

Studies on Combining Ability in Newly Developed Inbred Lines of Maize (*Zeamays L.*) for Yield and Quantitative Traits

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ABSTRACT

The present investigation entitled “Studies on combining ability in newly developed inbred lines of maize (*Zea mays L.*) for yield and quantitative traits” was conducted at Agricultural Research Station, Karimnagar to study heterosis in grain yield and yield contributing characters. The experimental material comprised of the crossing of 10 parental lines in half diallel mating design and 45 single cross hybrids were generated in Kharif, 2021. The hybrids along with parents and six standard checks were evaluated in Randomized Block Design with two replications in Rabi 2021-22 for twelve agro-morphological traits. Significant general and specific combining ability variances were observed for some of the characters. Parents, KML 140 and KML 132 were found to be good general combiner parents for days to 50% tasseling and days to 50% silking with the highest negative and significant *gca* effects. Parents KML 126 and KML 107 exhibited the highest positive and significant *gca* effects for grain yield and were good general combiners. Crosses, KML 110 × KML 132, and KML 111 × KML 132 were good specific combiners for days to tasseling and days to silking with negative and significant *sca* effects. Good specific combiners for grain yield were KML 107 × KML 128 followed by KML 132 × KML 120. These crosses could be selected and used in breeding programs for improving these traits. Finally, based on *per se* performance and standard heterosis KML 107 × KML 128 was a promising hybrid.

Keywords: Maize, Combining ability, GCA, sca, half diallel, yield, hybrid

INTRODUCTION

Maize (*Zea mays L.*) is a well-known cereal crop that is a member of the Maydeae tribe of the Poaceae grass family. According to speculation, it is a domesticated form of teosinte (*Zea mays ssp. parviglumis*). The largest production potential of all cereals is found in maize, which is why it is referred to as the “queen of cereals.” After rice and wheat, maize became the third-most significant crop in India. The suitability of maize to diverse environments is unmatched by any other crop as the expansion of maize to new areas

and environments still persists, owing to its wide range of plasticity. Among all the maize-growing countries, India ranks 4th and 7th in area and production respectively, representing 4% of the world’s maize area and 2% of the total production. In India, maize is grown throughout the year, though most of it (83%) is grown in the rainy or *kharif* season (July to October) followed by winter or *rabi* season (November to April) (15%) and spring season (February to May) (2%). Combining ability is a phenomenon with which inbred lines when crossed give hybrid vigour. Progeny tests should be performed in order to predict the

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combining ability of the characters governed by the recessive genes. Studies on combining ability are useful for evaluating the genetic worth of parental lines available in a breeding program. The present investigation was thus, conceptualized primarily to study the estimates of general and specific combining ability and gene action in maize for yield and yield components.

MATERIALS AND METHODS

The experiment was carried out at Agriculture Research Station, Karimnagar. Agricultural Research Station, Karimnagar is located in the Northern Telangana agro-climatic zone of Telangana state. Geographically, it lies at 18.44° N latitude, 79.13° E longitude with an altitude of 275 meters above Mean Sea Level (MSL). The average rainfall of the Research Station is 907 mm. The soils are sandy loam type with a pH of 7.3. The source of irrigation water is from Sri Ram Sagar Project (SRSP) and well. The experimental material used was 10 inbred lines developed by full-sibbing followed by two generations of selfing at ARS, Karimnagar. The data collected on several morphological traits were subjected to the combining ability analysis (Kempthorne, 1957) using the following biometrical analysis by assuming absence of reciprocal effects.

Statistical model for combining ability analysis is

$$Y_{ij} = \mu + g_i + g_j + s_{ij} + e$$

Where, Y_{ij} = mean of $i \times j^{\text{th}}$ genotypes, μ = experimental grand mean, g_j = gca effects of i^{th} female parent, g_i = effects of j^{th} male parent, s_{ij} = sca effects specific to the hybrid of the i^{th} female line and the j^{th} male line, e = experimental error.

The total variability in the population was partitioned into variance due to general combining ability, specific combining ability and error. The sum of squares obtained were as follows:

$$\text{S.S due to gca} = \frac{1}{n+2} \left[\sum (Y_{i.} + Y_{.i})^2 - \frac{4}{n} Y^2 \dots \right]$$

$$\text{S.S due to sca} = \frac{\sum \sum Y_{ij}^2}{n+2} - \frac{1}{n+2} \sum (Y_{i.} + Y_{.j})^2 + \frac{2}{(n+1)(n+2)} Y^2 \dots$$

Where, n = number of parents per diallel, $Y_{i.}$ = mean of $i \times n^{\text{th}}$ genotypes, $Y_{.i}$ = mean of $i \times i^{\text{th}}$ genotypes, $Y_{.j}$ = mean of $j \times j^{\text{th}}$ genotypes, Y_{ij} = mean of $i \times j^{\text{th}}$ genotypes

RESULTS AND DISCUSSION

In the present investigation, it was found that GCA variances were lower than SCA variances in most of the characters indicating the predominance of non-additive gene action. A similar trend of non-additive gene action for yield and its contributing characters under moisture stress conditions was in accordance with the findings of [14]

General Combining Ability Effects and Specific Combining Ability Effects

The general combining ability (GCA) effects for parental lines and the specific combining ability (SCA) effects of hybrids for twelve morpho-physiological characters were estimated and were presented in Table 1 and Table 2.

The average performance of the parental line in a series of cross combinations is generally referred to as general combining ability and is mainly attributed to additive and additive \times additive gene effects which are mainly intra allelic interaction and indicate part of inter allelic interaction also. The additive component of genetic variance is fixable through irrigated selection procedures, whereas the non-additive component is not fixable and its presence for the controlling traits necessitates the exploitation of hybrid vigor through heterosis breeding.

Deviation in the performance of a cross expected on the basis of the average performance of parental lines is mainly attributed to dominant and epistatic effects and is termed as specific combining ability i.e., non-additive part.

The general combining ability (GCA) effects of 10 parents and the specific combining ability (SCA) effects of 45 hybrids for yield and yield contributing characters were estimated and were presented in Table 4.3.

Days to 50 per cent tasseling:

The parental lines, KML-132 and KML-140 had negative and significant *gca* effects for days to 50% tasseling. The parental line, KML-140 is found to be a good general combiner for earliness with the highest negative and significant *gca* effects. These results are in agreement with the findings of [11] and [5] who reported additive gene action for days to 50 per cent tasseling.

Table 1: Estimates of general combining ability (GCA) and specific combining ability (SCA) effects for parental lines for yield and yield attributing traits

Parents	DT	DS	DM	PH	EH	TW	SP	CL	CG	KR	NKR	GY
KML-111	0.10	0.00	-0.10	11.26***	3.85**	0.80	-1.17***	-0.75***	-0.10	-0.45*	-0.89*	-772.44***
KML-110	0.30	0.20	0.40	1.60	2.98*	0.00	-1.28***	-0.30	2.07***	0.38*	0.40	15.80
KML-107	-0.40	-0.48*	-0.30	5.85***	9.02***	0.50	0.91***	0.00	0.88*	0.20	0.40	977.47***
KML-126	0.00	0.20	0.20	2.10	5.44***	1.32**	-1.74***	1.29***	4.79***	1.92***	1.1*08	1026.14***
KML-128	0.10	0.30	0.10	-4.40**	-1.80	-2.93***	4.06***	-0.10	-3.17***	-0.20	-0.40	531.97**
KML-132	-0.77***	-0.73**	-0.73*	-14.73***	-10.14***	-3.42***	-0.20	0.00	-2.06***	0.30	0.30	-737.94***
KML-135	1.26***	1.18***	1.05***	8.35***	2.73*	2.65***	-0.89***	0.30	0.50	-0.90***	0.40	217.50
KML-136	0.64**	0.55*	0.60	3.47*	0.50	0.20	0.93**	0.45*	-1.04**	-0.20	1.02*	-311.20
KML-120	1.05***	1.05***	1.01**	3.47*	-4.39**	2.98***	-0.20	-0.67**	-0.79*	-0.90***	-1.64***	-48.90
KML-140	-2.31***	-2.27***	-2.30	-16.90***	-8.22***	-2.11***	-0.40	-0.30	-1.03**	-0.10	-0.70	-898.44***

*Significant at 5% value

**Significant at 1% value

Negative and significant *sca* effects for days to 50 per cent tasseling were recorded in 2 hybrids viz., KML-111 X KML-132 and KML-110 X KML-132. These results were in accordance with the findings of [3] and [9].

Days to 50 per cent silking:

For days to 50% silking, parents viz., KML-107, KML-132 and KML-140 had negative and significant *gca* effects.

Parental line, KML-140 is found to be a good general combiner with highest negative and significant *gca* effects. These results were in agreement with the findings [11] and [5] who reported additive gene action for days to 50 per cent silking.

The hybrid KML-110 X KML-132 has negative and significant *sca* effects for days to 50 per cent silking. These results were comparable with the findings of [3] and [9].

Days to maturity

Among the parental lines, KML-132 has negative and significant *gca* effects for days to maturity which is found to be a good combiner for early maturity with negative and significant *gca* effects.

The hybrid KML-110 X KML-132 had negative and significant *sca* effects for days to maturity. These results were in agreement with the findings of [3] and [9] who reported the non-additive gene action for days to maturity.

Plant height (cm)

The parental line KML-111, KML-107, KML-135, KML-136 and KML-120 had positive and significant *gca* effects for plant height.

The parental line KML-111 and KML-135 had highest positive and significant *gca* effects and were good general combiners for tallness. These results were in agreement with the findings of [11] and [5] who reported additive gene action for plant height.

Of the 45 hybrids, 35 hybrids had the positive and significant *sca* effects for plant height. The highest positive and significant *sca* effect was found in KML-126 X KML-136 followed by KML-136 X KML-140. These results were comparable with the findings of [3] and [15] who reported non additive gene action for plant height.

Ear height (cm)

Among the parental lines KML-111, KML-110, KML-107, KML-126 and KML-135 had positive and significant *gca* effect. The parental line KML-107 and KML-126 had the highest positive and significant *gca* effects and were good general combiners for ear height. These results were in comparison with the findings of [11] and [5] who reported additive gene action for ear height.

32 crosses had shown positive and significant *sca* effects for ear height. The highest significant *sca* effect was found in cross KML-126 X KML-136 followed by KML-126 X KML-140. Similar results were obtained by [1], [2] and [15] who reported

Table 2: Estimates of general combining ability (GCA) and specific combining ability (SCA) effects for crosses for yield and yield attributing traits

Crosses	DT	DS	DM	PH	EH	TW	SP	CL	CG	KR	NKR	GY
KML 111 x KML 110	2.61***	2.68***	2.14*	14.37**	8.40	0.20	-4.61**	-1.59*	1.70	0.50	-2.50	-477.30
KML 111 x KML 107	1.30	1.40	1.90	15.08**	10.32*	1.70	0.20	0.50	0.30	0.20	-1.00	1590.98**
KML 111 x KML 126	4.94***	4.72***	4.39**	7.40	-5.10	-0.40	5.64***	-2.13**	-1.10	-0.50	-5.20	387.81**
KML 111 x KML 128	4.81***	4.64***	4.43***	8.80	12.15**	1.80	-1.10	1.97**	3.14*	-0.40	2.30	209.50
KML 111 x KML 132	-1.80**	-1.40	-0.20	10.66*	0.50	3.25*	-2.06*	0.70	4.45***	1.20	3.60	774.90*
KML 111 x KML 135	3.65***	3.22***	3.02**	16.08**	15.61***	2.30	-1.75*	2.43**	3.65**	0.80	4.60	1396.94*
KML 111 x KML 136	1.77*	1.85*	1.50	23.95***	8.30	4.70***	1.50	1.49*	2.38*	-0.90	0.40	1062.10
KML 111 x KML 120	3.36***	3.35***	3.06**	3.50	1.70	4.23**	-4.15***	1.10	2.20	0.80	2.10	-172.10
KML 111 x KML 140	3.73***	3.68***	4.35***	27.83***	20.07***	2.10	-3.30***	-0.10	-0.50	-0.50	0.10	99.40
KML 110 x KML 107	1.56*	1.68*	0.80	18.29***	11.70**	-1.20	-1.80*	1.40	-0.30	0.40	-1.30	-1209.76*
KML 110 x KML 126	2.23**	2.01**	1.40	8.10	11.78**	8.15**	-3.64***	-1.10	1.40	0.20	-1.00	-120.40
KML 110 x KML 128	2.61***	2.43**	1.90	18.54***	21.03***	0.00	0.90	1.46*	-2.10	-1.20	-2.50	381.20
KML 110 x KML 132	-3.01***	-3.06***	-2.72*	18.37***	14.86**	-1.80	3.54***	-1.20	-0.90	-0.20	-0.10	257.20
KML 110 x KML 135	0.40	0.50	2.00	24.79***	11.99**	4.36**	-1.10	1.40	3.41**	1.00	-1.70	337.70
KML 110 x KML 136	2.06**	2.14**	1.50	23.66***	19.70***	1.90	1.20	1.64*	1.00	-1.26*	3.60	1729.86**
KML 110 x KML 120	0.70	0.60	0.00	17.66***	15.11***	1.40	-0.10	1.10	2.40	0.00	1.80	1011.70
KML 110 x KML 140	4.02***	3.97***	4.81***	17.04***	8.95*	-2.10	0.20	0.40	1.00	1.20	2.30	1140.15*
KML 107 x KML 126	3.40***	3.22***	3.06**	25.29***	19.74***	1.80	2.05*	1.00	1.40	0.40	3.00	1212.90*
KML 107 x KML 128	1.77*	1.64*	3.10**	9.30	9.49*	3.62**	2.44**	-0.60	1.40	-0.50	-2.50	2989.06***
KML 107 x KML 132	3.65***	3.64***	2.98**	17.08***	20.82***	-1.50	-1.95*	1.42*	2.51*	1.53*	0.90	-280.00
KML 107 x KML 135	5.11***	5.22***	5.18***	42.50***	20.95***	5.46***	-4.19***	0.00	2.10	0.20	-0.20	275.00
KML 107 x KML 136	3.73***	3.85***	3.68***	20.37***	8.20	5.10***	0.10	1.76*	-0.20	-0.60	-0.90	-735.30
KML 107 x KML 120	3.31***	3.35***	3.73***	29.87***	15.57***	1.80	-1.20	1.40	2.20	0.20	1.30	573.00
KML 107 x KML 140	2.69***	3.18***	2.52*	32.25***	13.90**	1.40	1.40	0.20	3.78**	1.90**	1.30	1686.98**
KML 126 x KML 128	1.44*	1.47*	1.10	34.04***	17.57***	2.50	-2.04*	1.72*	3.15*	0.20	7.80	1180.90**
KML 126 x KML 132	3.31***	3.97***	3.52**	15.87**	11.90**	-0.10	-1.10	-0.30	0.70	1.28*	0.10	-1094.20
KML 126 x KML 135	3.27***	3.06***	2.73*	24.79***	13.03**	2.40	2.86**	1.20	-0.60	-0.60	-0.90	1411.36*
KML 126 x KML 136	1.90**	2.18**	3.73***	38.66***	23.74***	-0.70	-0.20	-0.20	0.20	0.70	-0.60	1156.52*
KML 126 x KML 120	1.48*	1.68*	1.30	32.66***	21.65***	-0.50	-0.80	1.10	0.20	0.40	1.60	-183.70
KML 126 x KML 140	-0.10	-0.50	1.60	33.04***	21.99***	3.47*	-1.98*	0.90	1.20	0.70	-0.40	679.30

continued.....

KML 128 x KML 132	2.19**	2.89***	2.56*	15.83**	11.65*	1.50	2.29**	1.40	1.30	-0.10	3.60	1176.98**
KML 128 x KML 135	2.65***	2.47**	2.27*	13.25**	11.28*	3.37*	0.80	0.00	-0.80	-1.42*	3.00	398.02*
KML 128 x KML 136	2.27**	2.10**	2.77**	16.62***	8.99*	1.00	0.20	0.80	1.30	-0.70	3.40	-218.80*
KML 128 x KML 120	2.36***	2.60***	2.81**	-2.40	5.90	-2.85*	2.95**	0.30	-0.20	0.10	1.00	-199.50
KML 128 x KML 1110	4.23***	4.93***	4.60***	11.00*	6.20	-0.80	0.30	1.60*	0.40	-1.72**	3.60	-1179.51**
KML 132 x KML 135	6.02***	5.97***	5.64***	11.58*	15.61***	1.10	-2.59**	1.48*	1.80	0.10	2.40	1599.44**
KML 132 x KML 136	6.15***	6.10***	6.14***	12.45**	8.82*	1.50	2.23*	-0.30	-1.20	-1.10	-0.30	-220.40
KML 132 x KML 120	3.73***	3.60***	3.18**	-1.00	4.70	3.73**	3.35***	1.30	0.50	0.10	3.90	2813.90***
KML 132 x KML 140	6.61***	5.43***	4.98***	2.80	2.10	-3.36*	2.76**	-2.61***	1.10	1.32*	-0.10	-1619.59**
KML 135 x KML 136	3.61***	3.68***	3.35**	23.37***	21.95***	3.11*	-1.90*	-0.70	0.10	1.53*	0.60	1351.15*
KML 135 x KML 120	3.69***	3.68***	3.39**	11.87*	7.90	1.40	0.40	0.30	2.49*	1.78**	2.30	1641.94**
KML 135 x KML 140	2.56***	3.01***	2.68*	7.80	9.20*	3.70**	0.10	-0.10	0.80	0.00	1.40	234.40
KML 136 x KML 120	3.81***	3.81***	3.39**	-0.80	2.10	3.75**	-3.35***	-0.30	0.00	0.50	0.10	-527.90
KML 136 x KML 140	3.19***	3.64***	3.18**	38.12***	21.90***	3.48*	-0.10	0.50	0.40	0.20	-2.30	1518.11**
KML 120 x KML 140	3.77***	3.64***	3.23**	15.12**	4.30	5.90***	0.70	2.40**	-0.50	-0.50	1.40	1039.90

*Significant at 5% value

**Significant at 1% value

the non-additive gene action for ear height.

Ear length (cm)

Among the parental lines, KML-126 and KML-136 had positive and significant *gca* effects. The parental line KML-126 had highest positive and significant *gca* effects and was a good general combiners for ear length. These results were comparable with findings of [11] and [5] who reported the additive gene action for ear length.

Positive and significant *sca* effects were observed in eleven hybrids for ear length. Highest positive and significant *sca* effects for ear length were found in KML-111 X KML-135 followed by the hybrid KML-120 X KML-140.

These results were comparable with findings of [3] and [15] who reported the non-additive gene action for ear length.

Ear diameter (cm)

The parental lines viz., KML-110, KML-107, and

KML-126 had shown positive and significant *gca* effects which are found to be good general combiners for ear diameter. These results were in agreement with that of [10], [12], and [11] who reported additive gene action for ear diameter.

Nine hybrids had shown positive and significant *sca* effects. The highest and positive significant *sca* effects for ear diameter were observed in KML-111 X KML-132 followed by KML-107 X KML-140.

Similar findings were reported by [2], [15] and [13] indicating the importance of non-additive gene action in the inheritance of ear diameter.

Number of kernel rows per ear

The parental lines KML-110 and KML-126 had positive and significant *gca* effects. The parental line, KML-126 was found to be good general combiners for a number of kernel rows per ear with the highest positive and significant *gca* effects for a number of kernels rows per ear. These results were comparable with the findings of [12] and [7] who indicated a number of kernels per ear

was governed by additive gene action.

Five hybrids had positive and significant *sca* effects for a number of kernel rows per ear. The highest positive and significant *sca* effect for this trait was found in cross KML- 107 X KML-140 followed by KML-135 X KML-120.

These results were in comparable with the findings of [10], [15] and [13] who reported the non-additive gene action for a number of kernel rows per ear.

Number of kernels per row

Among the parental lines, KML-126 and KML-136 had positive and significant *gca* effects for a number of kernels per row.

The parental lines, KML-126 and KML-136 are good general combiners with positive and significant *gca* effects for number of kernels rows per row. These results were comparable with the findings of [12] and [7] who mentioned that number of kernels per row was governed by additive gene action.

Ten hybrids had shown positive and significant *sca* effects for number of kernels per row. The highest positive and significant *sca* effect was found in cross KML-126 X KML-128 followed by KML-111 X KML-135 for a number of kernels per row. These results were in accordance with that of [3] and [14] who reported the non-additive gene action for a number of kernels per row.

Test weight

Among the parental lines, KML-126, KML-135, and KML-120 had positive and significant *gca* effects for the test weight. The parental line KML-120 had the highest positive and significant *gca* effects and were good general combiners for the test weight. These results were comparable with the findings of [11] and [7] who indicated the preponderance of additive gene action in the inheritance of test weight.

Sixteen crosses had shown positive and significant *sca* effects. Significant positive *sca* effect for test weight was highest in KML-110 X KML-126 followed by KML-120 X KML-140. These results were comparable with the findings of [10], [14]

and [9] who reported the importance of non-additive gene action in governing test weight.

Grain yield per hectare (kg/ha)

Among the parental lines, KML-107, KML-126, KML-128 had shown positive and significant *gca* effects.

The parental line, KML-126 had the highest positive and significant *gca* effects and was good general combiner for grain yield. Hence the parent will be utilized in the development of high-yielding hybrids. These results were supported by [11] and [5] who mentioned that grain yield was governed by additive gene action.

Nineteen hybrids had positive and significant *sca* effects. The highest positive and significant *sca* effect for grain yield was observed in KML-107 X KML-128 followed by KML-132 X KML-120. These results were comparable with the findings of [14] who indicated the importance of non-additive gene action in governing grain yield per plot.

Non additive gene action played an important role in the inheritance of all the studied traits indicating exploitation of heterosis, in deriving high-yielding early maturity hybrids amicable to climate change situations. Similar results were reported by El-Galfy *et al.* (2022).

Shelling percentage

The parental line, KML-107, KML-128 and KML-136 had positive and significant *gca* effects.

The parental line, KML-128 was a good general combiner with the highest positive and significant *gca* effects for shelling percentage. [4], [11] and [7] also reported similar findings indicating the importance of additive gene action in governing this trait.

Eleven hybrids had shown positive and significant *sca* effects for shelling percentage. Similar findings were reported by [10], [14] and [9] who reported a preponderance of non-additive gene action in the inheritance of shelling percentage.

CONCLUSION

Lines, KML 140 and KML 132 were found to be

good general combiners for days to 50% tasseling and days to 50% silking with the highest negative and significant *gca* effects. Inbred lines KML 126 and KML 107 had the highest positive and significant *gca* effects for grain yield and were good general combiners. Inbred lines, KML 140, KML 132 and KML 128 were found to be good general combiners for plant height having short stature with the highest negative and significant *gca* effects.

Crosses, KML 110 × KML 132 and KML 111 × KML 132 were good specific combiners for days to tasseling and days to silking with negative and significant *sca* effects. Good specific combiners for grain yield were KML 107 × KML 128 followed by KML 132 × KML 120 with the highest positive and significant *gca* effects. KML 128 × KML 120 and KML 132 × KML 120 were good specific combiners for plant height with the highest negative and significant *sca* effects.

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