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# Studies on combining ability of elite inbred lines of maize (*Zea mays* L.)

## N Tejaswini, K Sukumar, T Srikanth and B Mallaiah

### Abstract
Eight elite inbred lines were crossed to generate 28 experimental hybrids to study the combining ability of various traits. The study indicated the preponderance of non-additive (dominance × dominance and additive × dominance) gene action for the majority of the traits and heterosis breeding is rewarding the improvement of the characters.

**Keywords:** Maize, combining ability, gene action

### Introduction
Maize (*Zea mays* L.) crop is a highly cross-pollinated that was categorized in the family, Poaceae, tribe Maydeae which is widely adapted to diverse agro-climatic conditions. Its utility in various sectors made the crop significant and is often referred to as the 'queen of cereals' due to its high genetic variability and wider adaptability nature to varied agroclimatic conditions. It was grown worldwide in an area of 193.7 m ha with a production of 1147.6 MT while, productivity was 5920 kg ha^{-1} (FAO, 2020) [2].

### Materials and Methods
The experimental material consisted of eight elite inbred lines i.e., PFSR-73, PFSR-127, PFSR-151, BML-10, MGC-49, ML-14, PFSR-92, BPDT-5009 and the resultant 28 hybrids. Crossing programme was affected in Half-diallel, Method-II, Model-I mating design and developed 28 hybrids at Agricultural Polytechnic College, Polasa, Jagtial during *kharif,* 2021. Hybrid evaluation was done with 28 experimental hybrids, eight parents and one check, DHM-117 in Randomized Block Design (RBD) replicated thrice by adopting a spacing of 75 × 20 cm during *Rabi* 2021-22.

### Analysis of variance for combining ability based on half diallel design
The analysis of variance for combining ability of all the characters under present investigation has been presented in the Table 1.
The analysis revealed that treatments were found to be significant for all the characters included under this present study. The variance due to replications was non-significant for all the traits. Significant differences found in the parents indicated the presence of greater diversity among the parents. Further, hybrids also exhibited significant differences, indicating the varied performance of the cross combinations. Parents *vs.* hybrids showed significant differences for all the traits except the number of kernel rows per ear indicating that a considerable amount of variability was present in hybrids for these characters.

### Estimation of combining ability
The data was of F$_1$s and parents was analyzed as per Method II (F$_1$s + parents) and Model -I (fixed effect) of Griffing (1956a) [4] for combining ability. The concept of combining ability was given by Sprague and Tatum (1942) [11] which facilitates the partitioning of genotypic variation of hybrids into variation due to general combining ability (main effects) and specific combining ability (interaction effects).

### Analysis of variance for combining ability based on half diallel design
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The analysis revealed that treatments were found to be significant for all the traits included under the present study. The variance due to replications was non-significant for all the traits. Significant differences among the parents indicated the presence of greater diversity among the parents. Hybrids also exhibited significant differences, indicating the varying performance of the cross combinations. Parents *vs.* hybrids also exhibited significant differences for all the traits except number of kernel rows per ear indicating that a considerable amount of variability was present in hybrids for these characters.

## General combining ability effects and specific combining ability effects

The general combining ability effects of 8 parents and specific combining ability effects of the resultant 28 hybrid combinations were estimated as per the half diallel mating design. The trait-wise results *gca* effects of the parents under study are presented in Table 2 and *sca* effects of hybrids have been detailed in Table 3.

## Days to 50 percent anthesis

Among the parents, BML-10 (-3.58), PFSR-151 (-1.98), PFSR-127 (-1.78) and MGC-49 (-0.88) exhibited significant *gca* effect, implying that these lines are good general combiners for earliness. The hybrids, PFSR-73×MGC-49 (-7.53), PFSR-151×BPDT-5009 (-6.73), PFSR-127×PFSR-92 (-6.10), BML-10×BPDT-5009 (-5.80) and MGC-49×ML-14 (-5.66) exhibited negative and significant *sca* effects which are desirable for the trait, earliness. The findings are in concurrence with the earlier findings of Abd-Elaziz *et al.* (2021) [1] who reported earlier the importance of additive gene action and nonadditive gene action for the trait.

## Days to 50 percent silking

Among the 8 parents, four parents exhibited significant negative *gca* effects where the highest negative significant *gca* effect was recorded by BML-10 (3.40) followed by PFSR-151 (-1.77), PFSR-127 (-1.40) and MGC-49 (-0.70), indicating that these parents are good general combiners for early types. Similar findings were also reported by Sandesh *et al.* (2018) [9] who emphasized the importance of additive gene action in governing days to 50 percent silking. Among the 28 hybrids, sixteen hybrids exhibited significantly negative *sca* effects. The hybrid, PFSR-73×MGC-49 (-6.93) registered the highest negative significant *sca* effect followed by PFSR-151×BPDT-5009 (-6.73), PFSR-127×PFSR-92 (-5.83), BML-10×BPDT-5009 (-5.77) and PFSR-151×PFSR-92 (-5.13). The study indicated the predominance of non-additive (dominance × dominance and additive × dominance) gene action Hence, heterosis breeding can be exploited in the improvement of the trait. These findings are in accordance with the earlier findings of Sandesh *et al.* (2018) [9] who reported non-additive gene action for days to 50 percent silking.

## Anthesis silking interval

Highest negative significant *gca* effects were recorded by ML-14 (-0.42) followed by PFSR-73 (-0.29) and PFSR-92 (-0.29) and the remaining parents showed positive and significant *gca* effects. These results are in agreement with the findings of Patel (2022) [8].
The hybrid, PFSR-127×MGC-49 (-1.10) recorded the highest significant negative *sca* effect followed by PFSR-73×ML-14

(-0.94), MGC-49×BPDT-5009 (-0.90), PFSR-151×MGC-49 (-0.64), PFSR-73×PFSR-151 (-0.54) and MGC-49×PFSR-92 (-0.50).
The study indicated the predominance of non-additive (dominance × dominance and additive × dominance) gene action and heterosis breeding is rewarding the improvement of this character.

## Days to maturity

The parent PFSR-127 (-3.42) showed the highest negative significant *gca* effect followed by PFSR-151 (-2.55), PFSR-73 (-1.45), BML-10 (-1.09) and MGC-49 (-0.42).
The hybrid, BML-10×ML-14 (-9.37) exhibited the highest negative significant *sca* effect followed by PFSR-151×PFSR-92 (-8.40), PFSR-73×MGC-49 (-7.77), MGC-49×ML-14 (-7.04) and BML-10×BPDT-5009 (-6.40). The study indicated the predominance of predominance of non-additive (additive × dominance) gene action. Similar results were also reported by Yadav and Gangwar (2021) [13] for additive and non-additive gene action governing the trait.

## Plant height (cm)

For plant height, *gca* effects ranged from -20.00 (BPDT-5009) to 16.35 (PFSR-127). Three parents among eight showed significantly negative *gca* effects and are found good general combiners for dwarfness. For plant height, *sca* effects ranged from -66.25 (ML-14×PFSR-92) to 41.96 (PFSR-73×BPDT-5009). Among 28 hybrids, 10 hybrids showed significantly negative *sca* effects.

## Ear height (cm)

For ear height, *gca* effects ranged from -7.09 (ML-14) to 6.17 (PFSR-73). Four parents among eight showed significantly negative *gca* effects and were considered to be good general combiners. Six hybrids showed significantly negative *sca* effects. The hybrid, ML-14×PFSR-92 (-18.70) recorded the highest negative significant *sca* effect followed by PFSR-127×PFSR-92 (-13.38) and ML-14×BPDT-5009 (-12.79). Yadav and Gangwar (2021) [13] and Sayed *et al.* (2022) [10] also reported additive and non-additive gene action.

## Ear length (cm)

The parent, PFSR-127 (0.92) recorded the highest significant positive *gca* effect followed by BML-10 (0.90), PFSR-151 (0.87) and PFSR-73 (0.72) and these are considered as good general combiners. Similar kind of results were also reported by Mesekal *et al.* (2021) [5]. The hybrid, PFSR-151×MGC-49 (2.76) showed the highest significant and positive *sca* effect followed by PFSR-73×BPDT-5009 (2.59), BML-10×BPDT-5009 (2.37), MGC-49×ML-14 (2.18) and PFSR-73×MGC-49 (1.86). Mousa *et al.* (2021) [6] also reported similar kind of results.

## Ear girth (cm)

The parents, BML-10 (0.74), PFSR-127 (0.47), PFSR-151 (0.33) and ML-14 (0.23) recorded significant, positive *gca* effects and assumed as good general combiners for this trait. The results found similar to earlier findings of Ola *et al.* (2018) [7]. Fourteen hybrids recorded significantly positive *sca* effects, among which PFSR-73×PFSR-127 (1.68) exhibited the highest significant positive *sca* effect followed by PFSR-127×PFSR-92 (1.62), PFSR-73×BML-10 (1.13) and BML-10×PFSR-92 (1.01). The study indicated the presence of non-

additive gene action (additive × dominance and dominance × dominance). Mousa *et al.* (2021) [6] also reported similar kind of results.

**Number of kernel rows per ear**
Four out of eight parents BML-10 (0.79), PFSR-127 (033), ML-14 (0.17) and PFSR-151 (0.13) showed significantly positive *gca* effects implying that these four parents were found good general combiners. Similar findings were also reported by Ola *et al.* (2018) [7], Yadav and Gangwar (2021) [13] and Patel (2022) [8]. Eleven out of 28 hybrids recorded significantly positive *sca* effect, among which ML-14×PFSR-92 (1.61) recorded the highest positive significant *sca* effect followed by PFSR-127×BPDT-5009 (1.56), ML-14×BPDT-5009 (1.32), PFSR-73×MGC-49 (1.07) and PFSR-73×PFSR-92 (1.01). The study indicated the preponderance of non-additive gene action (additive × dominance and dominance × dominance). Similar results were reported by Patel (2022) [8].

**Number of kernels per row**
The parent BML-10 (3.11) recorded the highest significant *gca* effect followed by PFSR-151 (2.21), PFSR-73 (0.88) and PFSR-127 (0.78) and thus these parents are considered as good general combiners for this trait. The study found similarities with the findings of Patel (2022) [8]. The hybrid, MGC-49×ML-14 (8.47) registered high positive and significant *sca* effect followed by PFSR-73×PFSR-92 (7.95), PFSR-73×MGC-49 (7.66), PFSR-151×MGC-49 (5.87) and PFSR-92×BPDT-5009 (5.27).
The study indicated the predominance of non-additive gene

action (additive × dominance and dominance × dominance) where similar findings were reported earlier by Mousa *et al.* (2021) [6] and Patel (2022) [8].

**100-kernel weight (g)**
Three parents, PFSR-127 (2.88), BML-10 (0.90) and PFSR-151 (0.88) showed significantly positive *gca* effects and are as good general combiners. Significantly positive *gca* effect was also reported by Yadav and Gangwar (2021) [13]. The hybrid, PFSR-73×ML-14 (8.25) exhibited the highest significant *sca* effect followed by BML-10×BPDT-5009 (7.71), PFSR-151×BPDT-5009 (6.14), PFSR-127×BPDT-5009 (4.31) and PFSR-151×MGC-49 (3.85). The study indicated the predominance of non-additive gene action (additive × dominance and dominance × dominance) which found similarity with findings of Suresh *et al.* (2021) [12].

**Grain yield (g/plant)**
The parent, PFSR-127 (20.24) exhibited the highest significant positive *gca* effect followed by BML-10 (18.70) and PFSR-151 (17.24) demonstrating that these are good general combiners. The hybrid, PFSR-151×BPDT-5009 (47.93) exhibited the highest significant *sca* effect followed by PFSR-73×ML-14 (43.57), PFSR-127×BPDT-5009 (37.27), PFSR-151×MGC-49 (35.63), BML-10×PFSR-92 (31.67) and PFSR-127 ×BML-10 (31.50). The results are in agreement with the findings of Ola *et al.* (2018) [7], Sandesh *et al.* (2018) [9] and Patel (2022) [8] for both *gca* and *sca* effects which were significantly positive.

**Table 1:** Analysis of variance for combining ability for yield and its attributing traits in maize genotypes

| Source of variation | d.f. | Mean sum of squares | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | Days to 50% anthesis | Days to 50% silking | Anthesis silking interval | Days to maturity | Plant height (cm) | Ear height (cm) | Ear length (cm) | Ear girth (cm) | Number of kernel rows per ear | Number of kernels per row | 100-kernel weight (g) | Grain yield (g/plant) |
| Replications | 2 | 0.58 | 0.48 | 0.06 | 2.28 | 0.43 | 4.39 | 0.54 | 0.10 | 0.10 | 19.43 | 0.78 | 7.17 |
| Treatments | 35 | 88.79** | 81.08** | 1.51** | 115.49** | 3050.51** | 370.47** | 15.270** | 4.59** | 4.33** | 94.39** | 64.81** | 4134.84** |
| Parents | 7 | 97.94** | 78.37** | 2.75** | 111.69** | 1572.29** | 173.15** | 14.10** | 4.28** | 5.02** | 70.37** | 90.01** | 2071.51** |
| Hybrids | 27 | 89.37** | 84.59** | 1.20** | 119.77** | 3338.87** | 406.50** | 12.57** | 4.54** | 4.31** | 94.36** | 54.03** | 4346.31** |
| Parent Vs Hybrids | 1 | 9.05** | 5.47** | 1.20** | 26.45** | 5612.41** | 778.88** | 96.08** | 8.20** | 0.01 | 263.16** | 179.49** | 12868.33** |
| Error | 70 | 0.202 | 0.26 | 0.07 | 0.47 | 11.03 | 4.15 | 0.06 | 0.05 | 0.08 | 4.56 | 1.36 | 19.33 |
| Total | 107 | 29.18 | 26.70 | 0.54 | 38.13 | 1005.05 | 123.98 | 5.05 | 1.54 | 1.47 | 34.22 | 22.10 | 1365.30** |

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

**Table 2:** Estimates of general combining ability (*gca*) effects of the parents for yield and its attributing traits

| Source | Days to 50% anthesis | Days to 50% silking | Anthesis silking interval | Days to maturity | Plant height (cm) | Ear height (cm) | Ear length (cm) | Ear girth (cm) | Number of kernel rows per ear | Number of kernels per row | 100-kernel weight (g) | Grain yield (g/plant) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| PFSR-73 | 2.25** | 1.85** | -0.29** | -1.45** | 12.41** | 6.17** | 0.72** | -0.32** | -0.29** | 0.88* | -0.22 | -2.35** |
| PFSR-127 | -1.78** | -1.40** | 0.30** | -3.42** | 16.35** | 1.63** | 0.92** | 0.47** | 0.33** | 0.78* | 2.88** | 20.24** |
| PFSR-151 | -1.98** | -1.77** | 0.17** | -2.55** | 6.65** | -1.77** | 0.87** | 0.33** | 0.13** | 2.21** | 0.88** | 17.24** |
| BML-10 | -3.58** | -3.40** | 0.27** | -1.09** | 9.07** | 4.10** | 0.90** | 0.74** | 0.79** | 3.11** | 0.90** | 18.70** |
| MGC-49 | -0.88** | -0.70** | 0.14** | -0.42** | 4.32** | 5.71** | -0.12** | -0.30** | -0.24** | -0.20** | -0.55** | -12.09** |
| ML-14 | 1.05** | 0.59** | -0.42** | 2.47** | -16.83** | -7,…09** | -0.67** | 0.23** | 0.17** | -1.79** | -0.60** | -4.75** |
| PFSR-92 | 1.71** | 1.45** | -0.29** | 2.64** | -11.98** | -2.73** | -0.96** | -0.54** | -0.59** | -2.95** | 0.11 | -16.25** |
| BPDT-5009 | 3.21** | 3.39** | 0.10* | 3.84** | -20.00** | -6.02** | -1.67** | -0.61** | -0.29** | -2.04** | -3.40** | -20.72** |
| Gi at 95% | 0.18 | 0.20 | 0.11 | 0.27 | 1.34 | 0.82 | 0.10 | 0.09 | 0.11 | 0.86 | 0.47 | 1.77 |
| Gi-Gj at 95% | 0.27 | 0.31 | 0.16 | 0.42 | 2.02 | 1.24 | 0.16 | 0.14 | 0.17 | 1.30 | 0.71 | 2.68 |

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

**Table 3:** Estimates of specific combining ability (*sca*) effects of the hybrids for yield and its attributing traits

| Source | Days to 50% anthesis | Days to 50% silking | Anthesis silking interval | Days to maturity | Plant height (cm) | Ear height (cm) | Ear length (cm) | Ear girth (cm) | Number of kernel rows per ear | Number of kernels per row | 100-kernel weight (g) | Grain yield (g/plant) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| PFSR-151 × PFSR-92 | -5.23** | -5.13** | 0.12 | -8.40** | 31.93** | 3.71** | 0.91** | 0.58** | -0.61** | 0.55 | 2.36** | 20.47** |
| PFSR-151 × BPDT-5009 | -6.73** | -6.73** | 0.05 | -5.27** | 0.17 | 5.25** | 0.32* | 1.68** | 0.56** | 3.04* | 6.14** | 47.93** |
| BML-10 × MGC-49 | -0.70** | -0.67* | -0.07 | 2.19** | 16.60** | -0.77 | 0.46** | 0.08 | -0.42** | -1.36 | -2.72** | -15.49** |
| BML-10 × ML-14 | -3.96** | -3.63** | 0.15 | -9.37** | 2.34 | 4.29** | 0.96** | 1.13** | -0.83** | 5.16** | 2.30** | 13.83** |
| BML-10 × PFSR-92 | -2.63** | -2.17** | 0.35* | -3.20** | 16.39** | 4.71** | 1.78** | 1.01** | 0.99** | 2.45* | 0.14 | 31.67** |
| BML-10 × BPDT-5009 | -5.80** | -5.77** | -0.04 | -6.40** | 28.02** | 9.53** | 2.37** | 0.17 | -0.63** | 0.74 | 7.71** | 25.80** |
| MGC-49 × ML-14 | -5.66** | -5.00** | 0.62** | -7.04** | 32.60** | 8.56** | 2.18** | 0.30* | -0.33* | 8.47** | 4.26** | 42.97 |
| MGC-49 × PFSR-92 | 5.00** | 4.46** | -0.50** | 8.12** | 1.16 | 8.91** | 0.13 | -0.58** | 0.30 | -2.03 | -2.52** | -28.86** |
| MGC-49 × BPDT-5009 | 5.50** | 4.53** | -0.90** | 4.25** | -5.83** | -2.21* | -1.29** | -1.44** | -2.26** | -7.74** | -0.63 | -39.73** |
| ML-14 × PFSR-92 | -0.60** | -1.50** | -0.27 | -4.77** | -66.25** | -18.70** | -3.90** | 0.18 | 1.61** | -6.57** | 1.90** | -18.19** |
| ML-14 × BPDT-5009 | 4.23** | 4.56** | 0.32* | 6.35** | -45.03** | -12.79** | -0.71** | -0.15 | 1.32** | -9.88** | -2.91** | -32.06** |
| PFSR-92 × BPDT-5009 | 3.56** | 4.36** | 0.85** | 7.19** | -11.11** | -1.12 | 0.22 | -1.14** | -0.58** | 5.27** | -6.45** | -18.56** |
| Sij at 95% | 0.48 | 0.55 | 0.29 | 0.74 | 3.56 | 2.19 | 0.28 | 0.25 | 0.30 | 2.29 | 1.25 | 4.72 |
| Sij-Sik at 95% | 0.71 | 0.81 | 0.43 | 1.09 | 5.27 | 3.24 | 0.41 | 0.37 | 0.45 | 3.39 | 1.85 | 6.98 |
| Sij-Skl at 95% | 0.67 | 0.76 | 0.40 | 1.03 | 4.97 | 3.05 | 0.39 | 0.35 | 0.43 | 3.20 | 1.74 | 6.58 |

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

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