

**Genetic Studies of Medium Maturing Maize  
(*Zea mays* L.) Inbred Lines**

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(MSA-2019-1283)



**Division of Genetics & Plant Breeding**  
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Technology of Kashmir**  
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# Genetic Studies of Medium Maturing Maize (*Zea mays* L.) Inbred Lines

**Rahila Amin**  
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## Thesis

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*Dedicated To*  
***“My family”***

*“Parents” are teachers, guides, leaders, protectors and providers for their children. Parents are the ultimate role models for children. Every word, movement and action has an effect. No other person or outside force has a greater influence on a child than the parent.*

**“ To Serve Whom was my dream  
and Dream of serving them remain  
forever ”**

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**Certificate-I**

This is to certify that the thesis entitled “**Genetic Studies of Medium Maturing Maize (*Zea mays* L.) Inbred Lines**” submitted in partial fulfilment of the requirements for the award of the degree of **Master of Science in Agriculture(Genetics and Plant Breeding)**, to the **Faculty of Agriculture, Sher-e-Kashmir University of Agricultural Sciences and Technology of Kashmir** is a record of bonafide research work carried out by **Ms. Rahila Amin(Regd. No. MSA-2019-1283)** under my supervision and guidance. No part of the thesis has been submitted for any other degree or diploma.

It is further certified that information received during the course of investigation has duly been acknowledged.

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Inbred Lines”**

**ABSTRACT**

The present investigation entitled, **“Genetic Studies of Medium Maturing Maize (*Zea mays* L.) Inbred Lines”** was carried out to generate information on combining ability, gene action and heterosis. The experimental material comprised of 28 F<sub>1</sub>'s derived from crossing 8 maize inbred lines in a half diallel fashion. All the crosses along with parental lines and two checks (DHM-117 and PMH-10) were evaluated in a Randomized Complete Block Design (RCBD) with three replications at FoA, Wadura, SKUAST-K during *Kharif*, 2020. Data recorded for morphological, maturity, yield and yield attributing traits was subjected to analysis of variance (ANOVA) which revealed highly significant differences among the parents and their crosses indicating that there is significant diversity among the parents and the crosses. Analysis of variance for combining ability revealed significant mean squares for GCA and SCA for all traits and revealed that, both additive and non-additive gene actions were at play in the inheritance of all traits. Among the parents, BML-6 and UMI-1200 depicted

desirable significant negative GCA effects for maturity and LM-13 and UMI1200 showed positive significant GCA effect for grain yield plant<sup>-1</sup>. Estimates of SCA effects showed that among the crosses, CML-451 X BML-6 and LM-14 X UMI1200 showed desirable highly significant negative SCA effect for days to maturity while as CML-451 X LM-13 and BML-10 X V-405 showed desirable highly significant SCA effect for grain yield plant<sup>-1</sup>. Cross combinations, CML-451 X LM-13, BML-10 X V-405 and BML-10 X UMI1200 depicted more than 30 per cent and more than 20 per cent economic heterosis over standard checks, DHM-117 and PMH-10 respectively. These three potential hybrids with substantial heterosis need to be evaluated further, over locations and years to have a realistic of the performance of these experimental hybrids. Also parental lines with significant negative GCA effects for maturity traits and significant positive GCA effects for yield attributing traits can be utilized in future crossing programmes as potential parents for development of medium maturing and high yielding hybrids.

**Keywords:** GCA, Genetic studies, Heterosis, Inbred lines, Maize, SCA

Signature of Student

Signature of Major Advisor

Dated \_\_\_\_\_

Dated \_\_\_\_\_

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***Rahila Amin***

**Place:** FoA Wadura

**Dated:-**

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## Chapter- 1

### INTRODUCTION

Maize (*Zea mays* L.) belongs to the grass family Poaceae, genus *Zea* and species *Zea mays*. It originated in Mexico. Maize is one of the most important cereal grain crop grown worldwide in a wide range of environments because of its better adaptability. The crop plays a major role in the global economy and trade as food, feed and an industrial crop. Maize has a high rate of photosynthetic activity because of its C4 pathway resulting in its enhanced grain yield and biomass potential. It is cross-pollinated crop which contributed to its wide morphological variability and geographical adaptability. Globally, the production of maize is 1147.6 million tons (mt) cultivated on an area of 193.7 million hectares (mha) with productivity of 5.92 t ha<sup>-1</sup> (FAO, 2018).

In India, maize is the third important food crop after rice and wheat grown on an area of 9.2 million hectares (mt) with annual production of 30.24 million tons (mt) and productivity of 30.23 q ha<sup>-1</sup> (FAO, 2018). In Jammu and Kashmir, maize is grown on an area of 3.1 lac hectares with production of 498 thousand tons and average productivity of 17.82 q ha<sup>-1</sup> (Anonymous, 2018).

Maize demand will rise at global, national and regional level, in view of increasing demand in poultry and livestock. The need to meet such demands acts as the key contributor for interventions like maize hybrid technology and novel molecular tools and techniques in maize improvement which ultimately shall contribute to increasing productivity.

Hybrid maize breeding brought many fold increment in yield and production of maize all over the world by replacing traditional varieties, composites, synthetics and open pollinated varieties (OPVs) which are comparatively lower in yield. However, there is a gap in productivity at global and national level which can be attributed to the fact that only 40 per cent of maize area in India is under hybrids and rest 60 per cent is under low-yielding

composites and traditional varieties. The area under low yielding traditional land races is mainly in special ecologies where maize is grown by marginal farmers with small land holdings. Therefore, in order to shift maize productivity towards higher levels, more and more area need to be brought under hybrids and simultaneously, specific breeding programme need to be devised to develop hybrids for these special niche areas. Since the commencement of the All India Coordinated Maize Improvement Project (AICMIP) in 1957, maize improvement in India has gone through numerous phases and single cross hybrids have provided considerable rewards in terms of area, output and productivity in India as compared to others. The fundamental breeding strategy for exploitation of heterosis in maize has been to identify single crosses with high heterotic effects by analysing cross combinations of superior inbred lines with high vigour.

For a hybrid development programme, information on the combining ability and heterotic pattern of germplasm is a key and critical aspect. Maize has been widely investigated in terms of combining ability and heterosis breeding (Bharathiveeramani *et al.*,2018). Heterosis, perhaps the greatest practical achievement of the science of plant breeding, can be exploited by developing and identifying high performing vigorous parental lines and then assessing their potential in various cross combinations through specific breeding designs. Maize has been witness to the massive application of heterosis concept. U.S corn yields witnessed a remarkable vertical increase on account of utilization of heterosis in maize.

The magnitude of genetic variability in the base population and superior inbred growth are almost entirely responsible for hybrid development Combining ability play a crucial role in the improvement of crops to analyze the inbred lines for their propensity to create potential hybrids. Therefore, combining ability is an assessment of the value of genotypes based on of their offspring performance in some definite mating design. As a result, this information can be utilised to pick good combiners that can be employed in crosses to exploit heterosis or

accumulate fixable genes, as well as the interpretation of gene action. In order to attain this goal, breeders use different mating designs and notable among them is diallel crossing technique (Jink, 1954;Hayman, 1954) which gives information on the inheritance pattern of gene action in early filial generations to breeders for hybrid development and it is a approach for statistically differentiating progeny performance into components related to general combining ability (GCA) and specific combining ability (SCA). Diallel mating designs are also useful in collecting genetic information regarding the traits of interest in a short period of time through random and fixed selection sets of parental lines (Hayman, 1954; Griffing, 1956) and relative importance of additive and non-additive gene action.

In crop breeding, the concepts of GCA and SCA have a major impact on inbred line assessment and population development. Sprague and Tatum (1942) defined GCA as the average performance of a genotype in a series of hybrid combinations and defined SCA as those instances where the performance of a hybrid is relatively better or worst than would be expected on the basis of average performance of the parental inbred lines involved. Parents with a high average combining ability in crosses are considered to have good GCA, while if their potential to combine well is bounded to a particular cross, they are considered to have good SCA.

According to statistics, GCA is main effect, whereas SCA is an interaction effect. According to Sprague and Tatum (1942),GCA is promoted by the activity of genes that have predominantly additive effects as well as additive x additive inetractions.SCA is interpreted as an indication of loci with dominance variance (non-additive effects) and all the three types of epistatic interaction components if epistasis were present. They involve additive × dominance and dominance × dominance interactions.

The contribution of heterotic effects from superior inbred lines is crucial for the efficient and successful hybrid maize breeding programme. The superior cross combination could be commercialised as a single cross hybrid.

Keeping the above cited facts in view, the present study entitled, “**Genetic Studies of Medium Maturing Maize (*Zea mays* L.) Inbred lines**” was undertaken with the following objectives:

1. To estimate general and specific combining ability of maize (*Zea mays* L.) inbred lines and crosses, respectively.
2. To estimate gene action and heterosis for various traits of maize (*Zea mays* L.) inbred lines.

## Chapter- 2

### REVIEW OF LITERATURE

Because of the growing demand for maize (*Zea mays* L.), breeders have been concerned about boosting productivity. The success of hybrid maize breeding has resulted in a significant increase in maize production. Hybrid maize breeding began in 1909, primarily as a result of Dr. G.H. Shull's creative idea. Early in the 1990s, researchers began attempting to unravel the genetic basis of heterosis. In order to investigate the mechanism of heterosis, the dominance theory, over dominance hypothesis, and epistasis hypothesis were proposed.

At the International Maize and Wheat Improvement Center (CIMMYT) and national breeding programmes, inbred line development efforts have been bolstered and assessed for combining ability. Improved populations were developed by CIMMYT and were supplied for direct use in field as OPVs, or individual plants were self-pollinated to generate inbred lines utilised in hybrid development. In 1957, the All India Coordinated Maize Improvement Project (AICMIP) was established and efforts on developing and evaluating multi-parent hybrids began. A lot of work has been done on maize hybrids to explore heterosis and combining ability using diallel and other mating designs, and the findings have been interpreted and discussed.

Saleem *et al.* (2002) carried out a study for estimating gene action for various quantitative traits in a complete diallel set involving six maize inbred lines and established that number of days taken to tasseling, number of days taken to silking, number of kernel rowsear<sup>-1</sup>, number of kernels row<sup>-1</sup>, 100-grain weight and grain yield plant<sup>-1</sup> are regulated by over dominance type of gene action, whereas number of days to silking exhibited partial dominance and most of the characters showed over dominance type of gene action, thus concluding that this material can be exploited for heterotic effects.

Muraya *et al.* (2006) conducted a study for two growing seasons with diallel cross, excluding reciprocals, involving seven maize S<sub>1</sub> lines for studying heterosis and the results exhibited that general combining ability (GCA) and specific combining ability (SCA) were significant (P<0.05) for all traits indicating the existence of both additive and non-additive gene effects for the traits. However, for all traits except cob diameter and 100 seed weight, GCA: SCA ratio was >1, indicating preponderance of additive gene effects for inheritance of these traits. Heterosis estimates showed that heterosis was more important in grain yield, yield components, plant height, number of leaves plant<sup>-1</sup> and leaf area index than in other traits studied. They suggested that, based on their combining ability, the lines were combined to generate synthetic maize varieties which could be marketed both as a variety or employed for further improvement using recurrent selection.

Similarly, Gissa *et al.*(2007) conducted a study on adapted maize inbred lines for yield and yield components and it was noticed that majority of crosses with desirable heterosis were combinations of CIMMYT and Ethiopian inbred lines. For ear and plant height, ear length, kernels row<sup>-1</sup> and grain yield, all crosses exhibited positive mid parental heterosis (MPH). Gutto LMS5, CML-202 and CML-387 were good general combiners for ear and plant height and days to maturity.They proposed that inbred lines and hybrid combinations that had desirable expression of relevant traits could be useful for breeders in generating high yielding maize varieties with good agronomic performance.

Kumar and Bharathi (2009) studied five lines and three testers to assess combining ability in line x tester (LxT) and the resultant fifteen hybrids were evaluated for nine characters. It was revealed that there is inconsistent relationship between GCA and SCA effects. The results exhibited that the hybrids best for exploitation of heterosis were L<sub>1</sub>/T<sub>3</sub> and L<sub>4</sub>/T<sub>2</sub>. The superior specific hybrids were derived from parents including all kins of combinations, high x high, high x low and low x low in terms of GCA and SCA.

Sher *et al.* (2012) conducted a study on four white grain maize inbred lines from flint corn group in order to estimate inheritance pattern and determine various genetic effects for maturity and flowering attributes. Two lines were late maturing and two were early maturing. These divergent inbred lines were crossed to form four crosses, six generations ( $P_1, P_2, F_1, F_2, BC_1, BC_2$ ) for each individual cross and finally it was concluded that both dominance gene action and epistatic interactions played major role in governing inheritance of days to pollen shedding, 50 per cent tasseling, anthesis silking interval (ASI) and maturity. Except for days to 50 per cent husk browning (maturity), investigation of six generations demonstrated preponderance of non-additive gene action for expression of most of traits studied. Preponderance of dominance gene action for the traits highlighted their usefulness in subtropical maize hybrid programme.

Estakhr and Heidari (2012) studied 14 maize inbred lines and 91 related crosses which were evaluated over two years in temperate zone of Iran and results revealed that lines with negative GCA effects for growing degree day to milky and maturity and positive GCA for grain yield can be taken into account for producing early mature and high grain yielding maize plants, while cross combinations with positive and negative SCA for growing degree day to physiological maturity and grain yield can be taken into account as short-season hybrids for use in breeding plans for earliness. The SCA estimates can predict hybrid performance better than the mid parent and the heterosis. Selections based on SCA values boost the efficiency of hybrid improvement in breeding programmes.

Crosses involving parents/inbred lines from most divergent clusters manifested maximum heterosis and created wide variability in genetic architecture. This conclusion was confirmed from a study on thirty yellow inbred lines which were divided into six different clusters evaluated for thirteen parameters at the experimental field for the purpose of studying the genetic divergence using multivariate analysis. Days to maturity and ear diameter

exhibited maximum contribution towards total divergence among different traits (Azad *et al.*, 2012).

In order to assess genetic and epistatic effects influencing the inheritance of grain yield and yield components, parental material comprising of six genetically different maize inbred lines were crossed to produce F<sub>1</sub>, F<sub>2</sub> and backcross generation. The generation mean analysis exhibited the preponderance of non-additive effects for all the traits under study and opposite sign of dominance and dominance x dominance suggested the existence of duplicate epistasis and the major role of dominance variance along with duplicate epistasis in the inheritance of traits, favouring the use of research material for the production of single cross hybrids (Haq *et al.*, 2013).

Gowda *et al.* (2013) crossed 34 lines with five testers and evaluated hybrids along with parents to estimate GCA effects of parents and SCA effects of crosses for yield and yield attributing traits. The inbred lines identified as good general combiners were MAI 708, MAI 109, MAI 111, MAI 121, Cymt 3 and Cymt 30. The crosses viz., MAI 109 X MAI 105, MAI 109 X CM 202, Cmyt 3 X SKV 50 and Cmyt 3 x CM 202 exhibited highest significant SCA effects among all hybrids.

Tajwar and Chakraborty (2013) crossed twelve inbred lines with five testers in LXT design to assess combining ability for yield contributing traits. The best general combiner for grain yield was determined as L9 among the parental lines and T2 among the testers. Among the hybrids, (L6 X T5) was identified as a potential cross combination for grain yield.

Avinashe *et al.* (2013) conducted an experiment involving 45 F<sub>1</sub>, their 18 parents and three standard checks( HQPM-1, HM-5 and Gujarat Makai-2), in a randomized block design with 3 replications. The hybrids 1-07-10-1 x HKI-163, 1-07-8-6 X CLQ-30 were recognised as superior hybrids as these had high

percentage of relative heterosis, heterobeltois and standard heterosis for grain yield plant<sup>-1</sup> along with other traits.

Singh *et al.* (2013) estimated heterosis for yield and yield attributing components in maize involving 45 crosses including 15 lines, 3 testers along with 3 checks and sown in randomized block design with 3 replications. The phenomenon of heterosis was of general occurrence for majority of traits under study. Over both mid parent and better parent, crosses L9 x T1 and L9 x T2 elucidated desirable and significant heterosis. Future breeding programmes can use the superior lines and crosses to develop synthetics/hybrid varieties.

Azad *et al.* (2014) carried out a study with six diverse maize inbred lines by using a half diallel mating design and it was reported that there is substantial general combining ability variances for cob height and specific combining ability variance for plant height, cob height, cob length, cob girth, number of kernels cob<sup>-1</sup>, cob weight and hundred grain weight. Heterosis over mid parent (MP), better parent (BP) and check variety (CV) was estimated for 15 F<sub>1</sub> hybrids, indicated that heterosis over MP and BP can be used for experimental issues but heterosis over CV is regarded either as a hybrid variety that would be accepted or rejected for commercial cultivation by the farmer. As evaluated through combining ability and standard heterosis, F<sub>1</sub> hybrid ML02×ML29 was the best combination. For all studied traits except shelling percentage, heterosis over MP showed positive significant heterosis values for all crosses and heterosis over BP exhibited significant heterosis values in all studied traits except shelling percentage and hundred grain weights in most cases. Three F<sub>1</sub> hybrids, *viz.*, ML02 X ML15, ML02 X ML29 and ML05 X ML15 have proved to be the outstanding hybrids for immediate commercial cultivation.

Sarac and Nedelea (2014) conducted the study on six inbred lines and 15 F<sub>1</sub> hybrids derived from a 6x6 half diallel mating. The aim of this research was to identify the combiners and their crosses based on their general and specific combining ability for grains number and weight ear<sup>-1</sup>. The lines TC208 and K1080

have additive effects that enhance both the number of grains/ear and their weight, whereas TC209 line has positive additive effects for grain and negative for grains yield /ear.

Nartam *et al.* (2015) conducted a study where they evaluated 32 F<sub>1</sub> crosses along with four females and eight males in line x tester fashion for studying the general and specific combining ability effects of parents and crosses respectively. For all the characters, high significant SCA effect in the desirable direction were reported. High significant variation observed by GCA and SCA effects. For yield and yield contributing characters, the parents NM-32-1-1, NM-62-4-1 and NM-60-4 were identified as good general combiner. Among the crosses, NM-32-1-1 X NM-62-4-1 and NM-32-1-1 X NM-60-4 were recognised as best crosses based on their higher per se performance and high significant SCA effects in the desirable direction.

Rajesh *et al.* (2015) identified the top five superior single cross combinations, BM5050 x BML10, BM 3511 x BML7, BM 1234 x BML10, BM 1234 x BML13 and BM5050 x BML7 from a study on heterosis and combining ability of 45 hybrids along with three testers. For grain yield plant<sup>-1</sup>, the lines BM 5050, BM 1234, BM 3511, BM 3521 and testers BML 10 and BML 7 were found to be good general combiners. Also, the superior crosses may be commercially exploited after critical assessment of its superiority in stability performance across the locations over years. Similarly, a study was carried out in a 7×7 half diallel cross in maize and the parents, P<sub>1</sub> (for early flowering and short duration), P<sub>4</sub> (for yield, early flowering, short plant and ear height), P<sub>5</sub> (short duration) and P<sub>6</sub> (for yield), were found as donors for combining high yield with desired traits. Also crosses, P<sub>2</sub>×P<sub>3</sub>, P<sub>4</sub>×P<sub>6</sub> and P<sub>6</sub>×P<sub>7</sub>, exhibited the highest heterosis for yield trait as compared to the checks NK40 and 900MG. The cross combinations revealed significant high SCA effects associated with per se performance and hence could be more profitable in a hybrid breeding program after intensive evaluation at multiple agro ecological zones (Talukder *et al.*, 2016).

Ahmad (2015) studied the heterotic relationship between 13 morphological traits in 10 inbreds of maize and their diallel crossing was done. For seed yield plant<sup>-1</sup>, the most favourable cross pair was between NAI-133 X NAI-123 and also exhibited desirable heterosis for cob length, kernal row<sup>-1</sup>, cob diameter and 100-grain weight over the standard check. The W3 x W5 (ear height), NAI-143 x NAI-147 (cob plant<sup>-1</sup>), W3 x NAI-142 (kernal rows cob<sup>-1</sup>), NAI-137 x NAI-143 (kernal row<sup>-1</sup>), NAI-152 x NAI-137 (cob diameter), W5 x NAI-116 (100 grain weight) and NAI-143 x NAI-116 (protein content) demonstrated high heterosis over checks.

Reddy *et al.* (2015) evaluated 45 hybrids for 11 characters to estimate standard heterosis and heterobeltosis. For days to 50 per cent tasseling, days to 50 per cent silking and days to maturity, three hybrids, BML-2782 X BML-5233-5, CM-211 X BML-5233-5 and BML-2486 X BML-2 showed negative standard heterosis. For grain yield, five crosses, *viz.*, BML-15 X BML-2910, BML-7 X BML-3044, CM-211 X BML-7, BML-6 X BML-2 and BML-2782 X BML-6 showed heterobeltosis.

Shah *et al.* (2015) evaluated 6 inbred lines along with 30 F<sub>1</sub> hybrids developed by diallel fashion and reported highly significant variation among genotypes for grain yield and its component traits. Except kernels ear<sup>-1</sup> and grain yield, mean square values due to general combining ability were highly significant for all characters. For all traits, highly significant variations for specific combining ability of direct and reciprocal effects were found. For grain yield, Islamabad White x Sadaf was the best combiner. For reciprocal cross effects, BS-1 x Sahiwa 12002 proved good combiner for kernal row<sup>-1</sup> and kernal ear<sup>-1</sup> while BS-1 x Islamabad White for grain yield.

El Shamarka *et al.* (2015) conducted study on eight inbred lines, 28 crosses along with check and reported highly significant mean square due to GCA and SCA for all traits. The parents P1, P6 and P7 showed positive significant GCA effects for grain yield and parent P5 and P7 for earliness. Crosses, P2 X P4 and P3

X P6 were found to be the best cross combinations for earliness whereas, crosses P1 X P6, P2 X P4, P3 X P6 and P7 X P8 exhibited the best SCA effects for grain yield.

Zelleke (2015) evaluated the heterosis for grain yield and yield component traits in maize in 8 x 8 diallel cross. The cross, L1 X L4 (29.3%) showed the highest percentage of heterosis for grain over standard heterosis followed by crosses L1 X L5( 28.3%), L3 X L5 (21.7%), L1 X L7 (20.8%). For days to maturity, mid parent heterosis ranged from -2.5 to -23.9%, whereas that of better parent heterosis ranged from 0 to -13% implying that the hybrid tend to mature earlier than the parents.

Hoque *et al.* (2016) evaluated 6 parents along with 30 crosses to study combining ability for grain yield, maturity and growth parameters in maize. For all characters, high significant GCA and SCA effects were observed except SCA in days to tasseling and days to maturity. Except cob length, 100 grain weight and ear height, variances due to GCA were higher in magnitude than SCA, indicating additive gene effects for all traits. Parent P5 was identified as the best general combiner for yield and the parents P1 and P2 were identified as the best combiner for dwarf and earliness.

Suthamathi (2016) studied 91 cross combinations along with 14 selected inbred lines to evaluate the combining ability and reported the predominance of non additive gene action for yield contributing traits. For grain yield plant<sup>-1</sup>, kernal rows cob<sup>-1</sup>, number of kernals row<sup>-1</sup> and 100 grain weight, the cross combinations P4 X P6 and P4 X P5 exhibited desirable per se performance and SCA effects. The parents P1, P2, P3 and P4 were identified as good general combiners.

Aliu *et al.* (2016) crossed ten inbred lines in a full diallel fashion and evaluated parents along with their hybrids to assess combining ability for yield and yield attributing traits. Except for number of kernal rows per cob<sup>-1</sup>, high

magnitude of SCA than GCA was observed in all crosses for all traits. Parents, L2, L5, L6, L7 and L9 showed significant positive GCA effect for grain yield whereas 35 crosses exhibited significant positive SCA effects for grain yield.

Patel and Kathiria (2016) conducted a study on 10 inbred lines of maize along with hybrids under four environments and observed that mean square due to SCA was higher than the GCA, implying predominance of non additive gene action for all traits. Analysis of variance exhibited high significant difference among genotypes for all traits for all the environments.

Al-Naggar *et al.* (2016) estimated mean efficiency, heterosis and combining ability and interactions in six maize inbreds and their 15 diallel  $F_1$  crosses under elevated plant densities. Three experiments were conducted using RCBD with three replicates in each of the seasons of 2013 and 2014 and each experiment was allocated to either low density, medium density, or high density. In high plant density, it was reported that SCA was greater than GCA mean squares for grain yield  $\text{plant}^{-1}$ , grain yield  $\text{hectare}^{-1}$ , protein yield  $\text{hectare}^{-1}$ , oil yield  $\text{hectare}^{-1}$  and starch yield  $\text{hectare}^{-1}$ , indicating that non-additive variance controls a major proportion of the inheritance of the above traits than additive variance, but for grain protein, grain oil, and grain starch, the case was opposite. According to the results derived from correlation analysis, it was revealed that for the majority of yield traits tested under three plant densities, the mean performance of a particular parent could be regarded as an indicator of its GCA whereas, the mean performance of a cross could be considered as an indicator of its SCA.

Yerva *et al.* (2016) performed experiments on the heterosis and combining ability (CA) using 6 x 6 full diallel design. The CA estimation showed existence of higher SCA than GCA for all characters under review. The additive dominance variance ratio was lower than unity for all characteristics, indicating a higher non-additive variance than a additive variance and revealed significant GCA effects in a favourable direction for days to 50 per cent tasselling. The inbred

liner UMI 213 was identified as the best parent for grain yield among the 6 parents. Moreover, results of SCA effects aided in the identification of best hybrids as UMI 66 x UMI 112, UMI 112 X UMI 213 and UMI 122 X UMI 133 since these hybrids exhibited significant and beneficial SCA effects for the majority of the traits included grain yield plant<sup>-1</sup>.

Following Griffing's Method 1, a study in a complete diallel fashion was conducted for development of single cross maize hybrids and it was found that the SCA variance components were significantly greater than GCA effects for ear diameter, ear length, grain rows ear<sup>-1</sup> and grains ear<sup>-1</sup>. For seedling emergence and 100-grain weight, GCA variance were higher than variance due to SCA effects. Results exhibited that inheritance of ear diameter, grain rows ear<sup>-1</sup> and grains ear<sup>-1</sup> was controlled by non-additive gene action and it was reported that non-additive (dominance and over-dominance) and epistatic genetic effects were responsible for development of hybrids outperforming their parents in terms of performance and vigour. Cross combinations with the desired SCA value can be used for future breeding programmes and other with high GCA values can be employed for production of synthetic varieties (Aslam *et al.*, 2017).

Kumar *et al.* (2017) evaluated 45 hybrids, 10 parents along with 4 checks to determine GCA and SCA effects of parents and crosses respectively for yield and yield attributing traits. For grain yield plant<sup>-1</sup>, positive significant SCA effects were observed in 20 and 17 hybrids in E1 and E2 environments respectively. The good general combiners for grain yield plant<sup>-1</sup> were E1Q-112, E1Q-109 and E1Q-106 in E1 environment while, E1Q-109 and E1Q-112 in E2 environment.

Matin *et al.* (2017) crossed seven inbred lines in diallel fashion in maize to estimate GCA and SCA of parents and crosses respectively. Some of the characters exhibited significant general and specific combining ability variances. The parent WL3 was significant as general combiner for yield, WL2 and WL3 for earliness and WL1 for short height, according to the overall analysis of GCA

effects. These parents could be employed in future breeding programme to boost maize yield including desirable traits.

Sharma *et al.* (2017) evaluated 63 hybrids obtained by crossing 9 inbred lines and 7 QPM inbred in LxT design and reported that hybrid HKI-1128 x HKI-163 showed a strong heterotic effect for seed yield and also for other characteristics, i.e, plant height, number of cobs plant<sup>-1</sup>, ear height, number of grain cob<sup>-1</sup> across check 2 (HM5) and 100-grain weight over check weight (HQPM-1) so although HKI-659-3 x HKI-194-6 exhibited high level of heterosis and for the number of grain cob<sup>-1</sup>,100-grain weight and grain yield plant<sup>-1</sup>suggesting that such research varieties can be employed for hybrids for high grain yield and early maturity.

Dar *et al.* (2017) evaluated the GCA of parents and SCA of their crosses for yield and its related trait among 8 inbred lines, 3 testers and their 24 hybrids. For grain yield plant<sup>-1</sup>,the parent KDM-445A was identified as finest combinerfollowed by CM-502 and KDM-347. Futhermore, kDM-445A was also accompanied with significant and desirable GCA for 100 grain weight, shelling percentage, protein content, number of kernals row<sup>-1</sup>, days to 50 per cent tasseling.KDM-347 X SMC-7, KDM-445A X DMR-N6 and V-351 X DMR-N6 revealed highly significant and deirable SCA effects for grain yield plant<sup>-1</sup>among the crosses.

Karad *et al.*(2018) evaluated 30 crosses developed by diallel mating design along with 6 parents and 2 checks to estimate combining ability for yield and its components. High significant variability exhibited among genotypes for all characters. The parents, NAUM-21, NAUM-8 and DC-7 were identified as best general combiner for yield.

Dar *et al.* (2018) used LxT design to evaluate the combining ability of yield-related traits in popcorn. With the help of RCBD, eight inbred lines, three testers and twenty-four subsequent crosses were examined for all traits. Anovafor

combining ability exhibited significant mean squares for GCA and SCA. For traits, viz., plant height, grain width, kernel rows per cob, shelling rate, 100-grain weight, protein content, grain yield plant<sup>-1</sup>, dominance component variance estimates were higher than additive component. The parent KDPI-8 has been demonstrated as the best combiner for grain yield plant<sup>-1</sup> and followed by KDPI-4 and KDPI-6 for majority of its contributing traits. KDPI-6 × WIN POP, KDPI-8 × VL POPCORN-1 and KDPI-1 × VL POPCORN-1 exhibited significant and desirable SCA effects for grain yield plant<sup>-1</sup>, among the crosses.

Gami *et al.* (2018) evaluated 30 single cross hybrids, 6 lines and 5 testers for yield and its attributing traits. The results revealed that non-additive gene action found to be predominant for inheritance of flowering character as kernal yields, cob yield, cob girth and cob length. The parents, BLD-250, BLD-221, BLD-210 and BLD-107 were reported as best combiners for yield and its contributing traits. Good GCA was reported by the hybrid combinations, viz., Z-488-4 X VL-1032 and BLD-250 X BLD-46. Whereas, the cross combination, WNC-18242 X VL-1032 exhibited desirable SCA for flowering and maturity traits. Cross combination reported as superior for kernal yield and related traits involves both parents with either good or average general combiner.

Khan *et al.* (2018) while conducting a study on 45 hybrids of maize along with 18 parents and 3 checks, identified five hybrids L<sub>7</sub> × T<sub>3</sub>, L<sub>4</sub> × T<sub>3</sub>, L<sub>15</sub> × T<sub>2</sub>, L<sub>2</sub> × T<sub>1</sub> and L<sub>12</sub> × T<sub>1</sub> which depicted positive significant economic heterosis for grain yield<sup>-1</sup> over the best check HM-9 and stated that merging of population improvement with inbred line development could result in new superior lines for single cross hybrid breeding as well as other options for hybrid development. The superior hybrids for different traits as grain yield, oil content and protein content can be further used in breeding programmes for improving essential quantitative and qualitative traits.

Patel *et al.* (2019) studied estimates of gca effects among parents and revealed that BLD-11(5.19), CML-338(4.28), VL-1032 (1.68), VL-109178(1.25)

were good general combiners as they expressed significant and positive GCA effects. The assessment of SCA effects exhibited 23 hybrids with significant positive SCA effects. The magnitude in SCA effects ranged from 2.70 (CBE-98 X CML-338) to 27.57 (CBE-98 X MRCN-3) and on the basis of specific combining ability effects, the top most three hybrids for kernal yield plant<sup>-1</sup> were CBE-98 X MRCN-3 (27.57), CBE-98 X BLD-11 (23.16) and CBE-26 X BLD-11 (21.20).

Darshan and Marker (2019) revealed significant differences among the parents and experimental hybrids for all characters except anthesis silking interval for analysis of variance. Estimates of SCA variances were higher than GCA variances for majority of traits under study, as per combining ability analysis, exhibiting predominance of non-additive gene action for these traits. For yield and its related traits, the parents LM-13 and DMR-N21 were identified as best combiners. On the basis of SCA effect for grain yield plant<sup>-1</sup> and its component, the best experimental hybrid was LM-13 X IC-32809 followed by DMR-N21 X IC-32809 and LM-13 X IC-31899.

Raihan *et al.* (2019) experimented with combining ability with 21 crosses developed from 7 x 7 diallel cross with no reciprocals for yield and yield attributing traits. Analysis of variance for combining ability exhibited that mean square due to GCA and SCA were highly significant for all traits excluding GCA for 1000- seed weight, ear length and plant height and also the SCA in case of maturity and row cob<sup>-1</sup> implying that all but mentioned traits were controlled by both additive and non-additive gene action .

Chandel *et al.* (2019) revealed that except for days to 50 per cent silking due to genotypes, kernal rows, days to 50 per cent tasselling and days to 50 per cent silking due to parents, the mean square due to genotypes, parents and parents v/s crosses were significant for all the traits. For all the studied traits, the ratio of GCA variance to SCA variance suggested the preponderance of non-additive gene affects in the inheritance of these traits. L<sub>9</sub> showed significant GCA effects for grain yield plant<sup>-1</sup> and yield component traits, among female inbred lines, whereas

among male parents T<sub>2</sub> was the best general combiner for yield contributing traits. Three hybrids, viz., L<sub>9</sub> X T<sub>2</sub>, L<sub>5</sub> X T<sub>1</sub> and L<sub>1</sub> X T<sub>1</sub> were determined as the most promising based on mean grain yield and SCA effects and may be further evaluated at multi environments for use as single cross hybrids.

Yu *et al.* (2020) conducted a study on diverse maize germplasm resources by using 28 temperate and 23 tropical maize inbred lines to estimate combining ability and heterosis. A large-scale multiple-hybrid population (MHP) with 725 hybrids were formed and splitted into three subsets, 325 temperate diallel hybrids and 136 tropical diallel hybrids generated in Griffing IV, and 263 temperate by tropical hybrids obtained in NCD II and results revealed that several widely used inbreds exhibited strong GCA and their derived hybrids showed strong SCA. For all the tested traits except plant height and hundred grain weight, NCDII (temperate×tropical) hybrids exhibited higher average heterosis than the temperate and tropical diallel hybrids with higher hybrid performance for ear length, ear diameter and hundred grain weight. The study concluded that tropical maize germplasm can be used to boost the yield potential for temperate lines and heterosis being more significantly and positively correlated with SCA than GCA, implying that SCA can be used to forecast heterosis to produce potential hybrids in commercial maize breeding.

Esan *et al.* (2021) studied two parental maize varieties and two hybrids in order to assess hybrid efficiency in comparison to its white and yellow parents and to determine genetic variability and heterosis between hybrids and parental lines. It was revealed that the two hybrids formed by crossing between yellow and white as well as between white and yellow showed higher performance than the parents. Hybrid1 recorded the highest number of rows cob<sup>-1</sup> (12.38), while the lowest number was recorded in white variety. In comparison with their parents, hybrid1 (75 cm) had the widest cob followed by hybrid2 (70.63 cm). The grain yield for mid parent heterosis (MPH) ranged from 14.73 to 44.54 per cent whereas for better parent heterosis (BPH), grain yield ranged from 14.1 to 43.95 per cent.

Makore *et al.* (2021) studied ninety-five maize hybrids derived from elite and new inbred lines crossed using a half diallel mating design in a variety of environments, with the goal of estimating genetic variances, heritability of traits, and genetic advance, as well as determining correlations between grain yield and its component characters in maize hybrids. For all the traits, estimates of phenotypic coefficient of variation were marginally larger than genotypic coefficient of variation, suggesting low influence of environment in the expression of these traits. High heritability and genetic estimates were recorded for grain yield (79%; 30.27%), plant height (85%; 102.42%) and ear height (86%; 117.15%) whilst high heritability and low genetic advance were for anthesis date (87%;5.8%), texture (75%; 8%) and ear position (71%; 0.23%). Path analysis showed that plant height, ears plant<sup>-1</sup> and ear position had direct and positive influence on grain, while anthesis date, ear height, ear position, grain moisture content at harvest and texture had indirect effects on grain yield.

## Chapter -3

### MATERIAL AND METHODS

The current investigation on “**Genetic Studies of Medium Maturing Maize (*Zea mays* L.) Inbred Lines**” was conducted at Faculty of Agriculture, SKUAST-K, Wadura, Sopore, during *Kharif*, 2020. The material used in the current research and the procedure followed are detailed as below:

#### 3.1 Experimental Material and Methodology

##### 3.1.1 Crossing programme

The experimental material consists of eight inter-institutional maize inbred lines which were crossed in all possible combinations, excluded reciprocals, in diallel mating fashion (half diallel fashion) suggested by Griffing (1956) to produce 28 cross combinations at Winter Nursery Centre, Rajendranagar, Hyderabad, during *Rabi*, 2019-2020.

##### 3.1.2 Evaluation programme

8 parents and 28 hybrids along with 2 checks were sown in randomized complete block design with 3 replications for evaluation programme at Faculty of Agriculture, SKUAST-K, during *Kharif*, 2020. The material was sown in single rows as plots of 4m length. Plant to plant spacing was maintained at 20cm and row to row distance at 75cm.

##### 3.1.3 Details of Experimental Material

##### 3.1.4 Parental Material used for crossing

S.NO	PARENTS (INBREDS)	SOURCE
1	CML-451	CIMMYT, Hyderabad
2	LM-13	PAU, Ludhiana
3	LM-14	PAU, Ludhiana
4	BML-6	PJTSAU, Hyderabad
5	BML-10	PJTSAU, Hyderabad
6	UMI1200	TNAU, Coimbatore
7	V-405	VPKAS, Almora
8	IML-187	IIMR, Ludhiana



**Plate 1: Evaluation of single cross maize hybrids at FoA,Wadura**

### 3.1.5 Cross Combinations for evaluation

S.No.	CROSS COMBINATIONS
1	CML-451 X LM-13
2	CML-451 X LM-14
3	CML-451 X BML-6
4	CML-451 X BML-10
5	CML-451 X UMI1200
6	CML-451 X V-405
7	CML-451 X IML-187
8	LM-13 X LM-14
9	LM-13 X BML-6
10	LM-13 X BML-10
11	LM-13 X UMI1200
12	LM-13 X V-405
13	LM-13 X IML-187
14	LM-14 X BML-6
15	LM-14 X BML-10
16	LM-14 X UMI1200
17	LM-14 X V-405
18	LM-14 X IML-187
19	BML-6 X BML-10
20	BML-6 X UMI1200
21	BML-6 X V-405
22	BML-6 X IML-187
23	BML-10 X UMI1200
24	BML-10 X V-405
25	BML-10 X IML-187
26	UMI1200 X V-405
27	UMI1200 X IML-187
28	V-405 X IML-187

### 3.1.6 Checks for evaluation of heterosis

S. No	Name of the check	Source
1	Punjab Maize Hybrid-10 (PMH-10)	PAU, Ludhiana
2	Deccan Hybrid Maize-117 (DHM-117)	PJTSAU, Hyderabad

### **3.2 Observations recorded**

The data was recorded on 12 morphological, maturity, yield and yield attributing traits detailed as below:

#### **50 per cent tasseling (days)**

The number of days taken from the date of sowing to the day on which 50 percent of plants in a plot showed full tassel emergence.

#### **50 per cent silking (days)**

The number of days taken from the date of sowing to the day on which 50 percent of the plants in a plot showed complete silk emergence.

#### **Anthesis silking interval (days)**

Anthesis silking interval recorded as difference in days between male flowering when 50 per cent of the plants of the plot had tassels realizing pollen, and female flowering, when 50 per cent of the plants of the plot have visible style-stigma in the ears.

#### **Maturity (days)**

It was recorded as the number of days taken from sowing to the day on which more than 50 per cent of plants in each genotype had displayed 75 per cent of husk browning.

#### **Plant height (cm)**

It was measured as length of plant stalk from the ground level to the base of the tassel of fully matured plant and expressed in centimeters.

#### **Ear height (cm)**

Height of the ear was measurement from the base of the plant to the node bearing the uppermost ear at dry silk stage and expressed in centimeters.

**Cob length (cm)**

Cob length was measured from base to the tip of the cob and recorded in centimetres.

**Cob diameter (cm)**

Cob girth was measured at the middle of the ear and recorded in centimetres.

**Number of cobs plant<sup>-1</sup>**

The number of cobs was counted on five plants and averaged to obtain the number cobs plant<sup>-1</sup>.

**Kernel rows cob<sup>-1</sup>**

The total number of kernel rows cob<sup>-1</sup> of five plants was counted and averaged as a number of kernel rows cob<sup>-1</sup>.

**Number of kernels row<sup>-1</sup>**

The total number of kernels in each kernel row was counted for five cobs and the average was recorded as a number of kernels row<sup>-1</sup>.

**Grain yield plant<sup>-1</sup>(g)**

Grain yield plant<sup>-1</sup> expressed in gram was recorded by weighing the grains obtained after shelling of cobs of five plants individually and then average was calculated.

The observations were recorded on 5 randomly selected plants except for days to silking, tasseling, ASI and maturity which would be recorded on plot basis.

**3.3 Statistical analysis**

The data collected during the present research work was subjected to statistical and biometrical analyses as per following headings:

- i Analysis of variance

- ii Estimation of general and specific combining ability
- iii Estimation of heterosis

### 3.3.1 Analysis of Variance

Analysis of variance was carried out according to standard statistical procedure for randomized complete block design (RCBD) to test the differences among the genotypes for all traits.

$$Y_{ij} = \mu + t_i + r_j + e_{ij}$$

Where,

$Y_{ij}$  = Performance of  $i$ th genotype in  $j$ th block

$\mu$  = General mean

$t_i$  =  $i$ th genotype effect

$r_j$  =  $j$ th block effect

$e_{ij}$  = Random error

**Table 3.1. ANOVA Table for RCBD**

Source of variation	Degrees of freedom	Mean sum of squares	Expected mean sum of squares	“F” calculated value
Replications	$r-1$	$M_r$	$\sigma^2_e + t\sigma^2_r$	$M_r/M_e$
Treatments	$t-1$	$M_t$	$\sigma^2_e + r\sigma^2_g$	$M_t/M_e$
Error	$(r-1)(t-1)$	$M_e$	$\sigma^2_e$	
Total	$(rt-1)$			

Where,

$r$  = Number of replications

$t = g$  = Number of genotypes

$M_r$  = Mean sum of squares of replication

$\sigma^2_e$  = Environmental variance

$\sigma^2_r$  = Variance due to replications

$\sigma^2_g$  = Variance due to genotypes

### 3.3.2 Test of Significance

Test of significance for various mean squares were carried out by “F” test.

### 3.3.3 Critical Differences (C.D) of the estimates

To test the significance of differences of the estimates, critical difference was calculated as:

$C.D = S.E(d) \times t$  value at error degree of freedom at 0.05 and 0.01 levels of probability

Where,

$S.E(d) = \text{standard error of difference of mean} = [2M_e/r]^{0.5}$

### 3.3.4 Combining ability analysis

The estimates of variance for GCA and SCA and their effects were computed according to model-1 (fixed effect model) and method II (Parents and crosses, excluding reciprocals) as given by Griffing (1956).

The analysis of variance for combining ability was based on the following model:

$$Y_{ijk} = \mu + g_i + g_j + s_{ij} + (1/b) e_{ijk}$$

Where,

$Y_{ijk}$  = Mean value of hybrid involving  $i^{\text{th}}$  and  $j^{\text{th}}$  parents in  $k^{\text{th}}$  block,

$\mu$  = population mean

$g_i$  = GCA effect of  $i^{\text{th}}$  parent

$g_j$  = GCA effect of  $j^{\text{th}}$  parent,

$S_{ij}$  = SCA effect for the cross between  $i^{\text{th}}$  and  $j^{\text{th}}$  parents,

$b_k$  = effect of  $k^{\text{th}}$  block

$e_{ijk}$  = error associated with the observation

**Table 3.2. ANOVA Table for combining ability**

Source of variation	d.f	Sum of squares	Mean sum of squares	Expected mean square
GCA	P - 1	Sg	Mg	$\sigma_g^2 + p + 2 \left( \frac{1}{p-1} \right) \sum g_i^2$
SCA	P(P-1)/2	Ss	Ms	$\sigma_s^2 + \frac{2}{p(p-1)} \sum \sum s_{ij}^2$
Error	(r-1) (t-1)	Se	M'e	$\sigma_e^2$

Where,

$$Sg \text{ (SS due to gca)} = \frac{1}{(p+2)} \left[ \sum_i (X_{i.} + X_{.i}) - \frac{4}{p} X^2_{..} \right]$$

$$Ss \text{ (SS due to sca)} = \sum_i \sum_j X_{ij}^2 - \frac{1}{(p+2)} \sum_i (X_{i.} + X_{.i})^2 + \frac{2}{(p+1)(p+2)} X^2_{..}$$

SS = sum of squares

P = number of parents

$X_{i.}$  = total of array involving  $i^{\text{th}}$  parent,

$X_{.i}$  = parental value of  $i^{\text{th}}$  parent,

$X_{..}$  = total of all  $\frac{P(P+1)}{2}$  items of diallel table

$M'e$  = The error mean square was obtained after dividing the error mean square (Me) from RCBD Anova by the number of replications =  $Me/t$

The significance of mean square due to GCA (Mg) and SCA (Ms) was tested against error mean square (Me) by F-test at  $p = 0.01$  and  $0.05$

### 3.3.5 Estimates of combining ability effects and their standard error

The GCA effect of parent (i) was calculated as under

$$g_i = \frac{1}{(P+2)}(X_i + X_{ii}) - \frac{2X_{..}}{P}$$

The SCA effect of a cross (i x j) was calculated as under:

$$s_{ij} = X_{ij} - \frac{1}{(p+2)}(X_i + X_{ii} + X_j + X_{jj}) + \frac{2}{(p+1)(p+2)} X_{..}$$

Where,

$X_i$  = total of array involving  $i^{\text{th}}$  parent,

$X_j$  = total of array involving  $j^{\text{th}}$  parent,

$X_{ii}$  = parental value of  $i^{\text{th}}$  parent,

$X_{jj}$  = parental value of  $j^{\text{th}}$  parent, and

$X_{..}$  = total of all  $\frac{P(P+1)}{2}$  items of diallel table

The standard errors for test of significance of GCA and SCA effects and differences between them were worked out as follows:

$$S.E(g_i) = \left[ \frac{P-1}{P(P+2)} Me \right]^{0.5}$$

$$S.E(S_{ij}) = \left[ \frac{P^2 + P + 2}{(P+1)(P+2)} Me \right]^{0.5}$$

$$S.E(g_i - g_j) = \left[ \frac{2Me'}{(P+2)} \right]^{0.5}$$

$$SE(s_{ij} - s_{ik}) = \left[ \frac{2(p+1)}{(p+2)} Me \right]^{1/2}$$

$$SE(s_{ij} - s_{kl}) = \left[ \frac{2p}{(p+2)} Me \right]^{1/2}$$

### 3.3.6 Genetic components of variance

The components of variance were estimated by the following formulae:

$$\text{Variance due to gca}(\sigma^2g) = \frac{Mg - M'e}{(p+2)}$$

$$\text{Variance due to sca}(\sigma^2s) = Ms - M'e$$

Where, Mg = Mean sum of square due to gca effect

Ms = Mean sum of squares due to sca effect

M'e = Me/r = Error mean square

These estimates were translated into genetic components of variance as per the methodology suggested by Griffing (1956).

$$2\sigma^2g = \sigma^2A$$

$$\sigma^2s = \sigma^2D$$

Where,

$\sigma^2A$  = Additive genetic variance

$\sigma^2D$  = Dominance genetic variance

### 3.3.7 Test of significance

Each GCA and SCA effect was tested against zero for its difference by t-test, respectively

$$t = \frac{g_i - o}{S.E. \text{ of } (g_i)} \text{ and}$$

$$t = \frac{s_{ij} - o}{S.E. \text{ of } (s_{ij})}$$

To test the significance of differences of two estimates, critical differences (C.D) was calculated as product of the t-value for error degree of freedom and the standard error of difference of two estimates.

### 3.3.8 Estimation of heterosis

Heterosis was estimated as standard heterosis over the checks namely Punjab Maize Hybrid-10 (PMH-10) and Deccan Hybrid Maize-117 (DHM-117). It was calculated by the formula given below:

$$SH(\%) = \frac{\overline{F_1} - \overline{SC}}{\overline{SC}} \times 100$$

Where,

SH(%)= Standard heterosis expressed in percentage

$\overline{F_1}$  = Mean performance of  $F_1$  generation

$\overline{SC}$  = Mean performance of Standard check

## Chapter-4

### EXPERIMENTAL FINDINGS

The present investigation entitled “**Genetic Studies of Medium Maturing Maize (*Zea mays* L.) Inbred Lines.**” was undertaken using eight maize inbred lines to generate information on the amount of variability present in the material, combining ability effects of parents and their crosses; nature and magnitude of gene action and heterosis for yield and its component traits.

The experiment findings are presented under the following headings:

- 4.1 Analysis of variance for the experimental design
- 4.2 Analysis of variance for the combining ability
- 4.3 Analysis of combining ability effects.
- 4.4 Estimation of heterosis

#### **4.1 Analysis of variance for the experimental design**

Analysis of variance (ANOVA) for randomized complete block design (RCBD) provided in Table 4.1 was performed for all the traits under investigation. The results showed that the mean squares due to treatments (genotypes) were highly significant for all traits except ASI and ear height indicating that the experimental material under study possessed sufficient genetic variability. The mean squares due to treatments (genotypes) were further partitioned into parents, hybrids and parents v/s hybrids. The mean sum of squares due to parents and hybrids showed highly significant differences for all the traits except for ASI and ear height, revealing the existence of significant variability among parents and hybrids. Parents vs hybrids showed a highly significant mean sum of squares for five traits, i.e., days to maturity, plant height, cob diameter, number of kernels row<sup>-1</sup> and grain yield plant<sup>-1</sup>, except days to 50 per cent silking, days to 50 per cent tasseling, ASI, ear height, cob length, number of cobs plant<sup>-1</sup> and kernal rows cob<sup>-1</sup>. The mean sum of squares for ASI and ear height were found non-significant under all components of variations mentioned.

**Table:4.1: Analysis of variance for experimental design for 12 morphological, maturity, yield and yield attributing traits in maize (*Zea mays* L.)**

Source of variation	D.f	Days to 50% tasseling	Days to 50% silking	ASI	Days to maturity	Plant height (cm)	Ear height (cm)	Cob length (cm)	Cob diameter (cm)	Number of cobs plant <sup>-1</sup>	Kernel rows cob <sup>-1</sup>	Number of kernels row <sup>-1</sup>	Grain yield plant <sup>-1</sup>
Replications	2	2.98	1.03	0.13	8.08	135.35*	51.49	1.20	0.04	0.001	0.60	2.05	251.53
Treatments	35	37.98**	86.31**	0.69	65.16**	1825.90**	862.01	25.50**	1.77**	0.08**	4.56**	327.66**	6597.72**
Parents	7	36.45**	110.71**	0.48	31.89**	3379.65**	1045.10	29.29**	2.27**	0.07**	6.89**	500.89**	9894.73**
Hybrids	27	38.96**	82.94**	0.7	70.20**	1397.76**	583.71	25.34**	1.62**	0.08**	4.13**	291.78**	5833.94**
Parents vs. hybrids	1	22.32	6.71	0.06	162.05**	2512.56**	898.5	3.33	2.30**	0.03	0.02	83.72**	4140.54**
Error	70	2.68	2.31	0.2	2.93	31.89	16.35	1.74	0.02	0.02	0.87	4.28	154.28
Total	107	14.23	29.77	0.47	23.38	620.68	381.0	9.50	0.59	0.04	2.07	110.02	2263.77

\*, \*\* significant at 5 and 1 percent level, respectively

## 4.2 Estimation of combining ability and gene action

Diallel analysis evaluation was carried in the current research to assess the combining ability of parents and crosses in order to gain information about the nature and magnitude of the gene action involved in the trait expression.

### 4.2.1 ANOVA for combining ability

Table 4.2 presents the analysis of variance for combining ability and estimation of variance components for various traits which was carried out as per procedure given by Griffing 1956 (Model I and Method II). Variance analysis for general and specific combining ability was highly significant for all the traits under examination. These results depicted the involvement and importance of both additive and non-additive gene actions for the expression of all the traits.

The magnitude of mean sum of squares due to SCA was higher than respective GCA mean sum of squares for all the traits except for days to maturity. Further, the level of the dominance variance was higher in magnitude than the additive variance for all the traits studied, illustrating the preponderance of non-additive gene action in the expression of traits. Therefore, across all traits, the proportion of additive genetic variance ( $\sigma^2_A/\sigma^2_D$ ) to dominance variance was less than unity. The Baker's ratio  $2\sigma^2_g/2\sigma^2_g+\sigma^2_s$  is used to estimate the relative importance of general and specific combining ability on the progeny performance. The closer this ratio to unity, the greater the proportion of a specific hybrid's performance can be predicted based on GCA alone. Here, the Baker's ratio estimated was less than unity for all the trait, thus indicating that performance of a hybrid combination cannot be predicted on the GCA alone instead, here SCA played a greater role on progenies performance and therefore implies predominance of non-additive gene effects in inheritance of all traits.

**Table 4.2: Analysis of variance for combining ability and estimation of components of genetic variation for 11 morphological , yield and yield attributing in maize (*Zea mays* L.)**

Source of variation	D.f	Days to 50% tasseling	Days to 50% silking	Days to maturity	Plant height (cm)	Ear height (cm)	Cob length (cm)	Cob diameter (cm)	Cobs plant <sup>-1</sup>	Kernal rows cob <sup>-1</sup>	Kernals <sub>1</sub> row	Grain yield plant <sup>-1</sup> (g)
GCA	7	10.88**	20.69**	23.25**	221.90**	127.75**	1.53*	0.08**	0.02**	1.06**	20.76**	186.96**
SCA	28	13.03**	30.85**	21.34**	705.46**	327.24**	10.24**	0.71**	0.03**	1.63**	131.37**	2702.31**
Error	70	0.91	0.77	0.97	10.62	5.45	0.58	0.009	0.008	0.29	1.42	51.43
$\sigma^2_g$		0.99	1.99	2.22	21.12	12.22	0.09	0.008	0.001	0.07	1.93	13.55
$\sigma^2_s$		12.12	30.08	20.36	694.83	321.78	9.66	0.70	0.01	1.34	129.94	2650.88
$\sigma^2_A$		1.99	3.98	4.45	42.25	24.45	0.19	0.02	0.003	0.15	3.86	27.10
$\sigma^2_D$		12.12	30.08	20.36	694.83	321.78	9.66	0.70	0.02	1.34	129.94	2650.88
$\sigma^2_A/\sigma^2_D$		0.16	0.09	0.21	0.06	0.07	0.02	0.02	0.18	0.11	0.02	0.01
$2\sigma^2_g/2\sigma^2_g+\sigma^2_s$		0.14	0.11	0.17	0.05	0.07	0.01	0.02	0.15	0.10	0.02	0.01

\*, \*\* significant at 5 and 1 percent level

### **4.3 Estimation of combining ability effects**

#### **4.3.1 General combining effects**

The estimates of GCA effects shown in Table 4.3 revealed that none of the parents was found to be a good general combiner for all the characters under consideration, yet some parents were found good general combiners for the majority of traits. A wide range of variability of GCA effects was observed among the parents. Parents with significant and negative GCA effect for days to 50 per cent tasseling, days to 50 per cent silking, days to maturity were considered good general combiners for these particular traits and therefore, ideal choice for use in developing medium maturing hybrids. Similarly, parents with significant and negative GCA effects for plant height and ear height were considered good combiners for these traits. On the other hand, parents with significant and positive GCA effects (i.e., in desirable direction) were considered as good general combiners for yield and yield attributing traits. The results are elucidated trait-wise as:

#### **4.3.2 Days to 50% tasseling**

Out of the eight parents, V-405(-1.33) and IML-187(-1.40) displayed significant negative GCA effects for 50 per cent tasseling and were considered as best general combiners for earliness, while the parent LM-14(1.65) was considered as poor general combiner for this trait as exhibited significant positive GCA effect. Non-significant negative GCA effect was depicted by UMI1200.

#### **4.3.3 Days to 50% silking**

Parents, V-405(-1.88) and IML-187(-1.61) showed significant negative GCA effects in desirable direction for days to 50 per cent silking and were considered as good combiners for the trait. While the parent LM-14 (2.69) was observed to be poor general combiner as it recorded significant positive GCA effect for the trait. Non-significant negative GCA effect were depicted by CML-451 and LM-13.

#### **4.3.4 Days to maturity**

Out of eight parents, BML-6 (-1.80) and UMI1200(-2.17) depicted significant negative GCA effects for days to maturity and considered as good general combiner for the trait. The lines V-405(1.79) and LM-14(2.12) showed positive and significant GCA effects.

#### **4.3.5 Plant height**

The parents, LM-14 (-3.52), UMI1200 (-4.82) and IML-187(-5.96) exhibited significant negative GCA effects for plant height, thus revealing these parents as good general combiners for the trait. While the lines, CML-451( 6.63) and V-405(3.60) showed positive significant GCA effects for the trait thus regarded as poor general combiners for the trait. The line BML-10 showed negative but non-significant general combining ability effect.

#### **4.3.6 Ear height**

Out of eight parents, UMI1200 (-4.3), V-405 (-1.83) and LM-13 (-2.25) seemed to be good general combiners with significant and negative GCA effects. The line CML-451(2.42) was observed as poor general combiner for this trait as it depicted positive significant GCA effect. Whereas BML-10 showed negative but non-significant GCA effect for the trait.

#### **4.3.7 Cob length**

The lines UMI1200(0.75) was good general combiner for cob length with significant positive GCA effect. Whereas the line LM-13 showed non-significant positive GCA effect and remaining lines revealed non-significant negative GCA effects for the trait.

#### **4.3.8 Cob diameter**

The parent LM-14 (0.21) showed desirable significant and positive GCA effect for cob diameter. On the contrary, the line CML-451(-0.11) displayed significant negative GCA effect. The lines BML-6 and BML-10 showed non-

significant positive GCA effects for the trait, whereas the remaining lines exhibited non-significant negative GCA effects.

#### **4.3.9 Number of cobs plant<sup>-1</sup>**

Out of eight parents, the line BML-6 (0.07) exhibited significant GCA effects in a positive direction. The line, LM-13(-0.06) showed significant negative GCA effect. Non-significant positive GCA effects for the trait were depicted by LM-14, UMI1200 and V-405, The lines, CML-451, BML-10 and IML-187 showed non-significant negative GCA effects.

#### **4.3.10 Kernel rows cob<sup>-1</sup>**

The line BML-6 (0.56) exhibited desirable significant and positive GCA effect and was considered as good general combiner for kernal rows cob<sup>-1</sup>. On the contrary, negative and significant GCA effect was observed for the line UMI1200(-0.41). The parents LM-13 and LM-14 showed positive but non-significant GCA effect and remaining lines showed negative and non-significant GCA effects.

#### **4.3.11 Number of kernels row<sup>-1</sup>**

The parents, BML-6(2.42) and IML-187 (0.87) were good general combiners with significant and positive GCA effects for number of kernels row<sup>-1</sup>. The lines, LM-14 (-1.11) and V-405 (-2.53) showed undesirable, negative and significant GCA effects. The lines, LM-13, BML-10 and UMI1200 showed positive but non-significant GCA effect, whereas, CML-451 showed non-significant and negative GCA effect.

#### **4.3.12 Grain yield plant<sup>-1</sup>**

LM-13(5.14) and UMI1200(5.17) were observed as good general combiners for the trait as they revealed positive and significant GCA effects. The lines, CML-451, LM-14, BML-6, BML-10, V-405 and IML-187 showed positive but non-significant GCA effects for the trait.

**Table 4.3: Estimation of general combining ability effects for 11 morphological, maturity, yield and yield attributing traits in maize (*Zea mays* L.)**

Parents	Days to 50% tasseling	Days to 50% silking	Days to maturity	Plant height (cm)	Ear height (cm)	Cob length (cm)	Cob diameter (cm)	Cobs <sub>1</sub> plant	Kernal <sub>1</sub> rows cob	Kernals <sub>1</sub> row	Grain yield <sub>1</sub> plant (g)
<b>CML-451</b>	0.23	-0.17	-0.27	6.63**	2.42*	-0.11	-0.11**	-0.01	-0.15	-0.13	0.32
<b>LM-13</b>	0.23	-0.43	-0.37	0.35	-2.25*	0.36	-0.02	-0.06*	0.11	0.40	<b>5.14*</b>
<b>LM-14</b>	1.65**	2.69**	2.12*	-3.52**	0.47	-0.02	0.21**	0.01	0.30	-1.11*	2.81
<b>BML-6</b>	0.76*	0.49	<b>-1.80**</b>	5.02**	7.37**	-0.03	0.02	0.07*	0.56**	2.42**	4.53
<b>BML-10</b>	0.39	0.75*	0.55	-1.30	-0.71	-0.37	0.008	-0.05	-0.32	0.21	2.46
<b>UMI1200</b>	-0.53	0.16	<b>-2.17**</b>	-4.82**	-4.3**	0.75*	-0.04	0.05	-0.41*	0.15	<b>5.17*</b>
<b>V-405</b>	-1.33**	-1.88**	1.79**	3.60**	-1.83*	-0.43	-0.007	0.002	-0.14	-2.53**	4.43
<b>IML-187</b>	-1.40**	-1.61**	0.15	-5.96**	-1.17	-0.14	-0.04	-0.01	0.04	0.87*	4.82
<b>SE(gi)</b>	0.28	0.25	0.29	0.96	0.69	0.22	0.02	0.02	0.15	0.35	2.12
<b>SE(gi-gj)</b>	0.42	0.39	0.44	1.45	1.04	0.33	0.04	0.03	0.23	0.53	3.20

\*, \*\* significant at 5 and 1 percent level

#### **4.3.13 Specific combining ability effects**

Table 4.4 presents the estimates of the specific combining ability (SCA) effects of all the crosses for various characteristics. None of the cross combinations showed significant SCA effects in a favourable direction for all the traits. But some cross combinations showed significant SCA effects for the majority of traits, if not all. Trait wise findings obtained for SCA effects are as follows:

#### **4.3.14 Days to 50% tasseling**

Crosses, CML-451 x LM-13(-2.64), LM-13 x UMI1200(-2.54), LM-14 x BML-6(-4.60) and BML-6 x UMI1200 (-3.74) displayed significant effect of SCA in favourable direction i.e. significant and negative. Crosses, LM-13 x V-405(4.25), LM-14 X BML-10 (2.42), LM-14 X IML-187 (3.56), BML-10 X UMI1200 (5.28), BML-10 X V-405 (3.41), BML-10 X IML-187(2.48) and UMI1200 X V-405 (4.68) exhibited positive and significant SCA effect for the trait.

#### **4.3.15 Days to 50% silking**

Cross combinations, CML-451 X LM-14(-2.26), LM-13 X UMI1200(-3.15), LM-14 X BML-6(-5.59), LM-14 X V-405(-3.88) and BML-6 X UMI1200(-3.74) demonstrated desirable significant and negative SCA effects. While CML-451 X V-405 (2.97), CML-451 X IML-187(2.71), LM-13 X BML-6(2.52), LM-13 X BML-10(3.58), LM-13 X V-405(4.56), LM-14 X BML-10(4.46), LM-14 X UMI1200(9.38), BML-6 X IML-187(2.37), BML-10 X UMI1200(4.32), BML-10 X V-405(2.71), BML-10 X IML-187(2.77) and UMI1200 X V-405(4.30) revealed a significant SCA effect in a positive direction.

#### **4.3.16 Days to maturity**

The cross combinations, CML-451 X BML-6(-8.00), LM-13 X UMI1200 (-4.20), LM-14 X UMI1200(-5.03), BML-6 X IML-187(-3.43) were observed to

have desirable significant and negative SCA effects. Crosses, CML-451 X LM-14(3.06),CML-451 X V-405 (3.40),CML-451 X IML-187(5.03),LM-13 X BML-6(6.43),LM-14 X BML-6(3.26), LM-14 X IML-187(5.30),BML-6 X V-405(7.26) and UMI1200 X V-405 (2.63) exhibited positive and significant SCA effects.

#### **4.3.17 Plant height**

Cross combinations, LM-13 X UMI1200(-12.63),UMI1200 X V-405(-1.69) and V-405 X IML-187(-11.00) exhibited favourable significant and negativeSCA effects.Positive and significant SCA effects were demonstrated by crosses,LM-13 X V-405 (16.73),LM-13 X IML-187 (14.37), LM-14 X UMI1200(16.43),LM-14 X IML-187(36.28), BML- 6 X UMI1200(20.32),BML-6 X V-405(12.13),BML-10 X UMI1200(10.32), BML-10 X V-405(20.69) and UMI1200 X IML-187 (37.78).

#### **4.3.18 Ear height**

The cross combinations, LM-13 X BML-6(-9.38), LM-14 X V-405(-6.20) and UMI1200 X V-405(-22.68) showed favourable negative and significant SCA effects.Crosses, CML-451 X BML-6 (40.70),CML-451 X V-405 (18.41), LM-13 X LM-14 (7.64),LM-13 X V-405 (16.42), LM-13 X IML-187 (11.86), LM-14 X UMI1200(12.70), LM-14 X IML-187(12.90),BML-10 X UMI1200(15.25)and UMI1200 X IML-187 (37.78)exhibited positive and significant SCA effects.

#### **4.3.19 Cob length**

Crosses combinations, CML-451 x BML-6 (3.07),LM-13 X UMI1200 (4.83),LM-13 X IML-187(3.03), LM-14 X BML-6 (2.78),LM-14 X IML-187(3.32), BML-6 X V-405(2.13), BML-10 X UMI1200(2.43), BML-10 X V-405(6.20) and UMI1200 X IML-187(1.94) exhibited desirable significant and positive SCA effects, whereas, cross combinations,UMI1200 X V-405(-3.26),LM-14 X V-405(-3.84) and LM-13 X BML-10(-2.46) had negative and significant SCA effects.

#### **4.3.20 Cob diameter**

Out of 28 crosses, 21 cross combinations, i.e., CML-451 X LM-13(0.53), CML-451 X LM-14 (0.49), CML-451 X BML-10 (0.29), CML-451 X UMI1200 (0.72), CML-451 X V-405 (0.41), LM-13 X LM-14 (0.52), LM-13 X BML-6(0.26), LM-13 X BML-10 (0.71), LM-13 X V-405 (0.26), LM-13 X IML-187 (0.66), LM-14 X V-405 (0.49), LM-14 X IML-187 (0.29), BML-6 X BML-10 (0.52), BML-6 X UMI1200 (0.48), BML-6 X V-405 (0.34), BML-6 X IML-187 (0.45), BML-10 X UMI1200 (0.53), BML-10 X IML-187 (0.39), UMI1200 X V-405 (0.45), UMI1200 X IML-187 (0.55), V-405 X IML-187 (0.48) exhibited desirable positive significant SCA effect for the trait. None of the crosses showed significant and negative SCA effect.

#### **4.3.21 Number of cobs plant<sup>-1</sup>**

None of the crosses showed desirable significant and positive SCA effect for the trait. Whereas, crosses, BML-6 X V-405(-0.29) and UMI1200 X IML-187(-0.09) showed significant and negative SCA effect for the trait.

#### **4.3.22 Kernel rows cob<sup>-1</sup>**

The cross combinations, CML-451 X BML-6(1.69), LM-13 X BML-6(1.46), LM-13 X BML-10(1.79), LM-13 X IML-187(1.45) and BML-10 X IML-187(1.79) had demonstrated a positive as well as significant SCA effect for trait. Crosses, CML-451 X BML-10(-1.24), LM-13 X V-405(-1.02) and BML-6 X UMI1200(-1.14) showed negative and significant SCA effect.

#### **4.3.23 Number of kernels row<sup>-1</sup>**

Crosses, CML-451 X LM-13 (7.75), CML-451 X BML-6 (8.59), CML-451 X UMI1200 (5.20), CML-451 X V-405(3.45), CML-451 X IML-187 (8.48), LM-13 X LM-14 (1.73), LM-13 X BML-6 (6.59), LM-13 X UMI1200 (8.83), LM-13 X V-405 (7.21), LM-13 X IML-187 (8.11), LM-14 X BML-6 (6.34), LM-14 X BML-10 (5.31), LM-14 X UMI1200 (9.25), LM-14 X IML-187 (9.42), BML-6 X BML-10 (5.84), BML-6 X V-405 (7.49), BML-6 X IML-187(7.19),

BML-10 X UMI1200 (9.19), BML-10 X V-405 (15.27) showed favourable positive and significant SCA effect for the trait. Negative and significant SCA effect were shown by crosses, CML-451 X BML-6 (-1.12), LM-13 X BML-10 (-4.42), LM-14 X V-405 (-5.03) and UMI1200 X V-405 (-3.89).

#### **4.3.24 Grain yield plant<sup>-1</sup>**

Crosses CML-451 X LM-13 (36.82), CML-451 X LM-14 (37.28), CML-451 X BML-6 (36.93), CML-451 X BML-10 (16.33), LM-13 X LM-14 (25.41), LM-13 X BML-10 (22.23), LM-13 X UMI1200 (26.72), LM-13 X V-405 (32.26), LM-14 X UMI1200 (25.34), BML-6 X BML-10 (37.33), BML-6 X UMI1200 (31.59), BML-16 X IML-187 (31.83), BML-10 X V-405 (47.94), UMI1200 X IML-187 (40.86) and V-405 X IML-187 (47.23) showed significant and positive estimates of SCA effect for the trait. Negative and significant SCA effect was shown by cross, BML-10 X IML-187(-23.53).

#### **4.4 Estimation of heterosis for grain yield plant<sup>-1</sup>**

Heterosis for grain yield plant<sup>-1</sup>(Table 4.5) of all the crosses was estimated over the standard check, PMH-10 and DHM-117. Estimates of standard heterosis (SH%) for grain yield plant<sup>-1</sup> revealed that four cross combinations showed the maximum positive standard heterosis over standard checks, i.e., >20 per cent SH over PMH-10 and >30 per cent SH over DHM-117. The four identified crosses are, CML-451 X LM-13 (26.72% and 35.08%), BML-6 X UMI1200 (26.47% and 34.80%), BML-10 X UMI1200 (26.85% and 35.21%) and BML-10 X V-405 (26.27% and 34.59%). Whereas some crosses exhibited maximum negative standard heterosis over both checks as BML-10 X IML-187(-28.78% over PMH-10 and -24.09% over DHM-117), CML-451 X IML-187(-12.78% over PMH-10 and -7.05% over DHM-117) and UMI1200 X V-405 (-9.86% over PMH-10 and -3.92% over DHM-117).

**Table 4.4: Estimation of specific combining ability effects for 11 morphological, maturity, yield and yield attributing traits in maize (*Zea mays* L.)**

Crosses	Days to 50% tasseling	Days to 50% silking	Days to maturity	Plant height(cm)	Ear height(cm)	Cob length (cm)	Cob diameter (cm)	Cobs plant <sup>1</sup>	Kernal rows cob <sup>1</sup>	Kernals <sup>1</sup> row	Grain yield <sup>1</sup> plant (g)
CML-451 X LM-13	-2.64**	-1.81*	-1.76	17.90**	0.55	1.27	0.53**	0.03	0.08	7.75**	36.82**
CML-451 X LM-14	-1.07	-2.26**	3.06**	0.55	-0.13	0.96	0.49**	-0.01	0.02	2.79*	37.28**
CML-451 X BML-6	2.15*	1.93*	-8.00**	46.70**	40.29**	3.07**	0.14	-0.07	1.69**	8.59**	36.93**
CML-451 X BML-10	1.18	0.66	4.63*	2.80	-2.14	-0.65	0.29**	0.02	-1.24*	-1.12**	16.33**
CML-451 X UMI1200	1.45	1.25	-1.96*	14.15**	3.94	-0.58	0.72**	-0.05	0.70	5.20**	25.39*
CML-451 X V-405	0.91	2.97**	3.40**	22.65*	18.41**	0.70	0.41**	-0.10	0.53	3.45**	13.90*
CML-451 X IML-187	1.98*	2.71**	5.03**	-1.43	1.64	-0.11	0.21*	0.01	0.22	8.48**	-4.80
LM-13 X -LM-14	0.59	-0.01	1.83	2.22	7.64**	1.21	0.52**	-0.09	1.03*	1.73**	25.41**
LM-13 X BML-6	1.81*	2.52**	6.43**	1.81	-9.38**	1.46*	0.26**	-0.02	1.46**	6.59**	-6.03
LM-13 X BML-10	4.18*	3.58**	-0.26	5.84	5.83*	-2.46**	0.71**	0.10	1.79**	-4.42**	22.23**
LM-13 X UMI1200	-2.54**	-3.15**	-4.20**	-12.63**	9.22**	4.83**	0.17	-0.07	0.41	8.83**	26.72**
LM-13 X V-405	4.25**	4.56**	1.83	16.73**	16.42**	0.26	0.26**	-0.01	-1.02*	7.21**	32.26**
LM-13 X IML-187	-1.01	-1.03	1.46	14.37**	11.86**	3.03**	0.66**	-0.10	1.45**	8.11**	40.52*
LM-14 X BML-6	-4.60**	-5.59**	3.26**	-0.67	2.95	2.78**	0.22*	-0.11	-0.02	6.34**	35.08*

Contd:-

Crosses	Days to 50% tasseling	Days to 50% silking	Days to maturity	Plant height(cm)	Ear height(cm)	Cob length (cm)	Cob diameter (cm)	Cobs plant <sup>1</sup>	Kernal rows cob <sup>1</sup>	Kernals <sup>1</sup> row	Grain yield <sup>1</sup> plant (g)
LM-14 X BML-10	2.42**	4.46**	2.23*	-2.57	3.04	1.62*	0.20*	-0.17*	0.10	5.31**	7.85
LM-14 X UMI1200	1.69	9.38**	-5.03**	16.43**	12.70**	1.78*	-0.13	-0.09	0.45	9.25**	25.34**
LM-14 X V-405	-1.83*	-3.88**	-3.33**	4.81	-6.20**	-3.84**	0.49**	-0.03	0.71	-5.03**	9.59
LM-14 X IML-187	3.56**	2.17*	5.30**	36.28**	12.90**	3.32**	0.29**	-0.04	0.06	9.42**	6.08
BML-6 X BML-10	1.65	0.66	1.16	6.34*	-4.15	0.30	0.52**	-0.24*	0.54	5.84**	37.33**
BML-6 X UMI1200	-3.74**	-3.74**	-0.43	20.32**	1.00	-0.83	0.48**	0.37*	-1.14*	2.78*	31.59**
BML-6 X V-405	-1.28	-1.35	7.26**	12.13**	5.13*	2.13**	0.34**	-0.29**	-0.77	7.49**	9.30
BML-6 X IML-187	0.78	2.37**	-3.43**	4.80	2.66	0.43	0.45**	-0.07	0.80	7.19**	31.83**
BML-10 X UMI1200	5.28**	4.32**	6.53**	10.32**	15.25**	2.43**	0.53**	0.01	-0.54	9.19**	39.09*
BML-10 X V-405	3.41**	2.71**	0.90	20.69**	20.25	6.20**	0.05	-0.03	0.74	15.27**	47.94**
BML-10 X IML-187	2.48**	2.77**	1.86*	6.53*	0.45	0.47	0.39**	-0.14	1.79**	1.86	-23.53**
UMI1200 X V-405	4.68**	4.30**	2.63**	-1.69**	-22.68**	-3.26**	0.45**	0.02	0.86	-3.89**	-6.86
UMI1200 X IML-187	-1.91*	-1.29	-2.06*	37.78**	27.38**	1.94**	0.55**	-0.09**	1.24*	1.03	40.86**
V-405 X IML-187	0.21	1.08	1.30	-11.00**	2.44	1.67*	0.48**	0.09	-0.98	1.71	47.23**
SE (sij)	0.86	0.79	0.89	2.95	2.11	0.68	0.08	0.08	0.48	1.07	6.50
SE(sij-sjk)	1.28	1.17	1.32	4.37	3.13	1.01	0.13	0.11	0.71	1.59	9.62

\*, \*\* Significant at 5 and 1 percent level

**Table 4.5: Heterosis estimation over standard checks (PMH-10 and DHM-117) for grain yield plant<sup>-1</sup> in maize (*Zea mays* L.)**

<b>Crosses</b>	<b>Grain yield plant<sup>-1</sup> (g)</b>	<b>S.heterosis over PMH-10 check (%)</b>	<b>S.heterosis over DHM-117 check (%)</b>
<b>CML-451 X LM-13</b>	165.43	26.72	35.08
<b>CML-451 X LM-14</b>	157.93	20.98	28.95
<b>CML-451 X BML-6</b>	164.93	26.34	34.67
<b>CML-451 X BML-10</b>	137.33	5.20	12.13
<b>CML-451 X UMI1200</b>	154.03	17.99	25.77
<b>CML-451 X V-405</b>	132.93	1.83	8.54
<b>CML-451 X IML-187</b>	113.83	-12.78	-7.05
<b>LM-13 X LM-14</b>	151.53	16.08	23.73
<b>LM-13 X BML-6</b>	127.43	-2.38	4.05
<b>LM-13 X BML-10</b>	148.70	13.91	21.4
<b>LM-13 X UMI1200</b>	160.83	23.20	31.32
<b>LM-13 X V-405</b>	156.76	20.09	28.03
<b>LM-13 X IML-187</b>	164.63	26.11	34.42
<b>LM-14 X BML-6</b>	160.60	23.02	31.13
<b>LM-14 X BML-10</b>	126.36	-3.19	3.18
<b>LM-14 X UMI1200</b>	151.50	16.05	23.70
<b>LM-14 X V-405</b>	126.13	-3.37	2.99
<b>LM-14 X IML-187</b>	122.23	-6.36	-0.19
<b>BML-6 X BML-10</b>	163.20	25.01	33.25
<b>BML-6 X UMI1200</b>	165.10	26.47	34.80
<b>BML-6 X V-405</b>	133.20	2.03	8.76
<b>BML-6 X IML-187</b>	155.33	18.99	26.83
<b>BML-10 X UMI1200</b>	165.60	26.85	35.21
<b>BML-10 X V-405</b>	164.833	26.27	34.59
<b>BML-10 X IM L-187</b>	92.96	-28.78	-24.09
<b>UMI1200 X V-405</b>	117.66	-9.86	-3.92
<b>UMI1200 X IML-187</b>	165.00	26.39	34.72
<b>V-405 X IML-187</b>	161.76	23.92	32.08

## Chapter- 5

### DISCUSSION

Knowledge of the combining ability of breeding materials is required for the generation of potential hybrids, and selection based on this has been utilised as a significant breeding method in crop improvement. Therefore, for the improvement of maize crop through systematic breeding approaches, selection of parents with good general combining ability for the desired traits are crucial and cross combinations having high heterotic effects along with high estimates of specific combining ability for the desired traits are also required to isolate superior cross combinations to exploit heterosis. The combining ability provides information about the nature of gene action involved in inheritance of various traits and there by breeding methods to be used.

The present investigation entitled, “**Genetic Studies of Medium Maturing Maize (*Zea mays* L.) Inbred Lines.**” was aimed to evaluate the combining ability of 8 inbred lines and their crosses in order to identify best parents and best cross combinations (hybrids) for the targeted traits, along with nature and magnitude of gene action involved in the inheritance of traits. It also depicts the extent of heterosis over standard checks for the yield trait. In the present investigation, half diallel mating design was used to study the combining ability of parents and crosses and unravel the gene action involved in inheritance of traits under study. Observations were recorded for different maturity, yield and yield attributing traits and data generated was subjected to statistical analysis. Data recorded for all the traits such as, days to 50% tasseling, days to 50% silking, anthesis silkiing interval (ASI), days to maturity, plant height, ear height, cob length, cob diameter, cobs plant<sup>-1</sup>, kernal rows cob<sup>-1</sup>, kernels row<sup>-1</sup> and grain yield plant<sup>-1</sup> were subjected to analysis of variance.

## **5.1 Analysis of variance for the experimental design**

The analysis of variance for experimental design is important as it is an indicator of the measure of amount of variability existing in the experimental material. It not only testifies the validity of selection of parents but also suggests whether further analysis needs to be conducted for a trait or not. ANOVA results of this study showed highly significant variations for all traits among treatments(genotypes) and between parents and their crosses, suggesting that the material selected was diverse and produced substantial genetic variation in the crosses. Several workers have used ANOVA to measure the variability in the experimental materials and dissected this variability into different components and came up with similar results, notable among them are Singh *et al.*(2013), Ali *et al.* (2014), Shadlou *et al.*(2015) and Karad *et al.*(2018). The mean sum of squares due to treatments, parents and crosses exhibited major differences for all the characteristics except for anthesis silking interval. Darshan and Marker (2019) also revealed the significant differences among the parents and experimental hybrids for all characters except anthesis silking interval. Parents vs hybrids showed a highly significant mean sum of squares for most of the traits and thus implies presence of significant differences of average performance of hybrids from the parents for traits except for days to 50 per cent silking, days to 50 per cent tasseling, ASI, ear height, cob length, number of cobs plant<sup>-1</sup> and kernal rows cob<sup>-1</sup>.

## **5.2 Analysis of variance for combining ability**

The combining ability analysis is one of the most significant biometrical methods to give an insight into gene action involved in the inheritance of traits. Information on gene action and combining ability aids to identify the best parents and the best combiners that can be hybridized either to exploit heterosis or to develop the transgressive segregants in F<sub>2</sub> and future generations. The exploitation of heterosis primarily relies on the screening and selection of lines from available germplasm that could create better combinations of important characters.

In the present investigation, analysis of variance for combining ability revealed significant mean sum of squares (MSS) due to GCA and due to SCA for all the characters studied, which indicate the importance of both additive and non-additive gene action in the inheritance of these traits. Similar results of significant GCA and SCA variances for all characters have been reported by, Muraya *et al.* (2006), Zelleke (2000), Amiruzzaman *et al.* (2013) and El Shamarka *et al.* (2015). MSS for GCA has higher magnitude than SCA for days to maturity, indicating preponderance of additive gene action for the trait, which are in line with the findings of Hoque *et al.* (2016) and Matin *et al.* (2017) who reported similar findings for days to 50 % tasseling, days to 50% silking and days to maturity, whereas SCA exhibited higher magnitude for all other traits, viz., days to 50% tasseling, days to 50% silking, plant height, cob length, number of cobs plant<sup>-1</sup>, kernels rows cob<sup>-1</sup>, kernels row<sup>-1</sup>, cob diameter, g rain yield plant<sup>-1</sup>, indicating preponderance of non-additive gene action for the traits. Similar results were also reported by Mahto and Ganguli (2003), Satyanarayana *et al.* (1990), Debnath and Sarkar (1990), Dass *et al.* (1997), Singh and Gupta (2009), Amiruzzaman *et al.* (2013), Niyonzima *et al.* (2015), Aslam *et al.* (2017). For all traits, dominance variance ( $\sigma^2D$ ) values were observed much higher as compared to additive variance ( $\sigma^2A$ ) and therefore the additive to dominance variance ratio was observed to be less than unity. This revealed that non-additive variance played a major role in the inheritance of all traits as compared to additive variance. Same findings were recorded by Yerva *et al.* (2016) where the additive to dominance variance ratio was lower than unity for all the traits.

The predictability ratio ( $2\sigma^2g/2\sigma^2g+\sigma^2s$ ) which determines the predictability of hybrid performance for a character based on GCA alone. In this study, this ratio was found to be less than unity for all the traits, indicating that the predictability of the performance of progeny based on GCA would be negligible. This indicates rather that progeny performance was based more on SCA which

accounted for major genetic variability. Similar findings were reported earlier by Loesch (1972), Dhillon and Singh (1977), and Prasad *et al.* (1988).

### 5.2.1 General combining ability effects

In the present study, the GCA effects ( $g_{ij}$ ) of inbred lines were calculated to know their genetic worth for use in the development of hybrids. The GCA estimates revealed that none of parent showed significant GCA effects in the desired direction for all the traits. However, general combining estimates for day to 50% tasseling and days to 50% silking, indicated that among parents, viz., V-405 and IML-187 were having highly significant negative GCA effects for both traits. The lines BML-6 and BML-10 were classified as desirable parents for days to maturity as it exhibited highest negative and significant GCA effect for the trait. Presence of high GCA effects for maturity traits in maize were also reported by Vasal *et al.* (1993), Sedhom (1994) and Zelleke (2000). LM-14, UMI1200 and IML-187 were considered as good general combiners for plant height and UMI1200, V-405 and LM-13 as good general combiners for ear height as reflected by their significant negative but desirable GCA effects. Satyanarayana *et al.* (1990), Mahajan and khera (1991), San Vicente *et al.* (1998) and Zelleke (2000) also reported the presence of high gca effects for plant type traits in maize. Considering the yield traits like cob length and cob diameter, UMI1200 and LM-14, respectively were good general combiners. BML-6 was considered as good general combiner for number of cobs plant<sup>-1</sup>, kernel rows cob<sup>-1</sup> and kernels row<sup>-1</sup>. LM-13 and UMI1200 were good general combiner for grain yield plant<sup>1</sup> as reflected by their significant positive GCA effects. These can be used directly as parents for developing high yielding single cross hybrids. There are several evidences in the literature where GCA effect has been used to identify good combiners for grain yield plant<sup>-1</sup> and its related traits. Beck *et al.* (1991), Vasal *et al.* (1993), Setiyono (1996), Sedhom (1994), Dass *et al.* (1997) and Marker *et al.* (2002) have successfully used significant positive GCA effect to identify good combiners for grain yield plant<sup>-1</sup> and its related traits.

### 5.2.2 Specific combining ability effects

SCA( $s_{ij}$ ) effect estimates are used to find out cross combinations that perform relatively worse, or better, than what is expected based on GCA ( $g_i$  and  $g_j$ ) estimates. Specific combining ability examines the efficiency of a particular cross/hybrid with respect to its parents and assesses the non-additive genetic effects. In such instances, where there is estimation of non-additive gene action, breeding strategy should focus on the development of hybrids. The evaluation of the result with respect to specific combining ability effects of the 28 F1's for various traits in this study, showed that none of the cross combination exhibited significant and desirable SCA effects for all the traits. However, several cross combinations were observed to give highest desirable significant SCA effect and per se performance for each trait. The results indicated that crosses having significantly high SCA effects involved high, average and low general combiners as parents. For maturity traits like days taken to 50% tasseling, CML-451 x LM-13, LM-13 x UMI1200, LM-14 x BML-6 and BML-6 x UMI1200 showed significant negative SCA effect in desirable direction. Similarly for days to 50% silking the significant negative desirable SCA effects exhibited by CML-451 X LM-14, LM-13 X UMI1200, LM-14 X BML-6, LM-14 X V-405 and BML-6 X UMI1200. The desirable cross combinations for days to maturity were CML-451 X BML-6, LM-13 X UMI1200, LM-14 X UMI1200, BML-6 X IML-187 which showed negative and significant SCA effect for maturity traits and were regarded as good combiners for earliness, as the ones with positive significant values are generally regarded as poor combiners. For morphological traits, the best cross combination exhibiting desirable significant SCA effect for plant height were LM-13 X UMI1200, UMI1200 X V-405 and V-405 X IML-187 and for ear height, LM-13 X BML-6, LM-14 X V-405 and UMI1200 X V-405 as it reflected desirable significant negative SCA effects. Similar findings for high SCA effects for maturity traits, plant height and ear height in maize were reported by Sedhom (1994) and Zelleke (2000), Malik *et al.* (2004), Subramanian and Subraman

(2006), Mahajan and khehra (1991), San Vicente *et al.* (1998), Devi *et al.* (2007), Gissa *et al.* (2007) and Moradi *et al.*(2014).

For number of cobs plant<sup>-1</sup>, none of the crosses showed the desirable positive SCA effect .Whereas,BML-6 X V-405 and UMI1200 X IML-187showed undesirable negative and significant SCA effect.

For cob length, five cross combinations,LM-13 X UMI1200,LM-13 X IML-187, LM-14 X IML-187, BML-10 X UMI1200 and BML-10 X V-405, were found as good specific combiners as they depicted highest significant and desirable SCA effects. For cob diameter, crosses, CML-451 X LM-13, CML-451 X UMI1200, LM-13 X LM-14, LM-13 X BML-10, LM-13 X IML-187, UMI1200 X IML-187 showed highest significant positive SCA effects and also revealed high to average per se performance.

For other yield component traits, the crosses like,CML-451 X BML-6,LM-13 X BML-6, LM-13 X BML-10, LM-13 X IML-187and BML-10 X IML-187exhibited significant and desirable SCA effects for kernal rows cob<sup>-1</sup> and for kernals row<sup>-1</sup>, the crosses CML-451 X BML-6, LM-13 X UMI1200,LM-14 X UMI1200,LM-14 X IML-187, BML-10 X V-405 were having highest significant and desirable positive SCA effects. These results are in conformity with the results of Satyanarayan *et al.* (1990) and Aslam *et al.* (2017) and signify the importance of non-additive gene action for the inheritance of cob length,cob diameter, kernals rows cob<sup>-1</sup> and kernals row<sup>-1</sup>.The specific cross combinations for these traits involved poor x poor, poor x average, average x good and poor x good general combiners. Most of the superior cross combination involved one of the parents as poor combiner.

The cross combinations CML-451 X LM-13,CML-451 XLM-14, BML-6 X BML-10, BML-10 X V-405, UMI1200 X IML-187and V-405 X IML-187 showed favourable significant and positive SCA effects for grain yield plant<sup>-1</sup>. The best crosses combination for this trait was BML-10 X V-405 showing highest and

superior SCA effect. Such cross combinations need to be exploited in hybrid breeding programme. Similar findings for identification of superior hybrids based on SCA effects for grain yield were also reported by Muraya *et al.*(2006), Subramanian and Suubbraman (2006), Beck *et al.* (1991), Ruswamdi *et al.* (2015). Devi *et al.* (2007),Gissa *et al.* (2007). From this study, it was found that grain yield was predominantly governed by non-additive gene action as also reported by Shanthi *et al.* (2010), Da Silva *et al.* (2010), Dass *et al.*(1997) and Wani *et al.* (2017).

Thus the result of the present investigation revealed that in general there was no relationship between GCA effects of the parents and the SCA effects of the single crosses. However, mean performance of single crosses was largely dependent upon the mean performance of the parents involved so high GCA value of parents is no guarantee of high SCA effects of their crosses and the selection of parents should be based on specific combining ability test. The valuable parents and crosses identified through this study are as follows:

**Table 5.1: Best parents and crosses based on GCA and SCA effects for days to maturity and grain yield plant<sup>-1</sup> in maize (*Zea mays* L.)**

<b>Traits</b>	<b>Best parents on the basis of GCA effects</b>	<b>Best crosses on the basis of SCA effects</b>
Days to maturity	BML-6 (-1.80), UMI1200 (-2.17)	CML-451 X BML-6 (-8.00), LM-14 X UMI1200 (-5.03), LM-13 X UMI1200 (-4.20)
Grain yield plant <sup>-1</sup>	LM-13 (5.14), UMI1200 (5.17)	CML-451 X LM-13 (36.82), BML-10 X V-405 (47.94), V-405 X IML-187 (47.23) BML-10 X UMI1200 (39.09)

### 5.3 Heterosis

Heterosis breeding has been extensively researched and used to increase production in a variety of crops, particularly those that are cross pollinated. Heterosis is the most effective method for use in assessing performance of numerous quantitative traits in hybrid combinations. In hybrid and varietal improvement programme, a firsthand information regarding performance of selected parents in cross combinations, i.e., expression of heterosis is essential. The magnitude of heterosis serves as a foundation for genetic diversity and a guide for selecting desirable parents for developing superior F<sub>1</sub> hybrids so as to exploit hybrid vigour or for assembling gene pools to be used in breeding programme by assisting in eradicating a large number of poor performing crosses in very first generation. With this aim, the magnitude of standard heterosis (SH%) for grain yield plant<sup>-1</sup> over checks, viz., PMH-10 and DHM-117 were estimated for all cross combinations and revealed that most of the cross combinations showed positive SH over both checks. The cross combinations, CML-451 X LM-13, BML-10 X UMI1200, BML-6 X UMI1200 and BML-10 X V-405 showed highest positive heterosis over both the standard checks (>20 % over PMH-10 and >30 % over DHM-117) followed by cross combinations, CML-451 X BML-6, LM-13 X IML-187 and among above crosses, BML-10 X V-405, LM-13 X IML-187, BML-10 X UMI100 and CML-451 X LM-13 were also recognized as good specific combiners for grain yield plant<sup>-1</sup> as they reflected highest significant and positive SCA effects. Singh *et al.* (2010), Kage *et al.* (2013), Amiruzzaman *et al.* (2013), Izhar and Chakraborty (2013), Ruswandi *et al.* (2015) and Kumar *et al.* (2014) also reported positive economic heterosis in maize for grain yield. Top ranking heterotic crosses for this trait was cross between low × high GCA parents.

The crosses, BML-10 X IML-187, CML-451 X IML-187, UMI1200 X V-405 and LM-14 X IML-187 showed negative heterosis over both the standard checks.

**Table 5.2: Best crosses based on standard heterosis over checks (PMH-10 and DHM-117) for grain yield plant<sup>-1</sup>**

TRAIT	S.HETEROSIS (%) OVER PMH-10 CHECK	S.HETEROSIS (%) OVER DHM-117 CHECK
Grain yield plant <sup>-1</sup>	CML-451 X LM-13 (26.72%), BML-10 X UMI1200 (26.85%), BML-6 X UMI1200 (26.47%)	CML-451X LM-13 (35.08%), BML-10 X UMI1200 (35.21%), UMI1200 X IML-187 (34.72%)



**Plate 2: Best cross combination (CML-451 X LM-13)**



**Plate 3: Best cross combination (BML-10 X V-405)**

## Chapter -6

### SUMMARY AND CONCLUSION

The present investigation entitled “**Genetic Studies of Medium Maturing Maize (*Zea mays* L.) Inbred Lines**” was undertaken to estimate general and specific combining ability of maize (*Zea mays* L.) inbred lines and crosses, respectively and to estimate gene action and magnitude of heterosis for various traits.

The results are summarized as below:

1. The mean squares due to treatments (genotypes) were highly significant for all traits except for ASI and ear height indicating that there is sufficient genetic diversity in the experimental material under study.
2. The mean sum of squares due to parents and hybrids showed highly significant differences for all the traits except for ASI and ear height, revealing the existence of significant variability among parents and hybrids.
3. The mean sum of squares due to parents vs hybrids showed a highly significant differences for most of the traits except for days to 50 per cent silking, days to 50 per cent tasseling, ASI, ear height, cob length, number of cobs plant<sup>-1</sup> and kernal rows cob<sup>-1</sup> which implies the presence of significant differences of average performance of hybrids from the parents for the characters.
4. Variance analysis for general and specific combining ability was highly significant for all the traits under examination. These results depicted the involvement and importance of both additive and non-additive gene actions for the expression of all the traits.
5. The magnitude of mean sum of squares due to SCA was higher than respective GCA mean sum of squares for all the traits except for days to maturity.

6. The level of the dominance variance was higher in magnitude than the additive variance for all the traits studied, illustrating the preponderance of non-additive gene action in the expression of traits.
7. The Baker's ratio ( $2\hat{\sigma}^2g / 2\hat{\sigma}^2g + \hat{\sigma}^2s$ ) estimated was less than unity for all the trait, thus indicating that performance of a hybrid combination cannot be predicted on the basis of GCA alone, instead, here SCA played a major role in progeny performance. This also implies predominance of non-additive gene effects in inheritance of the traits.
8. For all the characters under consideration, none of the parents was found to be good general combiners. A broad range of GCA effect variations was noticed among parents.
9. Parents with significantly negative GCA for silking, tasseling, maturity, plant height and ear height were considered the best general combiners and use of these parents might be helpful in the development of medium maturing hybrid varieties. Those with significant and positive GCA effects were considered as the best general combiner for yield and yield attributing traits.
10. None of the cross combinations demonstrated significant SCA effects in a favourable direction for all the traits. However, there were several cross combinations which demonstrated significant SCA effects for majority of the traits.
11. Heterosis for grain yield  $\text{plant}^{-1}$  was calculated over 2 standard checks (PMH-10 and DHM-117) for all cross combinations and was expressed in percentage. The results revealed that most of the cross combinations exhibited positive standard heterosis (SH%) over both the checks. The top ranking heterotic crosses for this trait was the cross between low  $\times$  high GCA parents.

Hence, it has been revealed through this study that there were highly significant differences among parents and their crosses for all traits;

indicating the diverse nature of the experimental material used in the study. This can serve as viable source material for future breeding programmes. None of the parents was found to be a good general combiner for all the characters under consideration but several parents depicted good general combining ability in a desirable direction. Similarly, none of the cross combinations exhibited significant SCA effects for all the traits in a desirable direction. However, there were several cross combinations which demonstrated significant SCA effects in desirable direction for maturity and yield traits. Parents with significant and negative GCA for silking, tasseling and maturity may be considered as potential lines for development of medium maturing hybrids in future programmes. The crosses with significant and positive SCA effect for grain yield and other yield attributing traits may be regarded as good specific combiners and can be used for developing high yielding hybrids. The best performing crosses, viz., CML-451 X LM-13, BML-6 X UMI1200, BML-10 X UMI1200 and BML-10 X V-405 with maximum standard heterosis for grain yield plant<sup>-1</sup> should be further evaluated over locations for stability.

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**CERTIFICATE**

Certified that all the corrections/amendments as suggested by the external examiner **Dr. N. Sunil**, Principal Scientist, WNC, IIMR, Hyderabad during viva-voce examination held on 15-03-2022 have been incorporated in the final manuscript entitled, “**Genetic Studies of Medium Maturing Maize (*Zea mays* L.) Inbred Lines**” submitted by **Ms. Rahila Amin (Regd. No. MSA-2019-1283)**.

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