth	Kernal length	Kernal breadth	L/B ratio	KLAC	Milling %	HRR	Kernal elongation ratio
1	R 1	2.41**	-1.19**	2.07**	-1.07**	0.83**	2.80**	1.12**	1.54**	1.21**
2	R 2	3.25**	-1.09**	-1.63**	-1.27**	-0.76**	1.62**	-1.59**	2.78**	-2.23**
3	R 3	-1.47**	-1.00**	-1.07**	0.97**	-0.46*	-1.76**	-2.14**	-1.08**	1.07**
4	R 4	2.83**	-1.21**	2.19**	-1.43**	0.82**	2.60**	1.61**	0.76**	2.65**
5	R 5	1.67**	-0.96**	1.47**	-0.73**	-0.88**	1.61**	0.79**	1.09**	0.86**
6	R 6	2.50**	-1.31**	-1.93**	-1.10**	0.71**	-2.93**	-1.40**	-1.81**	-1.51**
7	R 7	-2.86**	1.49**	1.97**	1.23**	-0.29*	-1.89**	2.24**	-1.98**	2.78**
8	R 8	2.80**	-2.46**	-1.56**	1.27**	-0.84**	-1.38**	-0.23*	0.38*	-1.83**
9	R 9	1.78**	0.69*	1.51**	0.54*	0.87**	2.41**	-1.77**	-1.49**	0.56*
10	R 10	-1.94**	-1.05**	-1.52**	0.95**	0.22*	1.18**	-0.97**	2.62**	-1.49**
11	R 11	-1.83**	1.28**	-1.49	-1.07**	0.70**	-0.94**	-2.85**	-0.92**	1.32**
12	R 12	-1.50**	1.48**	-1.22**	0.96**	-0.03	-1.45**	1.78**	-1.67**	-1.49**
SE (gi) testers		0.84	0.37	0.69	0.54	0.34	0.51	0.95	0.56	1.41
SE(gi – gj)		1.20	0.87	1.08	0.51	0.69	0.70	0.71	0.98	1.10
Lines										
1	CMS 4A	-2.83**	1.96**	2.63**	1.67**	0.79**	0.92**	-1.39**	-0.35*	1.73**
2	CMS 6A	3.67**	-2.69**	2.87**	-2.37**	1.52**	2.59**	0.59*	1.23**	2.45**
3	CMS 14A	2.91**	-1.49**	2.93**	-1.20**	-1.10**	-0.98**	-0.95**	-0.99**	-1.67**
4	CMS 15A	1.96**	-0.68*	1.57**	-0.61	0.90**	1.99**	2.35**	1.76**	0.78**
SE(gi) lines		0.42	2.64	0.36	0.23	0.75	0.43	1.89	0.78	1.98
SE(gi – gj)		0.92	1.26	0.84	0.45	0.68	0.43	1.54	1.34	2.60

*, ** Significant at 5% and 1% probability levels, respectively

Table 5: Estimates of specific combining ability (SCA) effects of crosses for 9 quality characters in rice

S. No.	Crosses	Grain length	Grain breadth	Kernal length	Kernal breadth	L/B ratio	KLAC	Milling %	HRR	Elongation ratio
1	CMS 4A × R1	-2.48**	1.26**	-1.93**	1.14	-0.34**	-0.73**	-1.34**	0.29**	0.49**
2	CMS 6A × R1	2.16**	-1.73**	1.71**	1.45**	0.06*	1.74*	0.56**	1.32**	2.43**
3	CMS 14A × R1	2.63**	-1.76**	2.43**	-1.09**	-0.09**	1.38**	1.51**	-2.76**	1.65**
4	CMS 15A × R1	1.80**	-1.53**	1.51**	-1.26**	0.10**	1.73**	0.19**	1.95**	2.49**
5	CMS 4A × R2	-2.61**	1.19**	2.39**	-0.94*	-0.43	2.97**	1.59**	-1.79**	-2.14**
6	CMS 6A × R2	-1.39**	0.82**	-1.58**	0.40**	0.46**	1.67**	-1.77**	-2.64**	-1.57**
7	CMS 14A × R2	1.54**	0.69**	-1.37**	0.27**	1.42**	1.42**	1.55**	0.54*	0.98**
8	CMS 15A × R2	-2.58**	-1.99**	2.56**	-1.66**	-0.89**	-1.87**	-1.59**	-1.88**	1.65**
9	CMS 4A × R3	-2.28**	1.79**	-1.89**	1.39**	-0.07**	-1.51**	0.38**	0.79**	0.95**
10	CMS 6A × R3	1.69**	1.32**	1.42**	1.10**	0.15**	1.20**	0.62**	1.39**	0.63**
11	CMS 14A × R3	-2.97**	1.69**	-2.59**	1.32**	0.06*	-0.23**	-1.89**	0.81**	-1.09**
12	CMS 15A × R3	2.87**	1.69**	2.36**	1.11**	0.09*	0.90**	1.22**	1.92**	1.34**
13	CMS 4A × R4	2.42**	1.19**	-2.31**	-1.05**	0.56**	-0.71**	-3.67**	-1.54**	-0.83**
14	CMS 6A × R4	-2.36**	1.02**	1.92**	0.75**	0.71**	1.10**	0.89**	2.01**	0.46**
15	CMS 14A × R4	-1.67**	0.69**	1.28**	0.37**	0.15**	1.57**	1.11**	1.45**	-0.67**
16	CMS 15A × R4	2.50**	0.92**	2.14**	0.76**	0.05*	1.32**	2.13**	1.90**	0.59**
17	CMS 4A × R5	-2.78**	1.96**	2.49**	1.74**	0.44**	-0.18**	-1.45**	0.89**	1.43**
18	CMS 6A × R5	1.86**	0.95**	1.28**	0.45**	0.34**	0.32**	1.59**	2.34**	1.10**
19	CMS 14A × R5	1.83**	1.29**	1.43**	0.87**	-0.07*	-1.59**	-1.37**	1.67**	1.22**
20	CMS 15A × R5	2.86**	-1.70**	2.44**	-1.36**	0.98**	1.44**	1.08**	0.54**	1.76**
21	CMS 4A × R6	1.05**	0.69**	0.89	.44**	-0.30**	-1.41	1.02**	0.87**	0.99**
22	CMS 6A × R6	2.08**	1.72**	-1.78**	-1.51**	-0.60**	-0.69**	-1.48**	-0.45**	-1.52**
23	CMS 14A × R6	-2.91**	1.70**	2.68**	-1.42**	-0.59**	0.32**	-1.53**	-0.76**	1.68**

24	CMS 15A × R6	1.67**	1.40**	1.36**	1.10**	0.12**	0.41*	0.68**	1.03**	1.53**
25	CMS 4A × R7	2.10**	1.61**	-1.88**	-1.20**	0.58**	-1.74**	-0.68**	-1.72**	1.33**
26	CMS 6A × R7	-2.06**	-1.02**	1.84**	1.52**	-0.01	0.35**	2.79**	0.65**	-1.88**
27	CMS 14A × R7	-1.71**	1.49**	1.53**	1.17**	0.02**	0.52**	0.59**	-0.66**	-1.54**
28	CMS 15A × R7	-1.40**	-0.99**	-1.21**	-0.56**	-0.09**	1.05**	-1.68**	0.98*	-2.67**
29	CMS 4A × R8	-2.28**	1.06**	-1.01**	-0.86**	0.12**	-1.24**	-0.42**	1.86**	1.21**
30	CMS 6A × R8	1.44**	1.05**	1.28**	-0.85**	-0.09*	1.85**	2.76**	-2.34**	-1.98**
31	CMS 14A × R8	-2.67**	1.19**	2.43**	0.77**	0.36**	-0.59**	-2.79**	2.10**	1.67**
32	CMS 15A × R8	1.75**	1.40**	1.44**	1.04**	-0.02*	1.33**	2.43**	1.91**	0.33**
33	CMS 4A × R9	-1.80**	1.19**	-1.53**	-1.06**	-0.05**	0.34**	-1.58**	-0.23**	1.66**
34	CMS 6A × R9	-2.56**	2.12**	2.14**	1.85**	-0.17**	-1.57**	0.58**	-1.26**	0.95**
35	CMS 14A × R9	1.83**	-1.47**	1.23**	-1.23**	0.11**	1.02**	1.00**	0.23**	0.87**
36	CMS 15A × R9	2.00**	-1.90**	-1.84**	1.04**	0.06*	-0.29*	-0.53**	2.84**	1.08**
37	CMS 4A × R10	-1.55**	-0.79**	-1.19**	-0.56**	-0.10**	0.76**	1.47**	1.34**	0.80**
38	CMS 6A × R10	2.86**	1.72**	2.58**	1.45**	0.06*	1.08**	-1.55**	0.89**	1.74**
39	CMS 14A × R10	1.91**	1.69**	1.53**	-1.33**	0.05*	-1.12**	-1.57**	-1.24**	-0.41
40	CMS 15A × R10	-1.66**	1.20**	-1.33**	1.04**	-0.01	-0.68**	-1.32**	0.87**	-2.44**
41	CMS 4A × R11	-1.52**	1.19**	1.29**	-0.86**	-0.39**	0.51**	2.63**	1.11**	-1.90**
42	CMS 6A × R11	2.11**	2.02**	-1.88**	1.75**	-0.09**	1.55**	-0.81**	1.67**	2.04**
43	CMS 14A × R11	-1.50**	1.09**	1.23**	-1.07**	0.04**	-0.84**	-1.97**	-0.21**	1.36**
44	CMS 15A × R11	1.83**	1.41**	1.46**	-1.16**	-0.06*	0.75**	1.72**	0.71*	1.80**
45	CMS 4A × R12	-2.28**	1.79**	2.36**	1.34**	0.09*	0.84**	1.38**	1.09**	0.71**
46	CMS 6A × R12	-2.06**	-1.62**	1.72**	1.25**	-0.03*	1.03**	-0.36**	1.83**	0.90**
47	CMS 14A × R12	2.03**	-1.96**	2.49**	1.22**	-0.76**	-0.84**	-1.24**	-0.67**	1.87**
48	CMS 15A × R12	-1.50**	-1.12**	-1.27**	-0.96**	-0.10**	-0.27**	-1.59**	2.65**	1.34**
	SE (S_{ij})	2.47	1.29	1.16	0.92	0.19	0.32	1.74	2.78	1.21
	SE ($S_{ij} - S_{kl}$)	2.79	1.61	2.34	1.27	0.28	0.77	1.42	1.67	0.56

*, ** significant at 5 and 1 percent probability levels, respectively

Table 6: Most promising cross combinations for different characters along with their mean performance and GCA effects of parents

Characters	Crosses with significant effects	Mean performance of crosses	GCA effects of parents
Grain Length	CMS 15A × R3	2.87	H × L
	CMS 6A × R10	2.86	L × L
	CMS 15A × R5	2.80	H × H
	CMS 14A × R1	2.63	H × H
	CMS 15A × R4	2.50	H × H
Grain Breadth	CMS 15A × R2	-1.99	L × L
	CMS 14A × R12	-1.96	L × H
	CMS 14A × R1	-1.76	L × L
	CMS 6A × R1	-1.73	L × L
	CMS 15A × R5	-1.70	L × L
Kernal Length	CMS 14A × R6	2.68	H × L
	CMS 6A × R10	2.58	H × L
	CMS 15A × R2	2.56	L × L
	CMS 14A × R12	2.49	H × L
	CMS 15A × R5	2.44	H × H
Kernal Breadth	CMS 15A × R2	-1.66	L × L
	CMS 6A × R6	-1.51	L × L
	CMS 14A × R6	-1.42	L × L
	CMS 15A × R5	-1.36	L × L
	CMS 15A × R1	-1.26	L × L
L/B Ratio	CMS 14A × R2	1.42	L × H
	CMS 15A × R5	0.98	H × H
	CMS 6A × R4	0.71	H × L
	CMS 4A × R7	0.58	H × L
	CMS 4A× R4	0.56	H × H
KLAC	CMS 4A × R2	2.97	H × H
	CMS 6A × R8	1.85	H × L
	CMS 15A × R1	1.73	H × H
	CMS 6A × R1	1.74	H × H
	CMS 6A × R2	1.67	H × H
Milling %	CMS 6A × R7	2.79	H × H
	CMS 6A × R8	2.76	H × L
	CMS 15A × R8	2.43	H × L
	CMS 15A × R4	2.13	H × H
	CMS 6A × R5	1.59	H × H
HHR	CMS 15A × R9	2.84	H × L
	CMS 15A × R12	2.65	H × L

	CMS 6A × R5	2.34	H × H
	CMS 6A × R4	2.01	H × H
	CMS 15A × R1	1.95	H × H
Kernal Elongation Ratio	CMS 15A × R1	2.49	H × H
	CMS 6A × R1	2.43	H × H
	CMS 6A × R11	2.04	H × H
	CMS 14A × R12	1.87	L × L
	CMS 6A × R5	1.80	H × H

H = High (significant and positive), L= Low (significant and negative), A= Average (non-significant)

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