Combining ability studies for yield and yield contributing traits in Rice (*Oryza sativa* L.)

ABSTRACT

The current study was carried out with an objective to study Combining ability studies for yield and yield contributing traits in Rice (*Oryza sativa* L.) to identify superior crosses for commercial cultivation after testing over years band locations. Agricultural Polytechnic, Polasa, Jagtial, during *Kharif*, 2021 and *Rabi*, 2021-22. Where, crossing programme was carried out during *Kharif*, 2021 and evaluation of the crosses was taken up during *Rabi*, 2021-22.Twenty-four (24) experimental hybrids were developed using eight lines and three testersand randomized block design was utilized for the evaluation studies.The variance due to the crosses, variance due to theparents*vs*crosses werealso found highly significant for all the characters. Lines,testersandlinextestereffects,theinteraction effects (lines x testers) were found to be significant for all the traits studied.Thisindicates thatthematerialunderinvestigation has adequatevariability.The study revealed that the line, CMS 46B and KNM 7787 among the testers were identified asgood general combiners for grain yield per plant while, JMS 18A x RNR 21278 wereidentifiedas best specificcombiners for thetrait.

Key words: Paddy- line x Tester mating design-General Combining ability,Specific Combining ability,

INTRODUCTION

Rice (*Oryza sativa* L.) is one of the major cereal crops in the world and is theprincipal staple food for half of the world's population. Rice has shapedthe culture,diets and economy of millions of people around the globe. For more than half of themankind "Rice is Life". India is an important centre for rice cultivation and it ranks firstin the area and second in production next to China (FAO,2019). Rice production plays an integralrole in the national economy of India and has the maximum share in grain production,accountingfor 22%oftheworld's riceproduction(Bandumula,2018).[(1)].

Globally, about 167.20 million hectares of rice are planted, yielding 769.60 million tons with 4600 kg of productivity per hectare (FAO, 2019) [(2)]. In India, rice has occupied 45.07 million hectares of land, yielding 122.27 million tons and producing 2713 kilograms per hectare. On a 2.31 Mha area, Telangana's production and productivity levels were 7.70 Mt and 3327 kg ha^{-1}, respectively(Directorate of Economics and Statistics,2021)[(3)]. Identification of good general and specific combiners is a continuous and very important process to exploit better heterosis for the development of high yielding hybrids to meet the global food demand.

MATERIAL AND METHODS

AgriculturalPolytechnicCollege,Polasa,Jagtialislocatedatanaltitudeof 243.4mabovemeansealevelon18°49'40"Nlatitudeand78°56'45"ElongitudesintheNorthernZoneofTelanganaState.Thefieldsareuniformlyfertilewitheventopography and a consistent texture. In addition, the fields are adjacent to a majorirrigation channel which provides quick, uniform and timely irrigation. The soil type isloamy clay in the experimental plot. Proper drainage facility is provided to removeexcesswater in thefields.

Theexperimental inbred linesutilizedforthepresentstudyconsistsofeightlines *viz.,*CMS23A,CMS46A,CMS59A,JMS11A,JMS13A,JMS17A,JMS18Aand CMS 64A, three testers *viz*., JGL 33124, KNM 7787 and RNR 21278.Crossing programme was affected in line x tester mating design during *Kharif*, 2021. All the parents were sown inthree staggerings at 10 days interval to achieve synchronous flowering so as to obtainsufficientquantityofcrossedseed.

The resultant 24 experimental hybrids were evaluated during *Rabi*, 2021-22 in Randomized Block Design along with the parents to delineate the general combining ability (*gca*) and specific combining ability effects (*sca*) for yield and yield attributing characters. Recommended crop management strategieswerefollowedandmaintainedahealthycropduringtheentireperiodoffieldevaluation.

RESULTS AND DISCUSSION

Analysisofvariance

The results of analysis of variance for the traits under investigation are presented in Table 1. The analysis revealed that the variance due to treatments and parents was highly significant for all characters examined. The variance due to crosses and parents versus crosses were highly significant for all characters. Furthermore, the variance attributed to lines was significant for all traits analysed, while the variance due to testers was significant for all characters except for single plant yield, which was not significant.

When the effects of parents were divided into lines, testers, and line x tester interactions, the interaction effects (lines x testers) were found to be significant for all traits studied. This indicates that the material under investigation exhibits adequate variability. These findings align with those of El-Shamey et al. (2022) and Nagamani et al. (2022).

Table1.AnalysisofvarianceforcombiningabilityLinexTester)foryieldandyieldattributingtraitsinthericegenotypes

Sourceofvariation	df	Days to 50%flowering	Plant height(cm)	Paniclelength(cm)	No. ofproductivetillers perplant	No. of filledgrains perpanicle	No. ofunfilledgrains perpanicle	Spikeletfertility(%)	1000 grain-weight (g)	Grain yieldperplant(g)
Replicates	2	0.085	2.23	0.03	0.02	34.26	35.94	2.42	0.61	0.04
Treatments	34	81.16**	57.54**	8.74**	4.88**	13501.09**	6565.75**	1587.01**	44.25**	240.48**
Parents	10	70.26**	65.69**	12.47**	2.35**	12327.54**	726.61**	67.05**	61.97**	57.91**
Parents(Lines)	7	21.47**	21.84**	7.98**	1.33**	4888.63**	508.58**	65.49**	65.49**	46.13**
Parents(Tester)	2	193.00**	252.03**	26.23**	1.00**	3076.35**	1344.83**	61.06**	1.57*	0.24
Parents(L*vs*T)	1	166.37**	0.01	16.41**	12.23**	82902.28**	1016.26**	89.99**	158.06**	255.64**
Parents*vs*Crosses	1	103.52**	116.34**	1.63**	1.68**	102877.04**	65837.77**	16960.22**	36.53**	1653.62**
Crosses	23	84.93**	51.44**	7.42 **	6.13 **	10125.42**	6527.46**	1579.44**	36.88**	258.42**
LineEffect	7	81.58	96.94	4.32	9.87	7922.46	5863.73	1347.66	54.25	310.05
TesterEffect	2	207.18	3.30	10.28	2.63	8624.34	6373.57	1627.12	52.02	356.58
LinexTesterEff.	14	69.13**	35.57**	8.56**	4.75**	11441.33**	6881.32**	1688.52**	26.04**	218.56**
Error	68	0.37	1.02	0.07	0.15	18.75	38.94	4.19	0.33	0.15
Total	104	26.77	19.52	2.91	1.69	4426.74	2172.64	521.6	14.69	78.71

*Significant at5percent level**Significant at1percent level

Generalcombiningabilityeffectsand specificcombiningabilityeffects

The general combining ability (GCA) effects of eleven parents comprising eight lines and three testers along with the specific combining ability (SCA) effects of 24 hybrid combinations were estimated using the Line x Tester mating design procedure outlined by Kempthorne in 1957. The GCA effects of the parents (lines and testers) for each character are presented in Table 2, while the SCA effects of the hybrids are presented in Table 3.

Daysto50%flowering

The GCA effects among the lines ranged from -4.53 (CMS 59B) to 4.47 (CMS 23B) and among the testers, it ranged from -2.15 (RNR 21278) to 3.35 (KNM 7787). Based on negative and significant GCA value the parent CMS 59B (-4.53) and the tester RNR 21278 (-2.15) showed good GCA for the days to 50% flowering. Negative GCA effects are desirable in breeding for early maturity. Conversely, the lines CMS 23B (4.47), CMS 46B (3.81), and JMS 11B (0.81) showed significantly positive GCA effects.

Out of the 24 hybrids, 21 displayed high significant SCA effects. Among these, 11 hybrids exhibited significant positive SCA effects, while 10 hybrids exhibited significant negative SCA effects. The hybrids, CMS 46A x RNR 21278 (-6.18) followed by JMS 11A x JGL 33124 (-5.14**),**CMS59AxKNM7787 and JMS 17A x KNM 7787 (-4.35) were observed good specific combiners with highest negative value for early maturity. These findings are consistent with the results reported by Malathi and Suresh (2019) and Sari et al. (2020).

Plantheight

Five lines and none of the testers among the parents recorded significant *gca*effects The lines, JMS 17B (-4.31), CMS59B (-3.97) and JMS 18B (-0.81) displayed highly significant negative *gca*effects. Lines with negativeeffects could be effectively used in thedevelopment of dwarf and semi-dwarf hybrids and are ideal general combiners fordwarfness. Conversely, two lines *viz.,* CMS 46B (5.53) and CMS 23B (3.13) exhibitedsignificantlypositive*gca*effects.

Table2.Estimatesofgeneralcombiningability(GCA)effectsforlinesandtestersofthestudyforyieldandyieldattributingtraits

Source	Days to 50%flowering	Plant height(cm)	Panicle length(cm)	No. ofproductivetillers perplant	No. of filledgrains perpanicle	No. of unfilledgrains perpanicle	Spikeletfertility(%)	1000 grain-weight(g)	Grain yieldperplant (g)
Parents									
Lines									
CMS23 B	4.47 **	3.13**	-0.48**	1.87**	32.54**	-14.46**	11.72**	3.27**	7.34**
CMS46 B	3.81 **	5.53**	0.22*	1.35**	30.94**	-38.91**	15.25**	4.24**	9.98**
CMS59 B	-4.53**	-3.97**	-1.05**	-0.45**	-23.79**	10.86**	-5.25**	-2.26**	-5.23**
JMS11 B	0.81**	0.16	1.18**	-0.38**	30.07**	-2.76	7.74**	-0.51*	1.27**
JMS13 B	-0.86**	0.03	-0.12	-0.18	-7.59**	-0.92	-3.79**	-1.41**	-2.55**
JMS17B	-2.53**	-4.31**	-0.25*	-0.62**	-13.33**	-6.39**	0.04	-0.66**	-3.10**
JMS18 B	-0.64**	-0.81*	0.68**	-0.38**	0.54	0.91	-1.77*	-0.29	-1.32**
CMS64 B	-0.53*	0.26	-0.18	-1.18**	-49.39**	51.67**	-23.94**	-2.37**	-6.40**
Testers									
RNR21278	-2.15**	0.12	-0.22**	-0.37**	-2.32*	-5.24**	1.67**	-1.21**	-1.54**
JGL33124	-1.19**	-0.42	-0.52**	0.23**	-17.69***	18.27**	-8.94**	-0.44**	-2.85**
KNM7787	3.35**	0.29	0.74**	0.15	20.01**	-13.03**	7.26**	1.64**	4.38**
CD95% GCA(Line)	0.408	0.69	0.18	0.26	2.98	4.24	1.37	0.38	0.25
CD95% GCA (Tester)	0.250	0.43	0.12	0.16	1.82	2.59	0.84	0.24	0.15

*Significant at5percent level**Significant at1percent level

Table3.Estimatesof specificcombiningability(SCA)effectsforyieldandyieldattributingtraitsintheexperimentalricehybrids

S. No.	Crosses	Days to50% flowering	Plant height(cm)	Panicleleng th(cm)	No. ofproductiv etillers perplant	No. of filledgrains perpanicle	No. ofunfilledg rains perpanicle	Spikeletferti lity(%)	1000 grain-weight (g)	Grain yieldperplan t(g)
1	CMS23A xRNR21278	-2.85**	-3.18**	-1.64**	-0.35	-43.22**	-2.78	-8.48**	-1.33**	-6.06**
2	CMS23AxJGL33124	1.19 **	3.85**	1.75**	0.83**	34.55**	35.39**	-1.82	-1.51**	-0.97**
3	CMS23A xKNM7787	1.65**	-0.66	-0.11	-0.48*	8.65**	-32.61**	10.31**	2.83**	7.03**
4	CMS46A xRNR21278	-6.18**	0.62	-0.84**	-1.42**	-80.22**	52.44**	-31.95**	-5.97**	-15.99**
5	CMS46AxJGL33124	3.86**	-1.75**	0.45 **	-0.03	20.56**	-41.64**	21.68**	3.53**	7.64**
6	CMS46AxKNM7787	2.32**	1.14	0.39*	1.45**	59.66**	-10.81**	10.27**	2.45**	8.35**
7	CMS59A xRNR21278	3.15**	0.92	0.13	-0.22	50.52**	-37.29**	18.43**	1.48 **	5.32**
8	CMS59AxJGL33124	1.19*	0.25	-0.08	-0.03	14.89**	-55.63**	17.20**	-0.85*	2.14**
9	CMS59AxKNM7787	-4.35**	-1.16	-0.04	0.25	-65.41**	92.93**	-35.63**	-0.64	-7.46**
10	JMS11Ax RNR21278	-0.18	-1.42*	2.39**	0.12	-25.35**	-21.56**	1.05	1.64**	-0.32
11	JMS11Ax JGL33124	-5.14**	-3.58**	-3.12**	-1.90**	32.63**	16.73**	2.76*	-0.03	-2.57**
12	JMS11Ax KNM7787	5.32**	5.01**	0.73**	1.78**	-7.27**	4.83	-3.83**	-1.62**	2.89**
13	JMS13Ax RNR21278	-0.52	-2.78**	-0.01	0.12	20.31**	-30.16**	16.52**	-0.86*	1.61**
14	JMS13Ax JGL33124	-3.47**	-0.25	-1.12**	-0.10	-86.91**	61.08**	-38.26**	-1.53**	-8.18**
15	JMS13Ax KNM7787	3.98**	3.04**	1.13**	-0.02	66.59**	-30.92**	21.74**	2.39**	6.58**
16	JMS 17A x RNR 21278	4.15**	3.85**	0.93**	1.55**	-21.95**	44.94**	-17.61**	1.68**	4.31**
17	JMS 17A x JGL 33124	0.19	1.68*	0.42 *	-0.36	55.43**	-38.39**	22.03**	-0.33	4.56**
18	JMS 17A x KNM 7787	-4.35**	-5.53**	-1.34**	-1.18**	-33.47**	-6.543	-4.43 **	-1.35**	-8.87**
19	JMS 18A x RNR 21278	6.26**	3.85 **	1.19**	1.12**	85.18**	-23.33**	20.51 **	3.24**	10.37**
20	JMS 18A x JGL 33124	-3.03**	-1.92*	0.58**	0.10	-29.24**	10.44 **	-7.09 **	1.28**	-0.42
21	JMS 18A x KNM 7787	-3.24**	-1.93*	-1.77**	-1.22**	-55.94**	12.88**	-13.41 **	-4.52**	-9.96**

22	CMS 64A x RNR 21278	-3.85**	-1.82*	-2.14**	-0.88**	1.72**	17.76 **	1.534	0.11	0.75 **
23	CMS 64A x JGL 33124	5.19**	1.72*	1.14**	1.50**	-41.91**	12.01**	-16.51**	-0.56	-2.18**
24	CMS 64A x KNM 7787	-1.35**	0.11	0.99**	-0.62**	27.19**	-29.77**	14.97**	0.46	1.43**
	CD 95% SCA	0.71	1.19	0.33	0.45	5.16	7.35	2.38	0.66	0.45

*Significant at5percent level**Significant at1percent level

Out of 24 hybrids,16 hybrids displayed significant *sca*effects.It was foundthat seven hybridsrecorded significantly positive*sca*effects while, nine hybrids displayed significantly negative *sca*effects. Highestand negative significantly negative *sca*effect was recordedby thecross,JMS17A x KNM 7787(-5.53)followed by JMS11A x JGL 33124(-3.58). The cross combination, JMS 17A x KNM 7787 was recognized asthe bestspecific combiner amongall the crosses. Similar results were reported by Sari *et al.*(2020)[8]andBarhate *et al.*(2021)[9].

Paniclelength

Six lines and all the three testers (Parents)displayed significant *gca*effects for panicle length. The lines, JMS 11B (1.18), JMS 18B (0.68) and CMS46B (0.22) exhibitedsignificantly positive *gca*effects and the testers, KNM7787 (0.74) recorded significantly positive *gca*effect. Hence, the line JMS 11B and thetester,KNM 7787were observed asgoodgeneral combinersforpaniclelength.

Among all the cross combinations, 19 hybrids displayed significant *sca*effects.12 hybrids displayed significantly positive *sca*effects.The cross, JMS 11A x RNR21278(2.39)displayed thehighestpositivesignificant*sca*effectfollowed byCMS23A x JGL 33124 (1.75) andCMS64Ax JGL 33124(1.14).Among the crosses,JMS 11A x RNR21278wasobservedas the bestspecificcombiner forthetrait. These results are in accordance with the findings of Ambikabathy*et al.*(2019)[10] and Nagamani*etal.* (2022)[5].

Numberofproductivetillersperplant

Seven lines displayed significant *gca*effects; out of 8 lines, two lines displayed significantly positive *gca*effects ranging from 1.87 (CMS 23B) followedby 1.35 (CMS 46B). Only one tester *i.e.,* JGL 33124 (0.23) displayedsignificantly positive *gca*effect. Hence, the line CMS 23B and thetester, JGL 33124 were observed as good general combiners for number of productivetillersperplant.

Out of 24 hybrids, 13 hybrids displayed significant *sca*effects. Out of 24 hybrids, Sixhybrids displayed significantly positive *sca*effects. The cross, JMS 11A x KNM7787(1.78)followedbyJMS17A xRNR21278(1.55),CMS64A xJGL33124(1.50)and CMS 46A x KNM 7787 (1.45) showed the highest significantly positive *sca*effect.The cross, JMS 11A x KNM 7787 was observed as the best specificcombinerfornumberofproductivetillers per plant. The findings are similar to the results of Patel *et al.*(2019)[11] and Salah*et al.* (2020)[12].

Numberoffilledgrains perpanicle

The line, CMS 23B (32.54) displayedthe highest significantly positive*gca*effect followed by CMS 46B (30.94) and JMS 11B (30.07) while the tester, KNM 7787(20.01) displayed significantly positive *gca*effect. Hence, it was observed that the line, CMS23B and the tester, KNM 7787 were good generalcombiners.

All the 24hybrids exhibited significant *sca*effectsin which, elevenhybrids displayed significantly negative effects and the remaining thirteen hybridsexhibited significantly positive *sca*effects. The hybrids, JMS 18A xRNR21278(85.18), JMS13AxKNM7787(66.59),CMS46AxKNM 7787(59.66)andJMS17AxJGL33124(55.43)displayedthehighestsignificantly positive*sca*effects.

In terms of the number of grains per panicle, the good general combiners wereCMS 23B (among lines) and KNM 7787 (among testers).The best specific combinerwasJMS 18AxRNR 21278. These findings are in concurrence with results reportedby Ramesh *et al.*(2018)[13]and Yuga*et al.* (2018)[14].

Numberofunfilledgrains perpanicle

Fivelines and allthe three testers displayed significant*gca*effects.Thelines,CMS46B(-38.91)followedbyCMS23B(-14.46)displayedsignificantly negative *gca*effects. Among the testers, KNM 7787 (-13.03) andRNR21278 (-5.24)displayed significantlynegative*gca*effects.

Twenty-one hybrids displayed significant *sca*effects. Tenhybrids displayedsignificantly positive*sca*effectswhile eleven hybrids displayedsignificantlynegative*sca*effects.Thehighestnegativesignificant*sca*effectwasexhibited by the cross, CMS 59A x JGL 33124 (-55.63) followed by CMS 46A x JGL33124(-41.64),JMS17Ax JGL33124 (38.39)and CMS59AxRNR 21278(-37.29).

The line, CMS 46B and KNM7787 among testers wereobserved as the good general combiners due to their highsignificantly negative *gca*effects. The hybrid, CMS 59A x JGL 33124 wasobservedas the best specificcombiner forthe character.CurrentfindingisinconcurrencewiththereportsofRamesh *et al*.(2018)[13].

Spikeletfertility(%)

Three lines, CMS 46B (15.25), CMS 23B(11.72) and JMS 11B (7.74) and two testers *i.e.,* KNM 7787 (7.26) and RNR 21278(1.67)displayed significantlypositive *gca*effects.

Out of 24 hybrids, 21 hybrids displayed significant*sca*effects out of which tenhybridsexhibitednegativesignificant*sca*effectsandremaining 11hybridsdisplayedsignificantly positive*sca*effects. The hybrid, JMS 17A x JGL 33124 (22.03) followedbyJMS13AxKNM7787(21.74),CMS46AxJGL33124(21.68)andJMS18Ax RNR21278(20.51)displayedthehighestpositiveandsignificant*sca*effects.

Based on combining ability effects, the line, CMS 46B andKNM7787amongthe testerswereobservedasgoodgeneralcombinersforspikeletfertility. The hybrid, JMS 17A x JGL 33124 was observed as the bestspecificcombiner forspikelet fertility. These findings are in consonance with results of Salah*etal.* (2020)[12]and Mohan *et al.* (2021)[15].

1000grain weight

Seven lines and three testers exhibitedsignificant*gca*effects.Amongthelines,CMS46B(4.24)displayedsignificantly positive *gca*effect followed by CMS 23B (3.27) and the tester, KNM 7787(1.64)exhibited significantlypositive*gca*effect.

Out of 24 hybrids, 18 hybrids displayed significant*sca*effects inwhich each nine hybridsdisplayed significantly positive *sca*effects and nine crossesexhibited significantlynegative *sca*effect indicating that this trait is under the control of non-additive gene action. The hybrids, CMS 46A x JGL33124 (3.53) displayed the highest positive *sca*effect followed by JMS 18A x RNR21278(3.24),CMS 23Ax KNM 7787(2.83)andCMS 46Ax KNM7787(2.45). These results are similar to the findings of Patel *et al.* (2019)[11] and Nagamani *etal.* (2022)[5].

Grainyieldperplant

All the parents, *i.e.,* eight lines and three testers exhibited significant *gca*effectsfor single plant yield. The lines, CMS 46B (9.98), CMS 23B (7.34) and JMS 11B (1.27) andKNM7787(4.38)amongtestersdisplayed significantly positive*gca*effcts.

Out of 24 hybrids, 22hybridsdisplayedsignificant*sca*effects.Thirteenhybrids displayed significantly positive effects and 9 hybrids displayed significantnegative effects. Highest positive significant effects are recorded in the hybrid, JMS18A x RNR 21278 (10.37) followed by CMS 46A x KNM 7787 (8.35),CMS 46A xJGL33124 (7.64), CMS23A x KNM7787 (7.03)andJMS13A xKNM7787 (6.58).

CMS 46B among the lines and KNM 7787 among the testers were identified asgood general combiners for grain yield per plant while, JMS 18A x RNR 21278 wereidentifiedas best specificcombiners for thetrait. The results are in agreement with the findings ofPatel *et al.* (2019)[11]and Salah *et al.*(2020)[12]and Gupta et al, 2024[16].

In general, negative effects are desirable for days to 50% flowering to obtainearly maturing types. Whereas, positive effects are desirable for the other characters.From the above findings it is understood that the line, CMS 46B was found to be goodgeneral combiner for spikelet fertility, number of unfilled grains per panicle, 1000 grainweightandgrainyieldperplant.CMS23Bwasidentifiedasgoodgeneralcombinerfor number of productive tillers per plant, number of filled grains per panicle. CMS59Bwas identified asgoodgeneralcombiner for days to 50% flowering.JMS 11B wasidentified as good general combiner for panicle length and JMS 17B was identified asgoodgeneralcombinerforplantheight todevelopdwarf andsemidwarfvarieties.

Among testers, KNM 7787 was identified as good general combiner for paniclelength,number of filledgrainsperpanicle,number ofunfilledgrainsperpanicle,spikelet fertility, 1000 grain weight and grain yield per plant. RNR 21278 was found tobe good general combiner for days to 50% flowering and JGL 33124 was identified asgoodgeneralcombinerfornumberofproductivetillers perplant.

The hybrids, CMS 46A x RNR 21278 and JMS 11A x JGL 33124were identified as good specific combiners for days to 50% flowering. Though, t hehybrids, JMS 17A x KNM 7787 and JMS 11A x JGL 33124 were identified as goodspecific combiners for dwarfness, the , JMS 11A x KNM 7787, CMS 23A x JGL33124, JMS 17A x RNR 21278 and JMS 18A x RNR 21278 were found to be goodspecific combiners to achieve higher yield.

The cross, JMS11A x RNR 21278 was identified as good specific combiner for panicle length. JMS11A x KNM 7787, JMS 17A x RNR 21278 and CMS 64A x JGL 33124 were identifiedas good specific combiners for number of productive tillers per plant. The crosses, JMS18A x RNR 21278 followed by JMS 13A x KNM 7787 were identified as good specificcombiners for number of filled grains per panicle.

The crosses, CMS 59A x JGL 33124followed by CMS 46A x JGL 33124 crosses were identified as good specific combinersfor number of unfilled grains per panicle. JMS 17A x JGL 33124 followed by JMS 13Ax KNM 7787 and CMS 46A x JGL 33124 wereidentified as good specific combinersfor spikelet fertility. CMS 46A x JGL 33124, JMS 18A x RNR 21278 crosses wereidentified as the best specific combiners for 1000 grain weight. JMS 18A x RNR 21278,CMS46AxKNM7787,CMS46AxJGL33124,CMS23AxKNM7787andJMS 13Ax KNM7787wereidentifiedasbestspecificcombinersforgrainyieldperplant.

CONCLUSION

The lines, CMS 46B, CMS 23B and the tester, KNM 7787 showed significantpositive *gca*effects for grain yield per plant. Parents having positive significant *gca*effects for grain yield per plant, emphasizing their capability of producing superiorcrosses from low yielding parents, with high *sca*effects. The pedigree method can beused to exploit superior crosses with high xhigh *gca*effects. Whereas, biparentalmating and recurrent selection methods can be used to develop the obtained bettercrosseswith high xlowand lowxlow *gca*effects.

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1.

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