Combining ability analysis and nature of gene action for grain **yield in Maize hybrids** Anupam Barh¹, N.K Singh², S. S Verma³, J.P Jaiswal⁴ and P.S Shukla⁵

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Abstract— In the present investigation combining ability analysis and nature of gene action was studied for twenty lines, four testers and eighty hybrids, which were obtained from Line x tester biparental crossing scheme. The twelve characters were studied for winter maize under this experiment. Parental variance, Line variance, and line x tester variance revealed that there were significant differences in all the characters, whereas only tester variance showed three non-significant characters, namely days to 50% anthesis, days to maturity and cob length. The nature and magnitude of gene action showed that the dominance variance major reason towards hybrid performance for all characters. This means that non-additive action is important for the hybrid performance. The most promising crosses for higher yield per ha were L8 x T1 (27.63), L9 x T4 (23.44), L3 X T3 (23.41), L16 x T2 (23.03), L3 x T3 (22.81), L1 x T3 (22.51), L20 x T2 (19.48), L13 x T4 (19.47), L7 x T1 (18.22) and L17 x T4 (17.58) which have shown high SCA effects for grain yield which high parental GCA effects can be exploited for the development of SCHs because of non-additive gene action.

Keywords—Combining ability, GCA, Gene action, Maize and SCA.

INTRODUCTION

Maize (Zea mays L.) is an important cereal crop belonging to tribe Maydeae, of the grass family, Poaceae. Maize always been a versatile crop and used for various purposes, for example, feed, fodder, silage and ethanol production. In plant breeding maize hybrid had contributed a lot in terms of production. The higher yield of maize hybrid than inbred and composites is the main reason of its preference for commercial production. The production of promising hybrids for commercial cultivation is only accomplished by a perfect parental combination, which can judge by their combining abilities. Combining ability can be defined as the ability of a genotype to inherit its required economic performance to its crosses. Therefore, combining ability analysis is an effective tool for identifying superior parents for hybrids and was first reported by Sprague and Tatum (1942). Combining ability is dissected into two parts general combining ability (GCA) and specific combining ability (SCA). Both GCA and SCA variances have been determined and related to the possible types of gene action involved. The variance of GCA includes an additive genetic portion, while, SCA variance usually includes the nonadditive genetic variance of the total genetic variance arising largely from dominance and epistatic deviation. In the current investigation, combining ability analysis and nature of gene action was tested using line x tester mating design in order to sort out promising maize inbred lines and hybrid which can be utilized for the commercial production.

II. MATERIAL AND METHODS

The present investigation was carried out during December 2013 in the winter season at N. E. Borlaug Crop Research Centre, G. B. Pant University of Agriculture and Technology, Pantnagar, Uttarakhand. Geographically, Pantnagar is situated on the latitude of 29° N, longitude 79.3° E and at an altitude of 243.84 meters above the mean sea level. The University falls under the subtropical zone and situated in the Tarai region at the foothills of the Shivalik range of the Himalayas. Experimental materials in the present investigation were comprised of eighty F_{1S} along with 20 parental lines, four testers and one standard check (Table-1) which were evaluated in randomized complete block design (RCBD) with two replications having plot consisted of one row of four meter lengths with row to row distance of 75 cm and plant to plant of 20 cm. The observations recorded on five randomly selected competitive plants from the rows of each plot for Plant height (cm), Ear height (cm), cob length (cm), Ear diameter (cm), Tassel Length (cm), Number of kernel rows/ear, Number of kernels/row, 100 kernel weight (g) days to 50 percent anthesis. Observations were recorded on the whole plot basis in respect of Days to 50% anthesis, Days to 50% silking, days to maturity and grain yield (kg/ha).

TABLE 1
DETAILS OF PARENTAL MATERIAL AND CHECKS TO BE USED IN EXPERIMENT

| S. NO. | Pedigree of Parental line | | | | | | | | |
|---------------------|---|--|--|--|--|--|--|--|--|
| | Lines | | | | | | | | |
| L1 | POP 31⊗ 23-3-3-1-1-1-2-1/2#⊗ 7-2 to 3⊗5 | | | | | | | | |
| L2 | POP 445⊗ 101-3-2-BBB-⊗-1 | | | | | | | | |
| L3 | POP 45 C ₈ -86-1-1-1-8-⊗-1 | | | | | | | | |
| L4 | DMR HYD- 1284 | | | | | | | | |
| L5 | V-341 | | | | | | | | |
| L6 | L6 V-25 | | | | | | | | |
| L7 | DTPY C9 -F67-2-2-1-3-2-1-3-B-B-B | | | | | | | | |
| L8 | CML358 | | | | | | | | |
| L9 | CML-421-1 | | | | | | | | |
| L10 | PANT 12-13R- 100 | | | | | | | | |
| L11 | PANT 12-13R- 105 | | | | | | | | |
| L12 | Tr. 61/7117 🛇 118 | | | | | | | | |
| L13 | Tr. 61/7117 🛇 121 | | | | | | | | |
| L14 | Tr. 61/7117 🛇 122 | | | | | | | | |
| L15 | Tr. 203/1206 | | | | | | | | |
| L16 DMR 1126 | | | | | | | | | |
| L17 | DMR 409 | | | | | | | | |
| L18 | PANT 11K-62- OP-5 | | | | | | | | |
| L19 | PANT 12K/NAIP/II/61 ⊗ | | | | | | | | |
| L20 | PANT 12K/NAIP/II/67 ⊗ | | | | | | | | |
| | TESTERS /POLLINATORS | | | | | | | | |
| T1 | POP 31⊗ 18-2-1-1-4-2-2-1/1-⊗ -2⊗10A | | | | | | | | |
| T2 | PANT 12-13R- 101 | | | | | | | | |
| T3 | PANT 12K/NAIP/II/129 ⊗ | | | | | | | | |
| T4 | PANT 12K/NAIP/II/203 ⊗ | | | | | | | | |
| | CHECKS (HYBRIDS) | | | | | | | | |
| C1 | PSM-1 | | | | | | | | |

III. RESULTS AND DISCUSSION

The analysis of variance for different characters has been presented in Table 2 which indicated that there were highly significant differences among the treatments for all the characters. ANOVA partitioned the variance into parental variance, line variance, tester variance and line x tester variance. Parental variance, line variance, and line x tester variance revealed that there were significant differences in all the characters. Whereas, only tester variance has three non-significant characters, namely days to 50% anthesis, days to maturity and cob length. Similarly, lines vs testers and parent's vs crosses were significant for all the characters. The present observations are in agreement with the earlier reports of Chen *et al.* (2000), Srivastava (2001), Jaykumar and Sundaram, (2007), Premlatha and Kalamani (2010), Al Nagger *et.al* (2011), El-Hosary *et.al* (2013) and Ali *et.al.* (2014).

For Yield, GCA range was found from -7.53 to 10.04. The GCA effects were found to be significant for L14 (16.64), L4 (9.73) L15 (8.44), L7 (6.39), L11 (5.76) and L9 (5.76) (Figure-1). The range of GCA for tester were -3.45 to 5.31 and significant GCA effects were recorded for T₃ (2.07). The most promising crosses for higher yield per ha were L8 x T1 (27.63), L9 x T4 (23.44), L3 X T3 (23.41), L16 x T2 (23.03), L3 x T3 (22.81), L1 x T3 (22.51), L20 x T2 (19.48), L13 x T4 (19.47), L7 x T1 (18.22) and L17 x T4 (17.58) Figure-2. It is concluded in the majority of crosses that higher desirable SCA effects for grain yield were shown the involvement of parents with high GCA effects.

The nature and magnitude of gene action also suggested that the dominance variance major reason towards a hybrid performance for all characters. This mean non-additive action is important for the hybrid performance, which is evident in

the Table-3. The role of non additive gene action for kernel yield and other some traits have been reported earlier by Vijayabharathi *et al.*, (2009) and Kanagarasu *et.al* (2010).

TABLE 2

ANALYSIS OF VARIANCE FOR LINE X TESTER HAVING MEAN SQUARE VALUES

| ANALYSIS OF VARIANCE FOR LINE X TESTER HAVING MEAN SQUARE VALUES | | | | | | | | | | | | | |
|--|-----|-----------------|----------------|--------------|------------|------------|--------|------------|--------------|---------------|-------------------|------------------|---------|
| Source | df | Days to | Days to | Days to | Plant | Ear | Tassel | Cob | Ear | No of | No of | 100- | Yield/h |
| of variation | | 50% Anthesis | 50% silking | Maturit y | heigh t | heigh t | length | lengt h | diame ter | kernel row | kernel per row | Kernel weight | a |
| | | | | | | | | | | | | | |
| Кер | 1 | 91.50 | 34.02 | 12.3 | 12 | 9 | 11.55 | 3.3 | 0 | 1.08 | 0.55 | 120.41 | 22.42 |
| Par | 23 | 11.52** | 4.40** | 23.03** | 1297. | 373.4 | 39.91* | 6.06* | 0.07** | 3.33** | 47.28** | 49.50** | 408.97* |
| | | | | | 08** | 7** | * | * | | | | | * |
| Lines 19 | 19 | 12.31** | 4.76** | 26.45** | 1413. | 419.2 | 35.01* | 6.80* | 0.06** | 2.50** | 41.43** | 50.60** | 258.66* |
| | | | | | 20** | 0** | * | * | | | | | * |
| Tester | 3 | 3.17 | 3.00** | 0.17 | 948.2 | 206.4 | 80.32* | 0.96 | 0.05* | 7.33** | 62.75** | 58.52** | 871.98* |
| | | | | | 1** | 8** | * | | | | | | * |
| LxT | 57 | 22.19** | 23.23** | 28.14** | 1501. | 306.5 | 41.39* | 7.22* | 0.04** | 3.28** | 37.26** | 65.09** | 472.13* |
| | | | | | 68** | 9** | * | * | | | | | * |
| Crosses | 79 | 29.79** | 28.78** | 34.29** | 1548. | 452.0 | 51.65* | 8.25* | 0.03** | 3.61** | 41.43** | 63.06** | 515.64* |
| | | | | | 01** | 9** | * | * | | | | | * |
| Par vs | 1 | 25.90** | 25.51** | 143.72** | 38395 | 1593 | 1713.1 | 28.83 | 1.07** | 21.94** | 114.80** | 372.29** | 13755.9 |
| cross | | | | | .36** | 1.07* | 6** | ** | | | | | 4** |
| Error | 103 | 2.03 | 0.76 | 1.55 | 52.71 | 17.21 | 6.59 | 0.57 | 0.01 | 1.28 | 2.93 | 4.44 | 23.29 |

TABLE 3
VARIANCE COMPONENT AND GENE ACTION VARIANCE OF ALL TWELVE CHARACTERS.

| Line x Tester Variance | Genotype Variance | Additive Variance | Dominance Variance | Environmental Variance | |
|------------------------|--|--|---|--|--|
| 9.054233 | 0.0000 | 0.0000 | 36.2169 | 0.7809 | |
| 12.62825 | 0.6718 | 2.6873 | 50.5130 | 0.1505 | |
| 1.497979 | 0.1664 | 0.6657 | 5.9919 | 0.5047 | |
| 370.761 | 9.1549 | 36.6196 | 1483.0440 | 85.2826 | |
| 122.594 | 1.5855 | 6.3418 | 490.3758 | 52.4479 | |
| 1.235643 | 0.0000 | 0.0000 | 4.9426 | 1.0821 | |
| 2.722159 | 0.0000 | 0.0000 | 10.8886 | 0.8357 | |
| 0.137055 | 0.0016 | 0.0064 | 0.5482 | 0.0398 | |
| 1.235643 | 0.0000 | 0.0000 | 4.9426 | 1.0821 | |
| 15.62221 | 0.0000 | 0.0000 | 62.4888 | 3.1445 | |
| 15.36756 | 0.1936 | 0.7742 | 61.4702 | 0.8088 | |
| 27.70934 | 5.7651 | 23.0605 | 110.8374 | 28.8854 | |
| | 9.054233 12.62825 1.497979 370.761 122.594 1.235643 2.722159 0.137055 1.235643 15.62221 15.36756 | 9.054233 0.0000 12.62825 0.6718 1.497979 0.1664 370.761 9.1549 122.594 1.5855 1.235643 0.0000 0.137055 0.0016 1.235643 0.0000 15.62221 0.0000 15.36756 0.1936 | 9.054233 0.0000 0.0000 12.62825 0.6718 2.6873 1.497979 0.1664 0.6657 370.761 9.1549 36.6196 122.594 1.5855 6.3418 1.235643 0.0000 0.0000 2.722159 0.0000 0.0000 0.137055 0.0016 0.0064 1.235643 0.0000 0.0000 15.62221 0.0000 0.0000 15.36756 0.1936 0.7742 | 9.054233 0.0000 0.0000 36.2169 12.62825 0.6718 2.6873 50.5130 1.497979 0.1664 0.6657 5.9919 370.761 9.1549 36.6196 1483.0440 122.594 1.5855 6.3418 490.3758 1.235643 0.0000 0.0000 4.9426 2.722159 0.0000 0.0000 10.8886 0.137055 0.0016 0.0064 0.5482 1.235643 0.0000 0.0000 4.9426 15.62221 0.0000 0.0000 62.4888 15.36756 0.1936 0.7742 61.4702 | |

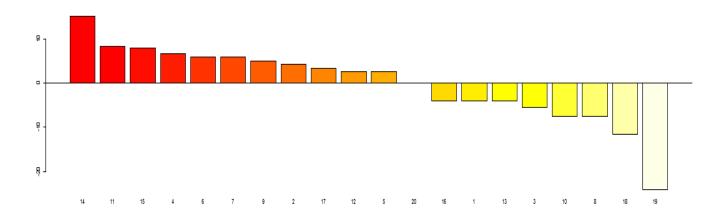


FIGURE-1 PICTORIAL REPRESENTATION OF GCA OF PARENTS

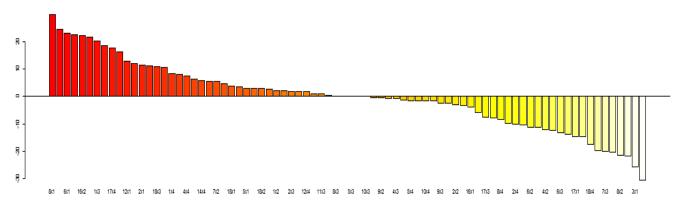


FIGURE-2. PICTORIAL REPRESENTATION OF SCA OF HYBRID

IV. CONCLUSION

In the current investigation SCA effects represent mainly dominance effect (additive × dominance, dominance × dominance effects). The crosses showing SCA effects involving parents with good GCA could be exploited. However, if a cross having high SCA has parents of which one is good combiner and another as poor or average combiners, such crosses are likely to throw some good segregants only if the additive genetic system is presently in a good general combiner and epistatic effects on the cross, act in the same direction so as to maximize the desirable expression of the characters in question (Lonnquist, 1961). Thus crosses namely, L8 x T1 (27.63), L9 x T4 (23.44), L3 X T3 (23.41), L16 x T2 (23.03) which have shown high SCA effects for grain yield, which high parental GCA effects can be exploited for the development of SCHs because of non-additive gene action for yield and yield component traits.

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