

**ESTIMATION OF HETEROSIS AND COMBINING
ABILITY IN MAIZE (*Zea mays* L.)**

BY

PATEL RAVIKUMAR DIPAKBHAI

B.Sc. (Hons.) Agriculture



**DEPARTMENT OF GENETICS AND PLANT BREEDING
CHIMANBHAI PATEL COLLEGE OF AGRICULTURE
SARDARKRUSHINAGAR DANTIWADA AGRICULTURAL UNIVERSITY
SARDARKRUSHINAGAR - 385 506 [GUJARAT]**

SEPTEMBER-2021

[Registration No. 04-AGRMA-02046-2019]

PATEL RAVIKUMAR D. M.Sc.(Agri.) GENETICS & PLANT BREEDING SEPTEMBER-2021

**ESTIMATION OF HETEROSIS AND COMBINING
ABILITY IN MAIZE (*Zea mays* L.)**

**A THESIS SUBMITTED TO
SARDARKRUSHINAGAR DANTIWADA AGRICULTURAL UNIVERSITY
IN PARTIAL FULFILMENT OF THE REQUIREMENTS
FOR THE AWARD OF THE DEGREE**

OF

**MASTER OF SCIENCE
(Agriculture)**

IN

GENETICS AND PLANT BREEDING

BY

PATEL RAVIKUMAR DIPAKBHAI

B.Sc. (Hons.) Agriculture



**DEPARTMENT OF GENETICS AND PLANT BREEDING
CHIMANBHAI PATEL COLLEGE OF AGRICULTURE
SARDARKRUSHINAGAR DANTIWADA AGRICULTURAL UNIVERSITY
SARDARKRUSHINAGAR – 385 506 [GUJARAT]**

SEPTEMBER - 2021

[Reg. No. 04-AGRMA-02046-2019]

ABSTRACT

ESTIMATION OF HETEROSIS AND COMBINING ABILITY IN MAIZE (*Zea mays* L.)

Name of student

PATEL RAVIKUMAR D.

Major Advisor

Dr. K. N. PRAJAPATI

**DEPARTMENT OF GENETICS AND PLANT BREEDING
CHIMANBHAI PATEL COLLEGE OF AGRICULTURE
SARDARKRUSHINAGAR DANTIWADA AGRICULTURAL UNIVERSITY
SARDARKRUSHINAGAR - 385 506**

ABSTRACT

Maize is an important allogamous cereal crop belongs to family *poaceae*. Maize has potential to improve crop as and when required due to presence of diverse genetic variability. Looking toward the importance of maize present investigation was carried out to identified superior genotype based on heterosis as well as combining ability. The experimental material consists of 14 parents, their 45 hybrids developed by 9×5 line by tester mating design along with one standard check GAYMH 1. The experiment was laid out in a randomized block design with three replications in *kharif* 2020 at Maize Research Station, Sardarkrushinagar Dantiwada Agricultural University, Bhiloda. The observations were recorded for thirteen characters including days to tasseling, days to silking, anthesis silking interval, plant height, ear height, days to maturity, cob length, cob girth, kernel rows per ear, kernels per row, 100 kernel weight, kernel yield per plant and shelling percentage. The objective of this study was to investigate the *per se* performance, magnitude of heterosis, type of gene action and combining ability effect with respect to thirteen different characters.

The analysis of variance depicted significant difference among all the genotypes for all the characters under study. Which means presence of sufficient amount of genetic variability and parents were differed significantly for all the characters. The analysis of variance due to hybrids were indicated the highly significant difference for all the traits under study except plant height. The variance due to lines vs. testers were significant for days to tasseling, days to silking, plant height, ear height and kernels row per cob. The variance due to parents vs. hybrids found

significant for the trait *viz.*, days to tasseling, days to silking, plant height, ear height, cob length, cob girth, kernels row per cob, 100 kernels weight and shelling percentage. This suggested the existence of differences between parents and hybrids for the characters under study.

In this experiment, out 45 crosses the crosses *viz.*, BLD 2 × BLD 103, BLD 2 × BLD 98 and WNC 40406 × BLD 125 were registered best three crosses based on significant heterobeltiosis for kernel yield per plant. While best three crosses based on standard heterosis were WNC 40406 × BLD 125, BLD 2 × BLD 103 and BLD 114 × IMR 113. Among the best three crosses for kernel yield per plant based on standard heterosis, WNC 40406 × BLD 125, and BLD 2 × BLD 103 were found significant with respect to standard heterosis as well as heterobeltiosis. The importance of standard heterosis is higher than heterobeltiosis therefore these three crosses were considered as best three crosses for kernel yield per plant. The results of heterosis analysis revealed that the crosses WNC 40406 × BLD 125, BLD 2 × BLD 103 and BLD 114 × IMR 113 were found as promising and need to be included for further evaluation.

The analysis of variance for combining ability revealed that specific combining ability variance for hybrids was highly significant for all the characters under study. Mean square due female was found significant for all the characters. Mean square due to line × tester interaction also found significant for most of the traits except plant height and ear height.

The *per se* performance hybrids were higher than parents in desirable direction for the traits like plant height, ear height, cob length, cob girth, kernels row per cob kernels per row and kernel yield per plant, which suggested the possibility, for existence of heterotic effects. In this trial, in respect to *per se* performance of parents, female parent BLD 114 and male parent IMR 113 were found to be superior for kernel yield per plant. Among the hybrids, WNC 40406 × BLD 125 and BLD 2 × BLD 103 manifested higher *per se* performance.

As per the estimates of *gca* effects the parent WNC 40406 was good general combiner for days to silking, anthesis silking interval (ASI), kernels per row and kernel yield per plant; BLD 2 was good general combiner for anthesis silking interval (ASI), cob length, kernels row per cob, 100 kernels weight, kernel yield per plant and shelling percentage. WNC 40080 was good general combiner for days to maturity, kernels row per cob and kernel yield per plant; BLD 125 was good

general combiner for kernel yield per plant. The estimates of *sca* effects showed that top five hybrids *viz.*, BLD 2 × BLD 103, WNC 40406 × BLD 125, BLD 114 × IMR 113, WNC 40456 × IMR 113 and BLD 114 × BLD 98 were exhibited maximum positive significant *sca* effect for kernel yield per plant and other contributing traits.

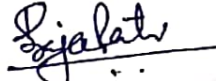
Based on the *gca* effect and overall performance, it can be concluded that the parental genotypes BLD 2, WNC 40080, WNC 40406 and BLD 125 were good general combiner for kernel yield per plant. Considering all the aspects *i.e.*, *per se* performance, heterosis and combining ability effects, the hybrids BLD 2 × BLD 103, WNC 40406 × BLD 125 and BLD 114 × IMR 113 for kernel yield per plant were found potential to generate desirable segregants for selection of superior plant. Therefore, these crosses may be exploited commercially after testing in wide range of environments. These crosses can also be used to throw off transgressive segregant in segregating generations for the improvement of yield and specific attributing traits.

**SARDARKRUSHINAGAR DANTIWADA AGRICULTURAL UNIVERSITY
CHIMANBHAI PATEL COLLEGE OF AGRICULTURE
SARDARKRUSHINAGAR – 385 506**

CERTIFICATE – I

Date: 14/09/2021

This is to certify that the thesis entitled, “ESTIMATION OF HETEROSIS AND COMBINING ABILITY IN MAIZE (*Zea mays* L.)” submitted for the degree of MASTER OF SCIENCE in the subject of GENETICS AND PLANT BREEDING is a record of bonafide research work carried by PATEL RAVIKUMAR DIPAKBHAI under my guidance and supervision and that no part of this thesis has been submitted for any other degree, diploma, associateship, fellowship or other similar title. The assistance and help received during the course of investigation have been fully acknowledged.



**(K. N. PRAJAPATI)
Major Advisor**



**(R. M. PATEL)
Minor Advisor**



**(J. M. PATEL)
Advisor**



**(G. K. CHAUDHARY)
Advisor**



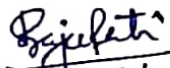
**(P. C. PATEL)
Advisor**

**SARDARKRUSHINAGAR DANTIWADA AGRICULTURAL UNIVERSITY
CHIMANBHAI PATEL COLLEGE OF AGRICULTURE
SARDARKRUSHINAGAR – 385 506**

CERTIFICATE – II

Date: 14/09/2021

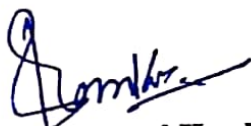
This is to certify that **PATEL RAVIKUMAR DIPAKBHAI**, Department of Genetics and Plant Breeding, C. P. College of Agriculture, S. D. Agricultural University, Sardarkrushinagar has made all corrections/modifications in the thesis entitled, “**ESTIMATION OF HETEROSIS AND COMBINING ABILITY IN MAIZE (*Zea mays* L.)**” submitted for the degree of **MASTER OF SCIENCE** in the subject of **GENETICS AND PLANT BREEDING** as suggested by the External Examiner and the Advisory Committee in the oral examination held on **8th SEPTEMBER, 2021**.



(K. N. PRAJAPATI)

**Major Advisor &
Assistant professor,**

**Vanbandhu Polytechnic in Agriculture,
S. D. Agricultural University,
Khedbrahma-383 255**

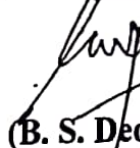


**Professor and Head,
Department of Genetics and
Plant Breeding,
C. P. College of Agriculture,
S. D. Agricultural University,
Sardarkrushinagar-385 506**



**Principal,
C. P. College of Agriculture,
S. D. Agricultural University,
Sardarkrushinagar-385 506**

APPROVED (Seal and Date)



(B. S. Deora) 14/09/21

**Director of Research and
Dean, Post-Graduate Studies,
S. D. Agricultural University,
Sardarkrushinagar-385 506**



ACKNOWLEDGEMENT

Pride, praise and perfection belong to almighty alone. So, first of all, I would like to offer my heartfelt salvation at the lotus feet of the supreme being for unbroken health and vigour, bestowed upon me and in whose faith, I was able to complete this task.

I consider, it my great fortune to have an opportunity to express my sincere and heartfelt gratitude towards **Dr. K. N. Prajapati**, Assistant Professor, Vanbandhu Polytechnic in Agriculture, S. D. Agricultural University, Khedbrahma and my Major Advisor, for his precious wealth of guidance, constructive criticism, ever present help, incessant encouragement and crisp scientific approach during the entire course of present investigation. His dynamism, vision, sincerity and motivation have deeply inspired me. He has taught me the methodology to carry out the research and to present the research works as clearly as possible. It was a great privilege and honour to work and study under his guidance. I am extremely grateful for what he has offered me. I am extending my heartfelt thanks to his wife, family for their acceptance and patience during the discussion; I had with him on research work and thesis preparation.

I emphatically express my venerable thanks to my minor advisor and eminent members of my Advisory Committee **Dr. R. M. Patel** (Minor Advisor), Assistance Research Scientist, Maize research station S. D. Agricultural University, Bhiloda, **Dr. J. M. Patel** (Committee Member), Associate Research Scientist, Wheat Research Station, S. D. Agricultural University, Vijapur and **Dr. G. K. Chaudhari** (Committee Member), Associate Professor, Department of Agril. Statistics, C. P. Collage of Agriculture, S. D. Agricultural University, Sardarkrushinagar **Dr. P. C. Patel** (Committee Member), Assistant Professor, Department of Genetics and Plant Breeding, C. P. College of Agriculture, S. D. Agricultural University, Sardarkrushinagar, who helped me to complete this manuscript with their suggestions.

I really feel short of words to express my heartfelt gratitude towards **Dr. R. M. Chauhan**, Honourable Vice Chancellor and **Dr. B. S. Deora**, Director of Research, S. D. Agricultural University for providing facilities for conducting the research work. I am cordially thankful to **Dr. S. D. Solanki**, Principle and Dean, C.

P. College of Agriculture, S. D. Agricultural University, Sardarkrushinagar who helped me to complete this thesis manuscript with their valuable suggestions.

My sincere thanks and gratitude to **Dr. S. D. Solanki**, Professor and head, my teachers **Dr. H. S. Bhadauria**, **Dr. L. D. Parmar**, **Dr. N. V. Soni**, **Dr. K. K. Tiwari**, **Dr. K. P. Pachhigar**, **Dr. A. K. Singh** and **Dr. P. C. Patel** for their persistent encouragement. I am also thankful to **Mr. M. M. Nayak** to help me throughout my research work.

It's privillage to my sincier thanks to **Mr. Bhaveshbhai Chaudhary**, other staff members **Kiritbhai**, **Dipakbhai**, **Ishvarbhai** and labours of Maize Research Station, S. D. Agricultural University, Bhiloda for their continuous help as and when required during by entire research work.

I am very thankful to **Dr. G. K. Chaudhary** for his guidance and providing help during the statistical analysis of experiment.

I will forever remain grateful to my batch mates **Kalpesh**, **Kavan**, **Avinash**, **Rutul** and **Kevan** for their direct and indirect help.

I owe my gratitude to **Alpeshbhai**, **Khatribhai** of the Department of Genetics and Plant Breeding and my immediate seniors **Dilipbhai**, **Pankajbhai**, **Chiragbhai**, and **Dhruvbhai** for their help during the investigation.

Thanks to all those who cannot find a separate name, but helped me directly or indirectly to achieve the goal.

I feel short of words to express my deep sense of reverence and indebtedness to my parents "**Shri Dipakbhai**" and "**Smt. Indiraben**" and my elder brother **Dr. Bhaumik** for their over helming moral support, affection, encouragement and patience. You encouraged me with your words. You did not allow me to give up and inspired me to start a new venture that flags success today.

Last but far from the least, I bow my head in extreme regards to the almighty goddess "**MAA UMIYA**", "**GURUMAHARAJ**" and "**LORD KRISHNA**" whose blessings enabled me to reach this destination.

Place: Sardarkrushinagar

Dated: 14th SEPTEMBER, 2021



(PATEL RAVIKUMAR D.)

CONTENTS

CHAPTER NO.	TITLE	PAGE NO.
I.	INTRODUCTION	1 - 3
II.	REVIEW OF LITERATURE	5 - 19
	2.1 Magnitude of heterosis	5
	2.2 Combining ability and gene action	11
III.	MATERIAL AND METHODS	21 - 32
	3.1 Location and climatic condition	21
	3.2 Geographic and edaphic details	21
	3.3 Experimental materials	21
	3.4 Crossing and selfing techniques	22
	3.5 Observations recorded	23
	3.6 Statistical analysis	25
IV.	RESULTS AND DISCUSSION	33 – 76
	4.1 Analysis of variance for experimental design	33
	4.2 <i>Per se</i> performance of parents and their F ₁ hybrids	35
	4.3 Magnitude of heterosis	38
	4.4 Combining ability analysis and gene action	56
	4.4.1 Analysis of variance for combining ability and gene action	58
	4.4.2 Estimation of general combining ability and specific combining ability effects.	60
V.	SUMMARY AND CONCLUSIONS	77 – 80
	REFERENCES	i - iv
	APPENDICES	A - E

LIST OF TABLES

Table No.	Title	Page No.
3.1	List of inbred lines used as parents	21
3.2	Experimental details	22
3.3	Crossing layout 9 × 5 Line × Tester in maize	23
3.4	Analysis of variance (ANOVA)	26
3.5	Analysis of variance for combining ability	29
4.1	Analysis of variance (mean sum of square) for kernel yield and its component characters in maize	34
4.2	Magnitude of heterobeltiosis (better parent) and standard heterosis over GAYMH 1 for days to tasseling and days to silking	40
4.3	Magnitude of heterobeltiosis (better parent) and standard heterosis over GAYMH 1 for anthesis silking interval (ASI) and plant height	42
4.4	Magnitude of heterobeltiosis (better parent) and standard heterosis over GAYMH 1 for ear height and days to maturity	44
4.5	Magnitude of heterobeltiosis (better parent) and standard heterosis over GAYMH 1 for cob length and cob girth	46
4.6	Magnitude of heterobeltiosis (better parent) and standard heterosis over GAYMH 1 for kernels row per cob and kernels per row	49
4.7	Magnitude of heterobeltiosis (better parent) and standard heterosis over GAYMH 1 for 100 kernels weight and kernel yield per plant	50
4.8	Magnitude of heterobeltiosis (better parent) and standard heterosis over GAYMH 1 for shelling percentage	52
4.9	Hybrids with significant heterosis in desirable direction for different traits in maize	55
4.10	Manifested of heterobeltiosis (HB) for other characters in five top ranking crosses for kernel yield per plant	57
4.11	Analysis of variance (mean sum of square) for combining ability, estimates of components of variance and their ratio for various characters in maize	59
4.12	Percent contribution of lines, testers and their interactions to total variance	60

4.13	The estimates of general combining ability (<i>gca</i>) effects of the parents for various characters in maize	63
4.14	The estimates of specific combining ability (<i>sca</i>) effects of the crosses for various characters in maize	66
4.15	Variance for general combining ability and specific combining ability along with gene action for different traits in maize	71
4.16	Classification of parents with respect to general combining ability for different characters in maize	72
4.17	Comparative study of most promising hybrids showing high specific combining ability (<i>sca</i>) effects for kernel yield per plant with various characters	73
4.18	Best performing parents and crosses on the basis of combining ability effects and mean performance for kernel yield per plant	74

LIST OF FIGURES

Figure No.	Title	After Page No.
4.1	Performance of males and females for kernel yield per plant	36
4.2	Performance of hybrid for kernel yield per plant	38
4.3	Percent contribution of lines, testers and their interactions to total variance	60
4.4	General combining ability effect of parents in maize for kernel yield per plant	64
4.5	Specific combining ability effects of hybrids for kernel yield per plant in maize	70

LIST OF PLATES

Plate No.	Title	After Page No.
1	Steps of crossing	24
2	Pictorial observation for cob of top five most promising heterotic hybrids and check (GAYMH 1) for kernel yield per plant	54

LIST OF APPENDICES

Appendix	Title	Page No.
A.	Weekly meteorological data recorded during the crop seasons (October-2019 to February-2020 and June-2020 to October-2020)	A
B.	Mean performance of parents and hybrids for various characters in maize	B - E

ABBREVIATIONS USED

%	:	Per cent
CD	:	Critical difference
CV	:	Coefficient of variance
cm	:	Centimeter
<i>et al.</i>	:	And associates
<i>etc.</i>	:	Etcetera
Fig.	:	Figure
g	:	Gram(s)
<i>i.e.</i>	:	That is
ha	:	Hectare
No.	:	Number
<i>viz.,</i>	:	Namely
GCA	:	General Combining Ability
SCA	:	Specific combining ability
S.Em.	:	Standard error of mean
S.E.	:	Standard error
Max	:	Maximum
Min.	:	Minimum
°C	:	Degree Celsius

INTRODUCTION



I. INTRODUCTION

Maize (*Zea mays* L.) is one of the most important cereal crop in the world after rice and wheat. It is one of the most versatile emerging crop having wider adaptability. Generally, maize is used as food for human and feed for animals. There is no cereal on the earth, which has such immense potential as maize therefore, it occupies the unique place as “Queen of cereals”. Being a C₄ plant, it is physiologically more efficient as well as resilient to changing climatic conditions and able to grow successfully throughout the world over a wide range of environmental conditions.

Maize belongs to the family *Poaceae* having chromosome number $2n = 2x = 20$. Mexico is accepted as the centre of origin of this crop. It was domesticated over the past 10,000 years from the grass teosinte (*Zea Mexicana* L.) in Central America and has been subject to cultivation and selection (Doebley *et al.*, 2006). Maize is a monoecious plant in that the reproductive organs are partitioned into separate pistillate (ear, female organ) and staminate (tassel, male organ) inflorescences. Maize is generally protandrous, that is the male spikelets mature earlier than the female pistillate. Within each male spikelets, there are usually two functional florets. Each floret contains three anthers and each plant produce about 3 to 5 million pollen grains. Each functional floret of the ear produces an ovary with elongated silk covered with hairs (trichomes). Pollen grain are very small, light in weight and easily carried or flown out by wind. The wind borne nature of the pollen grains and protendary leads to cross pollination.

However, the nutritional quality of maize protein is considered as poor, in which “Zein” protein of normal maize contain on an average about 2% lysine, which is less than one-half of the concentration recommended for human nutrition by the Food and Agriculture Organization (FAO) of the United Nations. Breeding maize crop with improved nutritional quality led to the discovery of the opaque-2 gene which is found to be associated with higher lysine and tryptophan content (Darshan and Marker, 2019). Nutritional composition per 100 g of edible portion of maize contain carbohydrate 71.88 g, protein 8.84 g, fat 4.57 g and fibre 2.15 g (Shah *et al.*, 2016).

Worldwide maize (*Zea mays* L.) plays a significant role in human and livestock nutrition. It accounts for 15 to 56 *per cent* of the total daily calories of the people in many developing countries. It is also a good feed for poultry, piggery, swine, fish and other domestic animals. It is utilized as raw materials for various industries for manufacturing starch, ethanol, acetic acid, glucose, synthetic rubber, dyes and resin, *etc.* Many by-products of maize like fructose syrup, maltodextrin, germ oil, germ meal fiber and gluten products which have applications in industries such as alcohol, textile, paper, pharmaceuticals, organic chemicals, cosmetics and edible oil.

It has great yield potential and attained the leading position among the cereals based on production as well as productivity. In India, maize ranks the third most important cereal crop with 9 million hectare area, the production of 30.25 million tonnes and 3100 kg/ha average productivity (Anonymous, 2020-21^a). The three largest maize producing states are Karnataka (3.96 MT), Madhya Pradesh (3.91 MT) and Telangana (3.00 MT) (Anonymous, 2019-20). While in Gujarat, it is widely grown in tribal areas of Panchmahal, Dahod, Sabarkantha, Aravalli, Banaskantha, Vadodara, Bharuch and Surat districts. In Gujarat, maize is cultivated in an area of 0.38 million ha with a production of 0.64 million tonnes and 1660 kg per ha average productivity (Anonymous, 2020-21^b).

Maize has been widely cultivated as a *kharif* crop in India, but with the evolution of new improved cross and assured availability of irrigation facility, it can be successfully grown during *rabi* in many parts of the country. The yield level of maize during the *rabi* season is considerably higher than that of *kharif* due to its higher water and fertilizer use efficiencies. In addition, the recent put more importance on the development of cross to meant for both the seasons has remunerated surplus in the terms of higher maize production and productivity in the country.

Heterosis and combining ability is a powerful tool for developing economically viable variety (Abuali *et al.*, 2012). Parental selection is very important in hybrid development. Line x Tester mating design developed by Kempthorne (1957), which provides reliable information on the general and specific combining ability effects of parents and their hybrid combinations were used to generate the information about the type of gene action involved in the expression of various quantitative characters. It is a prerequisite for developing a good and economically viable maize

hybrid. Information on the heterotic pattern and combining ability among maize genotypes is essential in maximizing the effectiveness of hybrid development. The effects of combining ability, both General Combining Ability (*gca*) and Specific Combining Ability (*sca*) introduced by Sparague and Tatum (1942) are important indicators of potential value for assessing inbred lines in hybrid combinations as a step to develop hybrid varieties in maize (Abdel-Moneam *et al.*, 2014). GCA is an effective tool used in selection of parents based on performance of the F₁ progenies. A high GCA value indicates higher heritability and less environmental effects. An elite parent with high *gca* effect indicates its large adaptability. GCA and SCA concept has become important to plant breeders because of its wide use in hybrids.

Keeping in view of all this fact, the present investigation on maize (*Zea mays* L.) has been undertaken with the following objectives:

1. To estimate the analysis of variances for yield and yield attributing traits
2. To estimate the magnitude of heterosis
3. To study the general combining ability and specific combining ability variances and effects for different traits

REVIEW OF LITERATURE



II. REVIEW OF LITERATURE

The available literature on maize pertaining to genetic aspect has been reviewed under the following headings.

2.1 Magnitude of heterosis

2.2 Combining ability and gene action

2.1 MAGNITUDE OF HETEROSIS

The phenomenon of heterosis has been proved to be the most important genetic tool in boosting the yield of self as well as cross pollinated crops, and is considered as the most important breakthrough in the field of crop improvement. Present investigation was planned to study the magnitude of heterosis and combining ability for different characters in maize (*Zea mays* L.). The available literature on these aspects is presented under the following head.

The term heterosis was coined by Shull (1914) and is now widely used in crop improvement programme. It refers to the phenomenon in which F_1 cross obtained by crossing two genetically dissimilar individuals shows increased or decreased vigour over the better or mid parent value. Exploitation of heterosis was first achieved in maize, which was followed subsequently in many crops like bajra, cotton, castor, sorghum etc. Later on, Fonseca and Patterson (1968) proposed a new term heterobeltiosis to described improvement of heterozygote in relation to better parent. As per Mather and Jinks (1971), heterosis as the amount by which the mean of F_1 progeny exceeds its better parent. Standard heterosis/ economic heterosis is refers to superiority of F_1 in comparison to adapted variety / hybrid. The term useful heterosis for standard heterosis was used by Meredith and Bridge (1972). Heterosis is complex phenomenon and no clear cut conclusive explanation is available to account for its manifestation.

The extent of heterosis expressed in hybrid depends upon the origin, relationship and compatibility between the parents involved. The hybrid develops from the crosses between diverse parents exhibit better hybrid vigour than those from closely related parents. According to East (1916) the amount of hybrid vigour expressed in F_1 is roughly proportionate to the genetic diversity between two parental lines involved in the development of hybrid.

For present study, the review of literature on maize crop in relation to heterosis for different characters is given below.

Heterosis for grain yield and its contributing characters in maize was studied by Alam *et al.* (2008). They evaluated genotypes was generated through 5×5 diallel mating analysis excluding reciprocal; the resulting 10 F_1 and their parents were grown in a randomized complete block design with three replications. The highest percentage of heterosis for grains per ear over mid parent as well as better parent was exhibited by the cross $P2 \times P3$. (85.83 and 46.17). Crosses $P1 \times P3$ (-1.66 and -6.83) and $P1 \times P5$ (-4.83 and -7.16) showed significant negative heterosis for days to maturity.

Bekele and Rao (2013) conducted study on heterosis in maize through line \times tester mating design. They observed twenty-four crosses from 6 lines and 4 testers in maize using randomized block design with three replications. The cross B-QPM-117 \times B-QPM-128 was the only hybrid that recorded positive and highly significant standard heterosis for grain yield over DHM-105 with a value of 31.95%. And the cross between B-QPM-114 \times B-QPM-118 showed the highest positive standard heterosis for oil content with the value of 0.71% and for grain yield per plot with value of 20% over the check Mandhuri.

Kage *et al.* (2013) studied heterosis in hybrids derived from new inbred lines in maize (*Zea mays* L.) through L \times T analysis by using ten lines and three testers. The resultant thirty cross and parents were evaluated for yield and yield related traits *viz.* days to 50% tasseling, days to 50% silking, plant height, ear height, days to 75% brown husk maturity, ear length, ear girth, number of kernel rows per ear, number of kernels per row, 100-grain weight and shelling percentage. Among thirty, three hybrids L2 \times KDMI-10, L1 \times KDMI-16 and L8 \times CI-5 showed significant positive standard heterosis over both EH434042 and 900M.

Rajesh *et al.* (2014) estimated heterosis for yield and yield attributing components in 45 crosses of maize developed through line \times tester design. They recorded out of 45 crosses, 42 crosses over better parent and 28 crosses over the standard check (DHM 117) significantly out yielded for grain yield. The crosses 5050 \times BML 10 (25.25%), 3511 \times BML 7 (23.97%), 1234 \times BML 10 (23.20%), 1234 \times BML 13 (23.03%) and 5050 \times BML 7 (21.03%) were recorded with high mean performance and standard heterosis over check DHM 117 for grain yield per plant and other yield contributing characters like number of kernels per row,

100-kernel weight, number of kernel rows per ear, ear girth and ear length. Thus, these crosses possess high heterosis which can be exploited commercially for higher yield in maize.

Rajitha *et al.* (2014) studied heterosis for grain yield per plant and its component traits. They revealed that almost all the line \times tester combinations registered significant positive heterosis over both mid and better parents for grain yield per plant. The crosses namely BM 256 \times BM 85 (134.12 and 131.81), BM 256 \times BM 143 (124.09 and 112.36), BM 3 \times RNBL 4351 (117.09 and 106.44) and BM 421 \times BM 85 (115.20 and 110.94) recorded a higher level of significant relative heterosis and heterobeltiosis for grain yield per plant.

Mir *et al.* (2015) studied heterosis in single crosses of inbred lines in maize (*Zea mays* L.) by using 10 \times 10 half diallel mating design. They evaluated 45 F₁ cross combinations, 10 parental lines and a check namely C₁₅. Among 45 crosses, NAI 113 \times NAI 123 for seed yield per plant also showed desirable heterosis for cob length, kernel rows per cob, kernels per row, cob diameter and 100-seed weight over the check. They also observed maximum positive heterosis for seed yield per plant in NAI 113 \times NAI 123 (89.94) followed by NAI 113 \times W3 (85.63), NAI 152 \times NAI 137 (81.95) and W5 \times NAI 116 (81.78) and for protein content, NAI 143 \times NAI 116 (36.30) showed the highest heterosis over the check.

Lahane *et al.* (2015) evaluated twenty-eight hybrids obtained by using an 8 \times 8 diallel crossing pattern excluding reciprocals for estimation of heterosis for quantitative traits in maize. They observed all the 28 F₁ hybrids, their parents along with standard check HQPM-1 for the characters *viz.* days to tasseling, days to silking, days to brown husk formation, plant height, number of ears per plant, ear weight, length of the ear, width of the ear, shelling (%) and 100-grain weight. Among these characters days to tasseling, days to silking, days to brown husk formation and plant height determine the earliness or lateness of a hybrid. In this study, they found that the magnitude of heterosis was varied from character to character. The standard heterosis for number of ears per plant was registered for the hybrid I-07-11-3-3 \times I-07-59-5 (28.57%). Maximum heterosis for ear height was manifested by hybrid I-07-59-5 \times I-07-7-1-1 (21.25%) followed by cross combinations I-07-11-3-3 \times I-07-65-18-3 (21.16%) and I-07-6-4-4 \times I-07-59-5 (18.39).

Ram *et al.* (2015) conducted heterosis studies in maize. They utilized ten maize inbreds as lines and eight testers for crossing in line \times tester mating design to generate eighty F₁ crosses. Total ninety-nine genotypes including eighty F₁ hybrids along with their eighteen parents and a check were evaluated in randomized block design. They observed Standard heterosis for grain yield ranged from -56.45 to 53.31 %. The maximum standard heterosis for grain yield was observed in the cross CM 141 \times CML 161 (53.31 %) followed by V335 \times CML 141 (34.71 %). The heterosis for grain yield over better parent ranged from -40.65 to 278.57 %. The maximum heterobeltiosis for grain yield was recorded in CM 141 \times CML 161 (278.57 %).

Reddy *et al.* (2015) have undertaken studies to estimate the heterotic, heterobeltiotic and standard heterotic effects of 11 characters of 45 maize hybrids developed by crossing in diallel fashion. They recorded five crosses *viz.*, BML 15 \times BML 2910 (42.79), BML 6 \times BML 2 (27.80), BML 2782 \times BML 7 (24.71), BML 7 \times BML 3044 (20.50) and CM 211 \times BML 7 (12.52) were identified as potential hybrids with standard heterosis for grain yield over better yielding commercial hybrid check DHM 117.

Heterosis for grain yield and its component traits in maize was studied by Habtamu Zeleke (2015) by using 8 \times 8 half diallel cross analysis. Heterosis estimation was carried out using one standard check (BH 660) for days to maturity, ear length, ear diameter, rows per ear, kernels per Row, 1000 kernel weight, grain yield. They estimated highest percentage of heterosis for grain yield over the standard check (BH 660) was the cross AL-165 \times AL-186 (29.3%) followed by crosses AL-165 \times AL99-AL-119 (28.3 %), AL-183 \times AL99-AL-119 (21.7 %) and AL-165 \times AL99-AL-270 (20.8 %) and maximum heterosis for grain yield over the better parent was AL-165 \times AL-186 (113.3%) followed by crosses AL-165 \times AL99-AL-119 (89.8 %).

Heterosis studied in maize by evaluating twenty-one F₁ crosses developed through 7 \times 7 diallel fashion (excluding reciprocals) mating design by Matin *et al.* (2016) for days to fifty *per cent* tasseling, days to fifty *per cent* silking, anthesis silking interval, plant height, ear height, days to maturity, cob length, cob diameter, thousand seed weight and yield. Heterosis for grain yield over the check ranged from -56.59 to 15.60% and the maximum heterosis was recorded in WL1 \times

WL6 (15.60 %) when BHM 7 used as check. Only one hybrid WL2 \times WL7 (-0.22) recorded negative heterosis against BHM 7 for days to maturity.

Heterosis for grain yield and quality traits in quality protein maize was studied by Patel and Kathiria (2016). They evaluated fifty-five genotypes generated through 10 \times 10 diallel mating analysis excluding reciprocal; involving ten maize inbred line. They reported that analysis of variance exhibited highly significant for all the traits *viz.*, kernel yield per plant, oil content, protein content and tryptophan content. Among all the cross, GWQPM6-3 \times GWQPM 11, GWQPM5-1 \times GWQPM 26-3 and GWQPM47-4 \times GWQPM46-2 for kernel yield per plant, GWQPM 55-2 \times GWQPM 46-2 for oil content, GWQPM46-2 \times GWQPM17-1 for protein as well as tryptophan content and GWQPM6-3 \times GWQPM 11 for lysine content gave a consistent performance in all the environment.

Gami *et al.* (2018) conducted study on maize by using six lines and five testers which were crossed in line \times tester mating design to produce 30 single cross hybrids. They evaluated the hybrids, their parents along with standard check GAYMH 1 in Randomized Block Design, for yield and attributing traits. Based on the heterobeltiosis and standard heterosis estimated they found best crosses, Z 4884 \times VL 1032 (58.44% and 88.99%) and BLD 250 \times BLD 46 (54.84% and 124.63%), respectively for kernel yield per plant. While WNC 18242 \times VL 1032 recorded significant better parent heterosis for days to silking (-8.77), ASI (-66.67) and days to dry husk (-6.17) as compared to its best parent for flowering and maturity traits.

Nandhitha *et al.* (2018) studied heterosis in 50 single cross hybrids of maize derived through line \times tester analysis. Among the fifty hybrid combinations they identified single cross hybrid N10-65-3 \times E.No.8 d as the best hybrid for grain yield and other major yield contributing traits followed by the hybrid N 44 \times UMI 1221. The best experimental cross, on the basis of standard heterosis for grain yield per plant, was N10-65-3 \times E.No.8 (16.33) followed by N 44 \times UMI 1210 (14.29) and N10-153-1-2 \times E.No.4 (12.68) that yielded more grain yield, respectively over standard check hybrid CO-6.

Reddy *et al.* (2018) studied on heterosis for grain yield traits in maize. They were used 6 inbreds as parents to make crosses in full diallel fashion to obtain total 30 possible F₁ hybrids. They reported that 13 hybrids show significant positive heterosis against the better parent. The range of heterobeltiosis was

from - 28.84 *per cent* (UMI 122 × UMI 213) to 39.59 *per cent* (UMI 122 × UMI 66). Heterosis over standard check was observed in positive direction for 15 hybrids. The magnitude of standard heterosis varied from -24.86 *per cent* (UMI 122 × UMI 112) to 30.01 *per cent* (UMI 122 × UMI 66).

Sandesh *et al.* (2018) carried out heterosis studies for yield and its component traits in maize. They evaluated thirteen genotypes which comprised of eleven inbreds as lines, two inbreds as tester and twenty-two hybrids which were developed through Line × Tester mating design. Among the twenty-two hybrids, N14 × UMI 1200-7-26-1-6-1 showed desirable standard heterosis percentage over the both checks CO 6 and NK 6240 for grain yield (26.73 and 51.01 respectively) and other important yield attributing traits.

Shrestha *et al.* (2018) studied Standard heterosis for grain yield in maize hybrids. They found the maize hybrids, RML-4 × RML-7, RML-5 × NML-1, NML-2 × RML-6, RML- 6 × RML-7, RML-5 × RL-47, RML-8 × RL-47, RML-5 × RML-8, NML-1 × RML-17, RML-7 × RML-18, RML-6 × RML-18 and RML-5 × NML-1 produced high heterosis (greater than 40%) indicating these hybrids are superior for commercial cultivation.

Darshan and Marker (2019) studied heterosis in maize through line × tester analysis by using six lines and two testers. The resultant twelve crosses were evaluated for seventeen characters *viz.*, days to fifty *per cent* tasseling, days to fifty *per cent* silking, anthesis silking interval, days to maturity, plant height, cob height, cob length, tassel length, cob diameter, number of cobs per plant, number of kernel rows per cob, number of kernels per row, 100-seed weight, grain yield per plant, protein content, oil content and starch content. They revealed that among the twelve cross the crosses LM 13 × IC32809, DMR N21 × IC 32809 and LM 13 × IC 31899 exhibited significant positive heterosis for grain yield and other yield attributing characters like 100 seed weight (test weight), number of grains per row, number of grain rows per cob, ear diameter and ear length. While some cross TSK 194 × IC 32809 and DMRN21 × IC 31899 exhibited the highest significant positive economic heterosis for protein content, starch content and oil content.

Kumar *et al.* (2019) studied heterosis in maize through line × tester analysis by using two male testers and thirty female inbred lines. They evaluated these sixty crosses along with fifteen parents and two commercial checks, *viz.*, Bio 9544 and Palam Sankar Makka-2. Among the crosses, two cross combinations TNAU/CBE

83 × BAJIM 08-27 and CML-292 × BAJIM 08-27 were identified as the best hybrid combinations as they showed highly significant heterosis and their per se performance more than that of the best check Bio-9544.

Aswin *et al.* (2020) was conducted study for heterosis using 16 parents and 28 F₁ cross combinations of maize hybrids in a Line × Tester mating design. They reported the standard Heterosis ranged from -21.62 to 4.51, -11.49 to 16.95 and -18.41 to 3.33 for cob weight, 100 kernel weight, and single plant yield, respectively. Among the hybrids, CBM-DL-360 × UMI 1200, CBM-DL-435 × UMI 1230, and CBM-DL-448 × UMI 1230 exhibited positive significant standard heterosis.

2.2 COMBINING ABILITY AND GENE ACTION

Ability of a parent to combine well and to produce promising segregants in succeeding generation is an important criterion in selecting parents for successful hybridization programme. The development of plant breeding strategy hinges mainly on the support provided by genetic information on the inheritance and behaviour of major quantitative characters associated with yield, quality or any economic trait of concern to the breeder.

The concept of general and specific combining ability was proposed by Sprague and Tatum (1942). The general combining ability (*gca*) is define as average performance of line in a series of crosses whereas, the specific combining ability (*sca*) is the deviation in the performance of specific cross predicted on the basis of *gca* effects. The general combining ability includes additive genetic variance and additive × additive interaction, while specific combining ability includes non additive portion arising from dominance and epistatic deviation. Griffing (1956^b) suggested a model to show that variance for GCA involved mostly additive genetic effects whereas, SCA resulted from dominance and epistatic components of genetic variance. Henderson (1952) defines *sca* in terms interactions that were due to the consequences of intraallelic interaction (dominance) and also due to inter-allelic (epistasis) gene action.

Estimation of combining ability in different crops has been reported by several workers using top crosses (Jenkins and Brunson, 1932), diallel cross analysis (Griffing, 1956^{a,b}) and line × tester analysis (Kempthorne, 1957).

The available literature pertaining to combining ability for different characters of maize pertinent to the present investigation are given here.

Alam *et al.* (2008) studied combining ability of maize for plant height, ear height, days to silking, days to maturity, grain per ear and 1000-grain weight in a diallel cross involving five maize inbred lines. They estimated additive genetic additive gene action for days to maturity, grains per ear and 1000-grain weight whereas non-additive gene action was involved in plant height, ear height, and days to silking. The inbred lines P2 (12.51) and P5 (6.69) were found to be best general combiner for 1000-grain weight. The crosses P1 \times P4 (16.44), P2 \times P3 (18.05) and P4 \times P5 (16.22) showed significantly positive *sca* effects for 1000-grain weight.

Senthil Kumar and Bharathi (2009) investigated relationship between *gca* and *sca* effects in maize. They were evaluated five lines and three testers of maize and resultant fifteen hybrids from line \times tester mating design. Among the lines, SW-99-L-8001-24 (8.15), SW-99-D-1005-128 (3.76), SW-99-L-3001-21 (1.11) and the tester Attur local (11.46) possessed desirable *gca* effects for grain yield per plant. Among the hybrids ML - 47 \times Attur local (27.18), SW-99-L-3001-21 \times Chidambaram local (25.07), SW-99-L-8001-24 \times African tall (19.47) and SW-99-D-1005-128 \times African tall (16.15), shows desirable *sca* effects for grain yield per plant.

Amiruzzaman *et al.* (2013) studied combining ability of maize for grain yield, days to tasseling, days to silking, plant height and ear height in a diallel cross involving seven elite maize inbred lines. They estimate predominance of non-additive gene action was observed for all the traits. They reported that parent Tzi 24 was the best general combiner for higher grain yield coupled with dwarfness and CML 487 was also good general combiner for grain yield and lateness in maturity by showing desirable significant *gca* effects. While the cross combinations CML 487 \times Tzi 24, CLG 1837 \times CML 480, CML 223 \times Ki 42 and Ki 42 \times Tzi 24 possessing significant desirable *sca* effects for grain yield, days to tasseling, and days to silking might be used for obtaining high yielding hybrids.

Habtamu Zeleke (2015) studied combining ability for yield and yield components in Maize (*Zea mays* L.) for days to maturity, ear length, ear diameter, rows per ear, kernels per Row, 1000 kernel weight and grain yield. They evaluated 28 F₁ hybrids developed from a cross between 8 inbred lines in a diallel fashion, the parental lines and one standard check BH 660. They observed the variance due to GCA and SCA were significant indicating role of both additive and non-additive types of gene action for controlling the traits. For grain yield the parents, AL-183

(0.459), AL99-AL-119 (0.185), AL-165 (0.165) and AL99-AL-270 (0.048) had good general combining ability. Among the hybrids *viz.* AL-165 × AL-186 (2.45) shows desirable specific combining ability effects for grain yield followed by AL99-AL-270 × AL99-AL-79 (2.13).

Lahane *et al.* (2015) evaluated twenty-eight cross combinations along with eight selected lines for their combining ability in maize. Based on the ratio of GCA/SCA variance they observed that all the traits *viz.*, days to tasseling, days to silking, days to brown husk formation, plant height, number of ears per plant, ear weight, length of ear, width of ear, shelling (%), 100-grain weight were controlled mainly under non additive genes. They found none of the parents as a good general combiner for all the yield attributing traits. However, parents I-07-11-3-3 (7.39), I-07-65-18-3 (4.66) and I-07-6-4-4 (2.01) for ear weight, parents I-07-11-3-3 (0.60), I-07-59-5 (0.72) and I-07-7-1-1 (0.66) for length of ear and parents I-07-13-1-3 (3.52) and I-07-59-5 (0.92) for width of ear were proved to be good general combiners. Out of 28 F₁'s hybrid combinations, I-07-11-3-3 × I-07-59-5 (0.475) and I-07-11-3-3 × I-07-65-18-3 (0.209) showed significant positive *sca* effects for number of ears per plant. These two crosses I-07-11-3-3 × I-07-59-5 (0.475) and I-07-11-3-3 × I-07-65-18-3 (0.209) showed the highest positive *sca* effect for number of ears per plant.

Ram *et al.* (2015) estimated combining ability and gene action in maize by line × tester method. They evaluated ninety-nine genotypes comprising of 80 F₁ hybrids along with their 18 parents and a check were evaluated in randomized block design to estimate the General Combining Ability (GCA), Specific Combining Ability (SCA). They reported both, non-additive and additive types of gene action were responsible to influence the expression of traits among the crosses. Among the lines, CM 141, V335 and V351 were found as the superior general combiner and the cross CM 141 × CML 161 was found among the best cross with desirable *sca* effect for grain yield and other important traits.

Suthamathi and Nallathambi (2015) studied combining ability for yield and yield attributing traits in maize (*Zea mays* L.). They evaluated ninety one cross combinations along with 14 parental lines. The ratio of GCA:SCA variance showed the predominance of non-additive gene action for important yield contributing traits *viz.*, cob length, cob girth, number of kernel rows, number of seeds per row, grain yield per plant and relative water content. They observed that the parents

UMI 285, UMI 1085, UMI 1058 and UMI 233 were found to be superior parents to develop hybrids with enhanced yield through improving yield related characters and UMI 233 × UMI 1069 and UMI 233 × UMI 1096 possessed desirable *per se* performance and *sca* effects for grain yield per plant, kernel rows per cob and number of kernels per row.

Kumar *et al.* (2016) studied combining ability analysis for grain yield and other agronomic traits in maize (*Zea mays* L.). They evaluated twelve parents along with their 132 F₁'s including reciprocals. They found preponderance of additive gene action for most of the traits studied except for the grain yield per plant, number of kernel rows per ear, number of kernels per row and ear length which showed preponderance of non-additive gene action. Among twelve parental lines, HKI 193-1 and VQL 1 were found to be good general combiner for 100 kernels weight (1.17, 0.78), grain yield per plant (4.33, 5.01) and grain yield per plot (0.08, 0.07), respectively. Parent VQL 1 was also found to be best general combiner for all traits studied including grain yield (5.01). Total 79 cross combinations were possessing significant desirable *sca* effects for grain yield. The top cross combinations possessing significant desirable *sca* effects for grain yield per plant were NAI 147 × CML 152-3058 (15.94), SE 547 × BLSB-RIL-92 (12.95), CM 142-393-1 × SE 547 (6.27) and SE 547 × VQL 1 (2.92) which may be used for obtaining high yielding hybrids in maize.

Patel and Kathiria (2016) evaluated fifty-five genotypes generated through 10 × 10 diallel mating design excluding reciprocal. They reported that analysis of variance exhibited highly significant for all the traits *viz.*, kernel yield per plant, oil content, protein content and tryptophan content. The ratio of GCA and SCA variance was less than unity thereby indicating the preponderance of non-additive gene action in the expression of all the characters studied. Parents GWQPM 6-3, GWQPM 47-4 and GWQPM 11 for kernel yield, GWQPM 6-3, GWQPM 55-2 and GWQPM 47-4 for oil content, GWQPM 40-3 and GWQPM 17-1 for protein content as well as tryptophan content, GWQPM 5-1, GWQPM 40-3 and GWQPM 17-1 for lysine content were identified as most desirable parents due to having good GCA in all environments. They recorded significant and desirable *sca* effects in GWQPM 6-3 × GWQPM 17-1, GWQPM 6-3 × GWQPM 11, GWQPM 5-1 × GWQPM 26-3, GWQPM 47-4 × GWQPM 46-2, GWQPM 46-2 × GWQPM 17-1, GWQPM 40-3 × GWQPM 22-5 and GWQPM 26-3 × GWQPM 17-1 for kernel

yield, GWQPM 5-1 \times GWQPM 26-3, GWQPM 55-2 \times GWQPM 46-2 and GWQPM 6-3 \times GWQPM26-3 for oil content and GWQPM 6-3 \times GWQPM 22-5 and GWQPM 46-2 \times GWQPM 17-1 for protein, tryptophan and lysine content, respectively.

Yerva *et al.* (2016) conducted combining ability studies for yield. They evaluated 30 single cross hybrids developed using 6 \times 6 full diallel method including reciprocal. They observed presence of high magnitude of SCA variance than GCA variance for all traits. The ratio of additive to dominance variance was lower than unity for all traits, which indicates preponderance of non additive variance than additive variance. Among the parents, inbred line namely UMI 133 (2.38), UMI 66 (2.07) and UMI 213 (1.04) was found to be the best parent for grain yield and hybrids *viz.*, UMI 66 \times UMI 112, UMI 112 \times UMI 213 and UMI 122 \times UMI 133 showed significant and favourable *sca* effects for majority of the characters including grain yield per plant.

Bharti *et al.* (2017) carried out combining ability analysis for grain yield and its contributing traits in maize. They used 15 inbred line and 3 tester parents to developed 45 hybrids using line \times tester cross analysis in three environments. In this study GCA and SCA indicating that both additive and non-additive gene actions were important in the inheritance of characters. Among the parents *viz.* EIQ 132, EIQ 134, EIQ 135, EIQ 136, EIQ 138, EIQ 144 and EIQ 145 were good general combiners for grain yield and majority of traits over the environments. Among the crosses *viz.* EIQ 137 \times EIQ 102, EIQ 143 \times EIQ 103, EIQ 140 \times EIQ 101, EIQ 131 \times EIQ 101 and EIQ 141 \times EIQ 103 were identified as potential ones for yield and yield components based on high *sca* effects along with high per se performance.

Kuselan *et al.* (2017) estimated combining ability for yield and its component characters in maize. They carried out line \times tester analysis, which involves forty-two lines and three testers in maize. They observed that variance due to SCA was higher than GCA, which indicating the predominance of non-additive type of gene action for all characters. Among the lines, RML 12 and the tester, RML 48 was identified as the good general combiner for most of the yield contributing traits. Among the hybrids, RML12 \times RML48 was found to be the superior with positive significant *sca* effects for grain yield, cob girth, number of grain rows per cob and number of grains per cob.

Gami *et al.* (2018) evaluated thirty crosses developed by crossing 6 line with 5 tester in maize. The results indicated that non-additive gene action found to be predominant for the inheritance of flowering traits, kernel yield, cob yield, cob girth and cob length. They reported BLD 250, BLD 221, BLD 210 and BLD 107 reported as best general combiners for yield and attributing traits. The cross Z 488-4 \times VL-1032 (27.32) and BLD-250 \times BLD-46 (23.36) with good specific combining ability for kernel yield per plant. Cross WNC 18242 \times VL 1032 reported desirable SCA for flowering and maturity traits *viz.*, days to silking (-3.40), ASI (-1.10) and days to dry husk (-3.90).

Anilkumar and Lohithaswa (2018) studied 108 F₁ crosses developed through crossing between twenty-seven lines and four testers by line \times tester mating design. The resultant 108 crosses were evaluated for six characters *viz.*, anthesis-silking interval (ASI), ear length (cm), ear circumference (cm), kernel rows per ear, kernels per row and grain yield per plant. They found preponderance of non-additive gene action for these traits. They observed that no single line or tester was desirable combiner for all the traits, but lines such as MAI 1-21-4 (-0.56), MAI 3-2-4-1 (-0.56) and MAI 1-17-2 (-0.47) were desirable general combiners for ASI, while MAI 1-41-3 (41.24), MAI 1-97-3 (27.27) and MAI 1-17-11 (23.70) were desirable general combiners for grain yield per plant. Similarly, hybrids such as MAI 1-31-2 \times NAI 137 (-1.27), MAI 1-21-4 \times CM 202 (-1.21) and MAI 1-41-3 \times NAI 137 (-0.85) were desirable specific combinations for ASI, MAI 1-58-3 \times NAI 137 (83.52), MAI 3-2-5 \times MAI 105 (78.20) and MAI 1-17-2 \times MAI 105 (69.62) were desirable specific combinations for grain yield per plant.

Combining ability analysis for grain yield and its component traits was studied by Nandhitha *et al.* (2018) by using ten lines and 5 testers through L \times T matting design and they revealed that non additive gene action was prevalent for most of the yield traits. Among the parents, the lines *viz.*, N67 (13.43), N10-65-3 (-1.71) and N10-153-1-2 (2.12) and the tester UMI 1210 (1.39) exhibited higher positive *gca* effects and found to be good general combiners among the parents. Most of the crosses which showed significant *sca* effects also showed desirable standard heterosis. Among the hybrids, N10-65-3 \times E.No.8 was found to be the best hybrid with desirable SCA for grain yield per plant along with other yield contributing traits *viz.*, cob weight and hundred seed weight.

Murtadha *et al.* (2018) studied combining ability analysis in maize (*Zea mays* L.). In this study, they evaluated fifteen F₁ hybrids which are developed by using 6 × 6 diallel mating design excluding reciprocals. They observed high significant GCA and SCA which revealed the importance of both additive and non-additive genetic actions. They found that KSU 6-47 had highest significant GCA for grain yield under E1 and E2 (0.35 and 0.53, respectively). Highly significant positive *gca* effect of leaf area index was found in CML 424 under all three environments E1, E2 and E3 (100.48, 90.63 and 106.54, respectively) and highly significant GCA for 1000-kernel weight under E2 and E3 with values of 77.77 and 48.63, respectively. While cross KSU 6-47 × KSU 3-69 with high SCA for grain yield (0.91, 0.96 and 1.48) and 1000-kernel weight (98.50, 99.70 and 142.00) under all the environments.

The experiment on combining ability and gene action studies for yield and its related traits in maize was performed by Rajesh *et al.* (2018). They evaluated forty-five hybrids which were generated from crossing fifteen lines with three testers in line × tester design. The estimates of variance due to SCA were higher than GCA variance indicating the predominance of non-additive gene action for all the characters *viz.*, days to fifty *per cent* tasseling, days to fifty *per cent* silking, days to maturity, plant height, ear height, ear length, ear girth, number of kernel rows per ear, number of kernels per row, 100-kernel weight and grain yield per plant. Among the female lines, five lines BM 5050 (20.62), BM 1234 (18.17), BM 3511-2 (16.07) and BM 3521 A-2 (12.93) and two testers *viz.*, BML 10 (5.74) and BML 7 (0.98) recorded desirable GCA values and found to be good general combiners for grain yield per plant. Among which BM 3521-3-1 × BML 10 (27.09) recorded the highest positive significant *sca* effect followed by 3530-3 × BML 7 (20.06), CML 409 × BML 13 (19.64), 5076 × BML 7 (16.78) and 5059 × BML 7 (14.62) for grain yield per plant.

Sandesh *et al.* (2018) carried out studies combining ability analysis for yield and its component traits in maize using twenty-two hybrids which were developed through Line × Tester mating design. The results showed that the predominance of non-additive gene action was observed for all the traits. The estimates of *gca* effects showed that the parents UMI 1230-2-70-9-6-1 (4.99) between the two testers and N 14 (23.81), N 42 (19.10), N 104 (7.97), N 285 (7.68) and N 107 (2.38) among the lines possessed highly significant positive *gca* effects for grain yield per plant.

Among the twenty-two hybrids, the hybrid N 14 × UMI 1200-7-26-1-6-1 manifested significant high *sca* effects.

Chandel *et al.* (2019) studied combining ability in maize (*Zea mays* L.) for twenty-two crosses were generated through crossing 11 newly developed yellow maize inbreds with 2 diverse testers using line × tester mating design. The ratio of GCA/SCA for all the studied traits indicated the preponderance of non-additive gene effects in the inheritance of these traits. Among female inbred lines, KI-13-182 had significant *gca* effects for grain yield per plant (21.64) and yield component traits like shelling percentage (3.24), ear length (2.37), ear diameter (1.07), number of kernels per row (3.84) and 1000-kernel weight (8.68), indicated that best general combiner for these traits, while in male parent KI 58 (HKI-1105) was the best general combiner for yield contributing traits *viz.*, ear length (0.47), ear diameter (0.19), number of kernel rows per ear (0.59), number of kernels per row (1.02) and 1000-kernel weight (10.05). Out of 22 crosses, six crosses have shown significant positive *sca* effects for grain yield per plant. The cross KI-13-315 × KI 58 (HKI 1105) (27.50) followed by KI 7C × KI 57 (CM 212) (18.98), KI-13-182 × KI 58 (HKI 1105) (15.93), KI-36A × KI 57 (CM 212) (11.73), KI 21A × KI 58 (HKI 1105) (9.28) and KI-13-194 × KI 57 (CM 212) (8.58) showed high positive significant effect for this trait.

Patel *et al.* (2019) studied on gene action and combining ability analysis for kernel yield and its attributing traits. Eight maize (*Zea mays* L.) genotypes were crossed in a half diallel mating design to generate a total of twenty- eight crosses. In present study the low ratio (< 1.0) of GCA to SCA variance for sixteen traits indicated that non-additive gene action was predominant in the expression of yield and component traits. The analysis for *gca* effects revealed that four parents BLD-11 (5.19), CML-338 (4.28), VL-1032 (1.68) and VL-109178 (1.25) were found good general combiners due to positive *gca* effects. The hybrids CBE-98 × MRCN-3 (27.57), CBE-98 × BLD-11 (23.16) and CBE-26 × BLD-11 (21.20) showed desirable *sca* effects for kernel yield per plant.

Kumar *et al.* (2019) evaluated sixty crosses developed by two male testers and thirty female inbred lines in line × tester design. The result shows ratio of $\sigma^2_{gca}/\sigma^2_{sca}$ was less than one for all the traits except plant height. This indicated that the preponderance of non-additive gene effects in the inheritance of these traits. Among the parent female inbred lines, TNAU/CBE-83 was observed to be a good general

combiner for grain yield, cob length, biological yield and protein content and tester BAJIM 08-26 was found to be a good general combiner for 1000 grain weight, biological yield and protein content whereas tester BAJIM 08-27 for grain yield, cob girth, harvest index, plant height and cob placement. Out of the 60 crosses *viz.* CML-292 \times BAJIM 08-27 (31.11) followed by BAJIM-15-11 \times BAJIM 08-26 (23.07), BAJIM-13-01 \times BAJIM 08-26 (22.47) and TNAU/CBE-83 \times BAJIM 08-27 (14.56) showed high significant *sca* effect for grain yield.

The experiment on combining ability and gene action was conducted by Aswin *et al.* (2020). The analysis showed that the ratios of SCA and GCA variance were high for all the characters studied revealed the preponderance of non-additive gene action. Among the parents CBM-DL-448, CBM-DL- 435, CBM-DL- 360 and UMI1230 were found to be good general combiners and the hybrids *viz.*, CBM-DL-360 \times UMI1200, CBM-DL435 \times UMI1230, and CBM-DL- 448 \times UMI1230 recorded positive *sca* effect and for desirable yield-related traits.

MATERIAL AND METHODS



III. MATERIAL AND METHODS

3.1 LOCATION AND CLIMATIC CONDITION

The present investigation on " **Estimation of heterosis and combining ability in maize (*Zea mays* L.)**" using 9×5 line × tester mating design was carried out to derive information on magnitude of heterobeltiosis, standard heterosis, general combining ability (GCA) of parental lines and specific combining ability (SCA) of hybrids in maize (*Zea mays* L.). The field experiment was conducted at Maize Research Station, Sardarkrushinagar Dantiwada Agricultural University, Bhiloda, during *rabi* 2019 and *kharif* 2020.

3.2 GEOGRAPHIC AND EDAPHIC DETAILS

The Maize research station is located in Agro-climatic zone-IV (North Gujarat) of Gujarat state. Geographically, Bhiloda is situated at 23° 76' North Latitude and 73° 24' East Longitude with an altitude of 259 meters above the mean sea level. The soil of experimental site is sandy to loamy sand. The climate of this region is sub-tropical monsoon type with semi-arid condition with an average temperature of 35 °C.

3.3 EXPERIMENTAL MATERIALS

Forty-five crosses were made during *rabi* 2019 using the 9 lines and 5 testers. The parents were obtained from Maize Research Station, SDAU, Bhiloda. Thus, the experimental materials consisted 60 entries comprising of 45 crosses, 14 parents and one standard check hybrid GAYMH 1 were evaluated in *kharif* 2020. The list of female and male parents used in crossing programmer is given with its pedigree in Table.3.1

Table 3.1 : List of inbred lines used as parents

	Name of genotype		Pedigree	Source
[A]	Lines (Female parents)			Maize Research Station, Sardarkrushinagar Dantiwada Agricultural University, Bhiloda (Aravalli)
	01	BLD 2	11-1-6-1-1	
	02	BLD 109	11-11-8-1-2	
	03	BLD 114	11-12-2-1-1	
	04	WNC 40080	SUP-N09-160-7	
	05	WNC 40324	CML31 POB 27 C5 HC 117-1-4-B	
	06	WNC 40406	TL02 A118432-12	
	07	WNC 40456	PC 123	
	08	WNC 52313	KDM 1156	
	09	WNC 52646	DMRSC 1	

Continue...

[B]	Testers (Male parents)			
	10	VL 109178	P31C4S5B-23-##-4-B*7-4-BBB	
	11	BLD 98	11-11-2-1-2	
	12	BLD 103	11-11-4-2-2	
	13	BLD 125	11-12-8-1-2	
	14	IMR 113	-	
[C]	Standard check			
	15	GAYMH 1	CML-307 × GYL-11	AAU, Anand

Table 3.2 : Experimental details

1.	Experimental title	:	“Estimation of heterosis and combining ability in maize (<i>Zea mays</i> L.)”
2.	Mating design	:	Line × Tester
3.	Experimental design	:	Randomized Blocked Design (RBD)
4.	Number of replication	:	3 (Three)
5.	Spacing	:	60 cm × 20 cm
6.	Number of inbred lines	:	14 (Fourteen) (9 line × 5 Tester)
7.	Year and season of experiment	:	Crossing season: <i>Rabi</i> 2019-20 Experiment season: <i>Kharif</i> 2020
8.	Number of genotypes	:	60 (14 parents and 45 crosses with 1 standard check)
9.	Length of row	:	4.0 m
10.	Location	:	Maize Research Station, S. D. Agricultural University, Bhiloda
11.	Agronomical practice	:	As per recommendations
12.	Plant protection measures	:	As per recommendations and requirement

3.4 CROSSING AND SELFING TECHNIQUES

Crossing block was raised in *rabi* 2019-20 at the Maize Research Station, S. D. Agricultural University, Bhiloda. Crossing was carried out in line × tester mating design. Cross and selfed seeds were harvest and threshed separately to prevent contamination.

Table 3.3 : Crossing layout 9 × 5 Line × Tester in maize

Female Parents		Male Parents				
		VL 109178	BLD 98	BLD 103	BLD 125	IMR 113
	
BLD 2	.	×	×	×	×	×
BLD 109	.	×	×	×	×	×
BLD 114	.	×	×	×	×	×
WNC 40080	.	×	×	×	×	×
WNC 40324	.	×	×	×	×	×
WNC 40406	.	×	×	×	×	×
WNC 40456	.	×	×	×	×	×
WNC 52313	.	×	×	×	×	×
WNC 52646	.	×	×	×	×	×

• indicates selfing while × indicates direct crosses.

3.5 OBSERVATIONS RECORDED

Five plants were randomly selected and tagged from each net plot of parents, standard check and F₁'s in all the replications to record the observations. The characters analyzed using their mean values. The methodology used for recording the observations for different characters in three replications is described as under .

3.5.1 Days to tasseling

The number of days from date of sowing to date of initiation of tassel in the fifty per cent plants per plot was recorded.

3.5.2 Days to silking

The number of days from date of sowing to date of emergence of silk in the fifty per cent plants per plot was recorded.

3.5.3 Anthesis Silking Interval (ASI)

The difference between days to tasseling and days to silking for each genotype was taken as Anthesis Silking Interval (ASI).

3.5.4 Plant height (cm)

The height of each tagged and randomly selected five plants per plot was measured in centimeter from the ground level to the base of tassel at the time of maturity. The mean plant height per plot was work out.

3.5.5 Ear height (cm)

The ear height of each tagged and randomly selected five plants were measured in centimeter from the ground level to the base of the upper most ear at the time of maturity. The mean ear height per plot was work out.

3.5.6 Days to maturity

The number of days was taken for drying husk from the date of sowing in 80 per cent plants per plot.

3.5.7 Cob length (cm)

The ears from the five randomly selected and tagged plants were taken for measuring the length of ear. Length of five ears were measured in centimeter from the base to the tip of dehusk ear and the mean length of ear was work out.

3.5.8 Cob girth (cm)

The ears used for measuring ear length were used to measure the girth of the ear. Ordinary string (thread) was be used for measuring the girth. The thread was be wrapped in the middle portion of the ear and the length of thread was be measured in centimeter as ear girth. By this method, girth of five ears was determine and mean ear girth was work out after dehusking.

3.5.9 Kernel rows per ear (No.)

The ears from the randomly selected and tagged five plants were used for counting the kernel rows per ear after dehusking in each plot of each replication. The mean values of kernel rows per ear was work out.

3.5.10 Kernels per row (No.)

The ears used for counting the kernel rows per ear were taken for counting the number of kernels per row per ear. The mean values of kernels per row was work out.

3.5.11 100-kernel weight (g)

One hundred kernels of composite samples of randomly selected five plants per plot per replication were collect and weigh for recording 100-kernel weight in gram.

3.5.12 Kernel yield per plant (g)

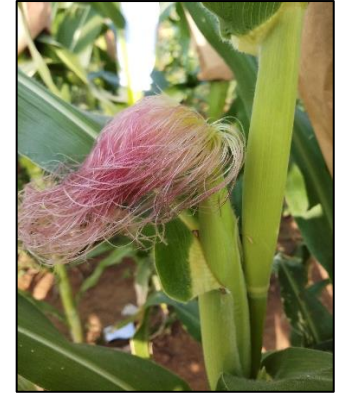
The ears of the randomly selected and tagged five plants were shell and kernels from ear will be weight in gram. The mean kernel yield per plant was work out after sun drying.



1. Selection of tassel



2. Covering of tassel with brown paper bag



3. Selection of silk



4. Covering of silk with white butter paper bag



5. Collection of pollen



6. Pollination on silk



7. Covering of ear after pollination

Plate 1: Steps of crossing

3.5.13 Shelling percentage (%)

The ratio of kernel weight to total weight of ear of randomly selected five plants was expressed in per cent.

$$\text{Shelling per cent} = \frac{\text{Kernel weight}}{\text{Total weight of ear}} \times 100$$

3.6 STATISTICAL ANALYSIS

The mean values for all the characters were subjected to statistical analysis. The analysis was carried out at Department of Agricultural Statistics, Chimanbhai Patel College of Agriculture, Sardarkrushinagar Dantiwada Agricultural University, Sardarkrushinagar. Following statistical parameters were employed.

3.6.1 Analysis of variance for RBD

3.6.2 Estimation of heterosis

3.6.3 Combining ability analysis

(a) Analysis of variance for combining ability (Line \times Tester)

(b) Estimation of general and specific combining ability effects

3.6.1 Analysis of variance

Analysis of variance technique suggested by Snedecor and Cochran (1967) and reviewed by Panse and Sukhatme (1985) for Randomised Complete Block Design was followed to test the differences among the genotypes for the characters under study.

The mathematical model for randomised complete block design is:

$$Y_{ij} = m + r_i + g_j + e_{ij}$$

Where,

Y_{ij} = Phenotypic value of j^{th} genotype in i^{th} replication,

m = General mean,

r_i = Effect of i^{th} replication,

g_j = Effect of j^{th} genotype, and

e_{ij} = Uncontrolled variation due to j^{th} genotype in the i^{th} replication.

The form of analysis of variance (ANOVA) including partitioning of variances due to various sources is as under Table 3.4.

Table 3.4 : Analysis of variance (ANOVA)

Sources of variation		d. f.	MS	Cal. 'F'
[A]	Replications	(r-1)	M_r	M_r/M_e
[B]	Genotypes	(g-1)	M_g	M_g/M_e
	(1) Parents	(p-1)	M_p	M_p/M_e
	(a) Females	(f-1)	M_f	M_f/M_{fm}
	(b) Males	(m-1)	M_m	M_m/M_{fm}
	(c) Females vs. Males	1	M_{mf}	M_{fm}/M_e
	(2) Hybrids	(h-1)	M_h	M_h/M_e
	(3) Parents vs. Hybrids	1	M_{ph}	M_{ph}/M_e
[C]	Error	(g-1)(r-1)	M_e	-
	Total :	(rg-1)	M_t	-

Where,

- r = Number of replications,
g = Number of genotypes,
p = Number of parents,
f = Number of females,
m = Number of males, and
h = Number of hybrids.

The estimates of Standard Error of Mean, Critical Difference and Coefficient of Variation were obtained as under

Standard error of mean (S.Em.)

$$S.Em. = \sqrt{\frac{M_e}{r}}$$

$$S.Ed. = \sqrt{\frac{2M_e}{r}}$$

Critical difference (C.D.)

$$C.D. = S.Em. \times \sqrt{2} \times t_{0.05} \text{ at error d.f.}$$

Where, T= Table 't' value for error degree of freedom at 0.01 and 0.05 levels of probability.

Coefficient of variation (C.V %)

$$C.V.\% = \frac{\sqrt{M_e}}{\bar{X}} \times 100$$

Where,

M_e = Error mean square, and

\bar{X} = General mean for the character.

3.6.2 Estimation of heterosis

Heterosis was estimated as per cent increase or decrease in the mean value of F₁ hybrid over better parent *i.e.*, heterobeltiosis Fonesca and Patterson (1968) and over standard check *i.e.*, standard heterosis Meredith and Bridge (1972) for each character.

3.6.2.1 Heterosis over better parent (Heterobeltiosis)

Heterobeltiosis was calculated using the method given by Fonesca and Patterson (1968). It was measured as the proportion of deviation of F₁ value from the better parent, expressed in percentage.

$$HB (\%) = \frac{\bar{F}_1 - \bar{BP}}{\bar{BP}} \times 100$$

Where,

\bar{BP} = Mean performance of better parent, and

\bar{F}_1 = Mean value of F₁.

3.6.2.2 Heterosis over the standard check (Standard heterosis)

It was measured as the proportion of deviation of F₁ value from the standard check, expressed in percentage suggested by Meredith and Bridge (1972).

$$SH (\%) = \frac{\bar{F}_1 - \bar{SC}}{\bar{SC}} \times 100$$

Where,

\bar{SC} = Mean performance of standard check GAYMH 1

\bar{F}_1 = Mean value of F₁.

The Standard Errors (S.E.) and critical differences were estimated using following relations.

$$S.E. (B.P.) = \sqrt{\frac{2M_e}{r}}$$

$$C.D. (B.P.) = S.E.(BP) \times t_{0.05} \text{ and } t_{0.01} \text{ at error d.f}$$

$$S.E. (SC) = \sqrt{\frac{2M_e}{r}}$$

$$C.D. (S.H.) = S.E.(SH) \times t_{0.05} \text{ and } t_{0.01} \text{ at error d.f}$$

Where,

r = Number of replications,

M_e = Error mean square, and

t = Value of 't' at error degree of freedom corresponding to 5 and 1 per cent level of significance.

3.6.2.3 Test of significance of heterosis

The significance of heterosis value was tested using 't' test

$$t = \frac{\overline{F_1} - \overline{BP} \text{ OR } \overline{SC}}{\text{S. E of heterosis over BP or SC}}$$

Calculated 't' value was compared with table 't' values at error degree of freedom for test of significance.

3.6.3 Combining ability analysis

The variation among the hybrids was partitioned further into sources attributable to general and specific combining ability components in accordance with the procedure suggested by Kempthorne (1957) and modified by Arunachalam (1974).

The analysis of variances for the combining ability was based on the following statistical model.

3.6.3.1 Statistical model

The statistical model used to study the general and specific combining ability was:

$$Y_{ijk} = m + g_i + g_j + s_{ij} + r_k + e_{ijk}$$

Where,

I = Number of female parent (1, 2.... f),

J = Number of male parent (1, 2....m), and

k = Number of replication (1, 2.... r).

The term,

Y_{ijk} = Value of the hybrid involving i^{th} female and j^{th} male parent in k^{th} replication,

m = General mean of all hybrids,

g_i = *gca* effect of i^{th} female parent,

g_j = *gca* effect of j^{th} male parent,

s_{ij} = *sca* effect of the progeny of $(i \times j)^{\text{th}}$ cross,

r_k = Effect of k^{th} replication, and

e_{ijk} = Uncontrolled variation associated with ijk^{th} observation.

The analysis of variance (ANOVA) table for combining ability is given as under (Table 3.5).

Table 3.5 : Analysis of variance for combining ability

Sources of Variation	D.F.		M.S.	Cal. F
Replication	(r-1)	2		
Hybrids (h)	(h-1)	23	M_h	
Lines (L)	(l-1)	5	M_l	$\sigma_e^2 + r\sigma_{lt}^2 + rt\sigma_l^2$
Testers (T)	(t-1)	3	M_t	$\sigma_e^2 + r\sigma_{lt}^2 + rl\sigma_t^2$
L x T	(l-1) (t-1)	15	M_{lt}	$\sigma_e^2 + r\sigma_{lt}^2$
Error	(r-1) (h-1)	46	M_e	σ_e^2

Where,

- l = Number of lines,
- t = Number of testers,
- h = Number of hybrids,
- r = Number of replications,
- σ_l^2 = GCA variance component of lines,
- σ_t^2 = GCA variance component of testers,
- σ_{lt}^2 = SCA variance component of hybrids, and
- σ_e^2 = Error variance.

3.6.3.2 Estimation of variance components

Following estimates of variance components were worked out based on the expectation of mean square as shown in ANOVA (Table 3.4).

$$\sigma^2_{g_i} = \sigma^2_{gca_i} = \frac{M_l - M_{lt}}{r \times t}$$

$$\sigma^2_{g_j} = \sigma^2_{gca_j} = \frac{M_t - M_{lt}}{r \times l}$$

$$\sigma^2_{s_{ij}} = \sigma^2_{sca_{ij}} = \frac{M_{lt} - M_e}{r}$$

Where,

$\sigma^2_{g_i} = \sigma^2_{gca_i}$ = Variance due to general combining ability for females/lines

$\sigma^2_{g_j} = \sigma^2_{gca_j}$ = Variance due to general combining ability for males/testers

$\sigma^2_{s_{ij}} = \sigma^2_{sca_{ij}}$ = Variance due to specific combining ability for hybrids

3.6.3.3 Estimation of GCA and SCA variances

Variances due to general and specific combining ability were calculated as follows:

$$\sigma^2_{gca} = \text{Cov. (H.S.)} = \frac{M_1 + M_t - 2M_{1t}}{r(1+t)}$$

$$\sigma^2_{sca} = \text{Cov. (F.S.)} - 2\text{Cov. (H.S.)} = \frac{M_{1t} - M_e}{r}$$

Where,

Cov. (H.S.) = Covariance of half sibs, and

Cov. (F.S.) = Covariance of full sibs.

Test of significance of estimates of variances

[1] **To test σ^2_g (i)**

$F = M_1 / M_{1t}$ at DF (1) and DF (1t), respectively.

[2] **To test σ^2_g (j)**

$F = M_t / M_{1t}$ at DF (t) and DF (1t), respectively.

[3] **To test σ^2_{gca}**

$F = 1/2(M_1 + M_t) / M_{1t}$ at DFG and DF (1t), respectively.

[4] **To test σ^2_{sca}**

$F = M_{1t} / M_e$ at DF (1t) and DF (e), respectively.

Where,

DF (1), DF (t), DF (1t) and DF (e) were the degrees of freedom with M_1 , M_t , M_{1t} and M_e , respectively and DFG were obtained by:

$$DFG = \frac{(M_1 + M_t) \times DF (1) \times DF (2)}{[DF (2) \times M_1^2] + [DF (1) \times M_t^2]}$$

3.6.3.4 Estimation of *gca* and *sca* effects

The general combining ability (*gca*) and specific combining ability (*sca*) effects were calculated using following relationships.

$$g_i = \bar{Y}_{i.} - \bar{Y}_{..}$$

$$g_j = \bar{Y}_{.j} - \bar{Y}_{..}$$

$$S_{ij} = \bar{Y}_{ij} - \bar{Y}_{i.} - \bar{Y}_{.j} + \bar{Y}_{..}$$

Where,

g_i = General combining effect of line (female),

g_j = General combining effect of tester (male),

S_{ij} = Specific combining effect of ij^{th} crosses,

$\bar{Y}_{i.}$ = The mean performance of i^{th} female parent with all male parents in hybrid combinations,

$\bar{Y}_{.j}$ = The mean performance of j^{th} male parent with all female parents in

hybrid combinations,

\bar{Y}_{ij} = The mean performance of hybrid from j^{th} male parent and i^{th} female parent, and

$\bar{Y}_{..}$ = The overall mean performance of hybrids all male and female parents in hybrid combination.

3.6.3.5 Standard errors and test of significance for combining ability effects

[i] Standard errors:

(1) for *gca* effects of females:

$$\text{S.E. for } g_i = \sqrt{\frac{M'_e}{rt}}$$

$$\text{CD} = \text{S.E. for } g_i \times t$$

$$\text{S.E. } (g_i - g_j)_{\text{lines}} = \sqrt{\frac{2M_e}{rt}}$$

$$\text{CD} = \text{S.E. } (g_i - g_j)_{\text{lines}} \times t$$

(2) for *gca* effects of males:

$$\text{S.E. for } g_j = \sqrt{\frac{M'_e}{rl}}$$

$$\text{CD} = \text{S.E. for } g_j \times t$$

$$\text{S.E. } (g_i - g_j)_{\text{testers}} = \sqrt{\frac{2M_e}{rl}}$$

$$\text{CD} = \text{S.E. } (g_i - g_j)_{\text{testers}} \times t$$

(3) for *sca* effects of hybrids:

$$\text{S.E. for } s_{ij} = \sqrt{\frac{M'_e}{r}}$$

$$\text{CD} = \text{S.E. for } s_{ij} \times t$$

$$\text{S.E. } (s_{ij} - s_{kl}) = \sqrt{\frac{2M_e}{rl}}$$

$$\text{CD} = \text{S.E. } (s_{ij} - s_{kl}) \times t$$

Where,

M_e = Error mean square for combining ability,

r = Number of replications,

t = Table 't' value at 5 and 1 per cent levels of significance for error degree of freedom,

g_i = *gca* effect of i^{th} female parent,

g_j = *gca* effect of j^{th} male parent,

- $(g_i - g_j)$ = To test difference between *gca* effects of lines/testers,
 s_{ij} = *sca* effect of the progeny of $(i \times j)^{\text{th}}$ cross, and
 $(s_{ij} - s_{kl})$ = To test the difference between *sca* effects of two crosses having a common line.

[ii] The test of significance was carried out using ‘t’ test as under:

For *gca* effects of females: $t = \frac{(\hat{g}_i - 0)}{SE(g_i)}$

For *gca* effects of males: $t = \frac{(\hat{g}_j - 0)}{SE(g_j)}$

For *sca* effects of hybrids: $t = \frac{(\hat{s}_{ij} - 0)}{SE(s_{ij})}$

3.6.3.6 Per cent contribution of lines, testers and their interactions to total variance

Per cent males (testers) contribution = $\frac{SS_{th}}{SS_h} \times 100$

Per cent females (lines) contribution = $\frac{SS_{lh}}{SS_h} \times 100$

Per cent lines \times testers contribution = $\frac{SS_{lth}}{SS_h} \times 100$

Where,

SS_{th} = Sum of squares of males in hybrids,

SS_{lh} = Sum of squares of females in hybrids,

SS_{lth} = Sum of squares of line \times testers, and

SS_h = Sum of squares of hybrids.

RESULTS AND DISCUSSION



IV. RESULT AND DISCUSSION

The experiment entitled as “Estimation of heterosis and combining ability in maize (*Zea mays* L.)” was conducted during *kharif* 2020 at Maize Research Station, S. D. Agricultural University, Bhiloda. The experimental material includes 45 single cross hybrids, 14 parents (9 lines and 5 tasters) and 1 standard check were evaluated for thirteen traits. The experiment was carried out to determine the heterosis and combining ability. The result obtained from present investigation are presented and discussed under the suitable sub headings.

4.1 Analysis of variance for experimental design

4.2 *Per se* performance of parents and hybrids

4.3 Magnitude of heterosis

4.4 Combining ability analysis and gene action

4.4.1 Analysis of variance for combining ability and gene action

4.4.2 Estimation of general combining ability and specific combining ability effects

4.1 ANALYSIS OF VARIANCE FOR EXPERIMENTAL DESIGN

The analysis of variance was computed to test the difference amongst parents and hybrids for all thirteen characters and presented in Table - 4.1. The variance was further partitioned into parents, hybrids and parent vs hybrids. The mean sum of square due to parents were highly significant for all the characters *viz.* days to tasseling, days to silking, anthesis-silking interval, days to maturity, plant height, ear height, cob length, cob girth, kernels row per cob, kernels per row, 100 kernel weight, kernels yield per plant and shelling percentage. Which indicated that significant genetic variability was existing in parents used in the study. Among the parents mean square due to females differed significantly for days to tasseling, days to silking, plant height, ear height, days to maturity and kernels per row. The mean square due to male was highly significant for kernels row per cob. The mean sum square due to hybrid were indicated the highly significant difference for all the traits under study except plant height.

Table 4.1 : Analysis of variance (mean sum of square) for kernel yield and its component characters in maize

Source of variation	d.f.	Days to tasseling	Days to silking	ASI	Plant height (cm)	Ear height (cm)	Days to maturity	Cob length (cm)	Cob girth (cm)	Kernels row per cob	Kernels per row	100 kernels weight (g)	Kernel yield per plant (g)	Shelling (%)
Replications	2	9.77**	16.48**	2.06**	1112.77**	263.07*	2.82	7.89**	6.88**	3.93**	37.67**	22.90**	658.66**	4.01
Parents	13	21.58**	19.05**	1.15**	1302.49**	496.07**	12.34**	2.23**	0.59**	1.10**	10.28**	35.99**	243.46**	13.90**
Females	8	32.26**	27.23**	1.25	1589.00**	474.31**	15.20**	0.90	1.28	6.37	40.68*	315.74	13.80	1.28
Males	4	1.43	4.67	1.10	298.90	312.17	9.10	0.10	0.95	16.85*	33.57	157.48	15.55	0.95
Female vs. Male	1	16.76**	11.12*	0.58	3024.80**	1405.77**	2.38	0.03	0.28	15.22**	8.14	9.11	7.95	0.28
Hybrids	44	4.07**	5.44**	0.83**	247.01	160.95**	9.22**	0.52**	1.79**	6.77**	22.88**	474.64**	22.16**	1.79**
Parent vs. hybrid	1	153.41**	152.15**	0.02	14406.08**	7787.31**	4.95	3.82**	2.11*	8.57**	2.07	121.26*	0.01	2.11*
Error	116	1.97	2.14	0.37	175.65	60.31	1.88	0.40	0.25	0.35	1.21	2.31	25.75	4.71

Note : * and ** indicate level of significance at 5 % and 1 %, respectively

Further, the analysis of variance for parents vs hybrids revealed that significant difference among them for the characters under study *viz*, days to tasseling, days to silking, plant height, ear height, cob length, cob girth, kernels row per cob, 100 kernels weight and shelling percentage. This indicated that the presence of wide genetic variability among the parents as well as hybrids with respect to most of the character under study. The analysis of variance for female vs male found highly significant for days to tasseling, days to silking, plant height, ear height and kernels row per cob. Parents vs hybrid comparison also showed significant differences for all the traits except anthesis silking interval (ASI), days to maturity, kernels per row and kernel yield per plant. Which indicated that crosses thereby supporting the presence of mean heterosis for most of the traits.

4.2 PER SE PERFORMANCE OF PARENTS AND HYBRIDS

The mean data pertaining the performance of parents and hybrids with range for thirteen different characters are presented Appendix-B. The character-wise details of mean performance are summarized as under.

4.2.1 Days to tasseling

For days to tasseling genotypic variance had significant estimates. However, among the different sources mean square due to parents were significant. The mean performance among all the parents used for days to 50% tasseling is ranged from 47.00 days (WNC 52646) to 57.33 days (WNC 40456) for attain 50% tasseling. While in respect to hybrids ranged from 44.67 days (WNC 40324 × BLD 98) to 50.67 days (BLD 2 × BLD 103). Among the parents, WNC 52646 (47 days) followed by WNC 52313 (47.33 days) and WNC 40406 (47.67) were most promising for early tasseling character. In case of hybrids, WNC 40324 × BLD 98 (44.67 days) followed by BLD 109 × IMR 113 (45.67 days) and WNC 52646 × VL 109178 (45.67 days) were recorded for early tasseling character.

As per the mean performance of days to tasseling, the lower value is desirable. Looking at the overall result, it was revealed that out of 45 hybrids, 30 hybrids were earlier for days to tasseling as compared to a standard check GAYMH 1 (48 days).

4.2.2 Days to silking

Among the various sources of genotypic variance parents contributed largely to hybrids and contrast comparison due to parents, hybrids were highly significant which suggested possibility of heterotic crosses for days to silking. The variation for days to 50% silking in parents is ranged from 51.33 days (WNC 40406) to 60.67 days

(WNC 40456) for attain 50% silking. While in respect to hybrids ranged from 48 days (WNC 40324 × BLD 98) to 55 days (BLD 2 × BLD 103). Among the parents, WNC 40406 (51.33 days) followed by WNC 52646 (51.67 days) and BLD 98 (51.67 days) and in hybrids WNC 40324 × BLD 98 (48 days) followed by WNC 40406 × BLD 103 (49.33 days) were recorded for early silking character. Mean performance of days to silking revealed that out of 45 hybrids, 17 took fewer days to silking as compared to a standard check GAYMH 1 (51.33 days).

4.2.3 Anthesis-silking interval (Day)

Among the various sources of genotypic variance hybrid contributed more for anthesis silking interval. Among the parents the variation for anthesis-silking interval is ranged from 3 days (WNC 40080) to 5 days (IMR 113). Among the hybrids, WNC 40080 × IMR 113 (3 days) had minimum anthesis-silking interval and the cross BLD 109 × BLD 125 (5 days) and WNC 52646 × BLD 98 (5 days) possessed maximum anthesis-silking interval.

4.2.4 Plant height (cm)

For the character plant height all the genotypic variance had significant estimate and possibility for expression of hybrid vigor. The parents were more dwarf as compare to hybrids and checks. Looking at the mean performance for plant height, dwarf nature is desirable. Plant height for parents was ranged from 105.33 cm (BLD 109) to 170.67 cm (WNC 52646). Among the crosses under study the variation is ranged from 152 cm (BLD 2 × BLD 98) to 190 cm (BLD 109 × BLD 125). Parents were more dwarf as compare to hybrids and check.

4.2.5 Ear height (cm)

Among the sources genotypic variance of female had a large variation as compare to males. The parental genotypes had higher value of mean square than hybrids. The variation for ear height for parental genotype is ranged from 46 cm (BLD 109) to 88.33 cm (BLD 125) and in hybrid, it ranged from 73.67 cm (WNC 52313 × VL 109178) to 108 cm (BLD 109 × BLD 125). Mean values showed that parents *viz.* BLD 109 (46 cm) and WNC 40080 (57 cm) while in hybrids *viz.* WNC 52313 × VL 109178 (73.67 cm) and WNC 40324 × BLD 125 (77.67 cm) were found most promising for ear height character.

4.2.6 Days to maturity

For the characters days to maturity parents and hybrids had significant variances. The parental line BLD 125 (80 days) was found early maturing genotype, whereas

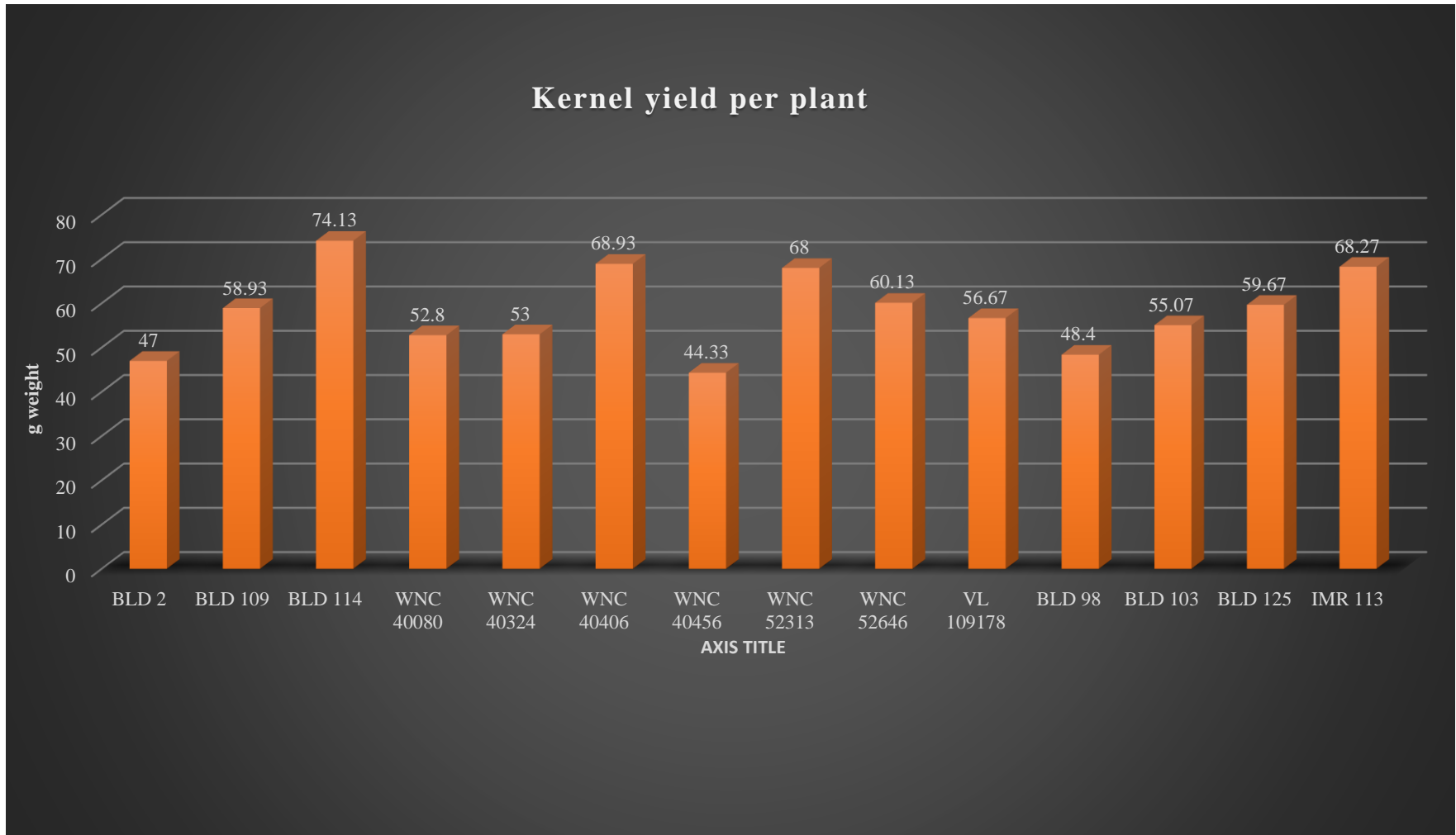


Fig 4.1 *Per se* Performance of male and female parents for kernel yield per plant

WNC 40456 (88.33 days) was late maturing genotype based on days to maturity. Among the crosses under study, the cross BLD 109 × VL 109178 (79 days) took minimum days and the cross WNC 52646 × BLD 103 (85.67 days) took maximum days to reached the maturity. Earliness is desirable character and three hybrids BLD 109 × VL 109178 (79.00), BLD 109 × BLD 103 (80.00) and WNC 40324 × BLD 98 (80.00) recorded superior performance as compared with check GAYMH 1.

4.2.7 Cob length (cm)

For cob length variance due to parents and hybrids were significant. The trait cob length was reported maximum for the parental genotype IMR 113 (16.57 cm) and minimum for BLD 109 (13.33 cm). The cross which recorded maximum cob length was WNC 40456 × BLD 125 (18.14 cm) while the cross WNC 40406 × BLD 98 (14.45 cm) had minimum cob length.

4.2.8 Cob girth (cm)

For cob girth, genotypic variance had significant estimates. However, among the different sources of genotypic mean square due to genotype and hybrid were significant. The general mean for cob girth was found 15.06 cm. Among the parental genotype under study, cob girth is found maximum for WNC 52313 (15.64 cm) and minimum for BLD 109(13.96 cm). While in hybrids, WNC 40324 × BLD 125 (15.95 cm) possessed maximum cob girth and the cross WNC 52313 × BLD 103 (14.27 cm) had minimum cob girth.

4.2.9 Kernel rows per cob

Among the various sources of genotypic variance hybrids contributed largely in comparison to parents. Parents and hybrids were highly significant, which suggested possibility of heterotic crosses for kernel rows per cob. Among the parents, the maximum number of kernels rows per cob was found in IMR 113 (13.60) and the genotype WNC 40080 (11.33) had minimum number of kernels rows per cob. Among all crosses under study, the cross WNC 40080 × BLD 125 (14.67) and WNC 40456 × BLD 98 (11.47) recorded with maximum and minimum number of kernels rows per cob, respectively.

4.2.10 Kernels per row

For kernels per row hybrid had higher contribution than parents, whereas among male parents have higher variation in comparison to female parents. Kernels per row for parental genotype is ranged from 24.07 (BLD 103) to 17.87 (BLD 109). Out of 45

crosses, the cross WNC 40406 × BLD 125 (25.07) and BLD 109 × BLD 103 (18.73) were possessed highest and lowest number of kernels per row, respectively.

4.2.11 100 kernel weight (g)

Among the different sources of variation genotypic variances were significant. The parents contributed significant estimates of variances however, male and parents vs hybrid shows non-significant mean square. The mean square indicated presence of heterotic effect due to parents was highly significant. The present mean data revealed that the variation for 100 kernel weight in parents is ranged from 30.33 g (BLD 114) to 40.33 g (WNC 40080 and BLD 103). Whereas, the crosses having range between 30.00 g (WNC 40456 × BLD 98) to 41.67 g (BLD 109 × BLD 98 and BLD 114 × BLD 98). The parents *viz.*, WNC 40080, BLD 103 (40.33 g) and WNC 40406 (39.33 g) while in hybrids, BLD 109 × BLD 98, BLD 114 × BLD 98 (41.47 g) and BLD 109 × BLD 103 (41.00 g) were recorded most promising for 100 kernel weight.

4.2.12 Kernel yield per plant (g)

For the character kernel yield per plant, among the genotypic variance parents, hybrids and parents vs hybrids have significant estimates of variances suggested possibility for expression of hybrid vigor. As per the mean performance general mean for kernel yield per plant is 59.52 g. Among the parental genotype under study, the genotype BLD 114 (74.13 g) reported highest while WNC 40456 (44.33 g) had lowest kernel yield per plant. Maximum amount of kernel yield per plant was recorded by the cross WNC 40406 × BLD 125 (95.13 g) while the cross WNC 40456 × BLD 103 (42.33 g) observed with minimum amount of kernel yield per plant.

4.2.13 Shelling percentage

In case of shelling percentage parents hybrids had significant variances. The general mean for shelling percentage was 76.53 %. For parental genotypes, shelling percentage were recorded maximum by WNC 52313 (78.79 %) and minimum by BLD 98 (72.62 %). Out of 45 crosses, the cross BLD 114 × IMR 113 (82.81 %) and BLD 109 × BLD 125 (70.02 %) possessed highest and lowest shelling percentage, respectively.

4.3. MAGNITUDE OF HETEROSIS

The aim of estimation of heterosis in present study was to spot out superior hybrids with high degree of useful heterosis for quantitative and qualitative characters in maize and for their future use in breeding programme. The heterosis was measured as percent increase or decrease of F₁ over mid parent (RH), better parent (heterobeltiosis) and

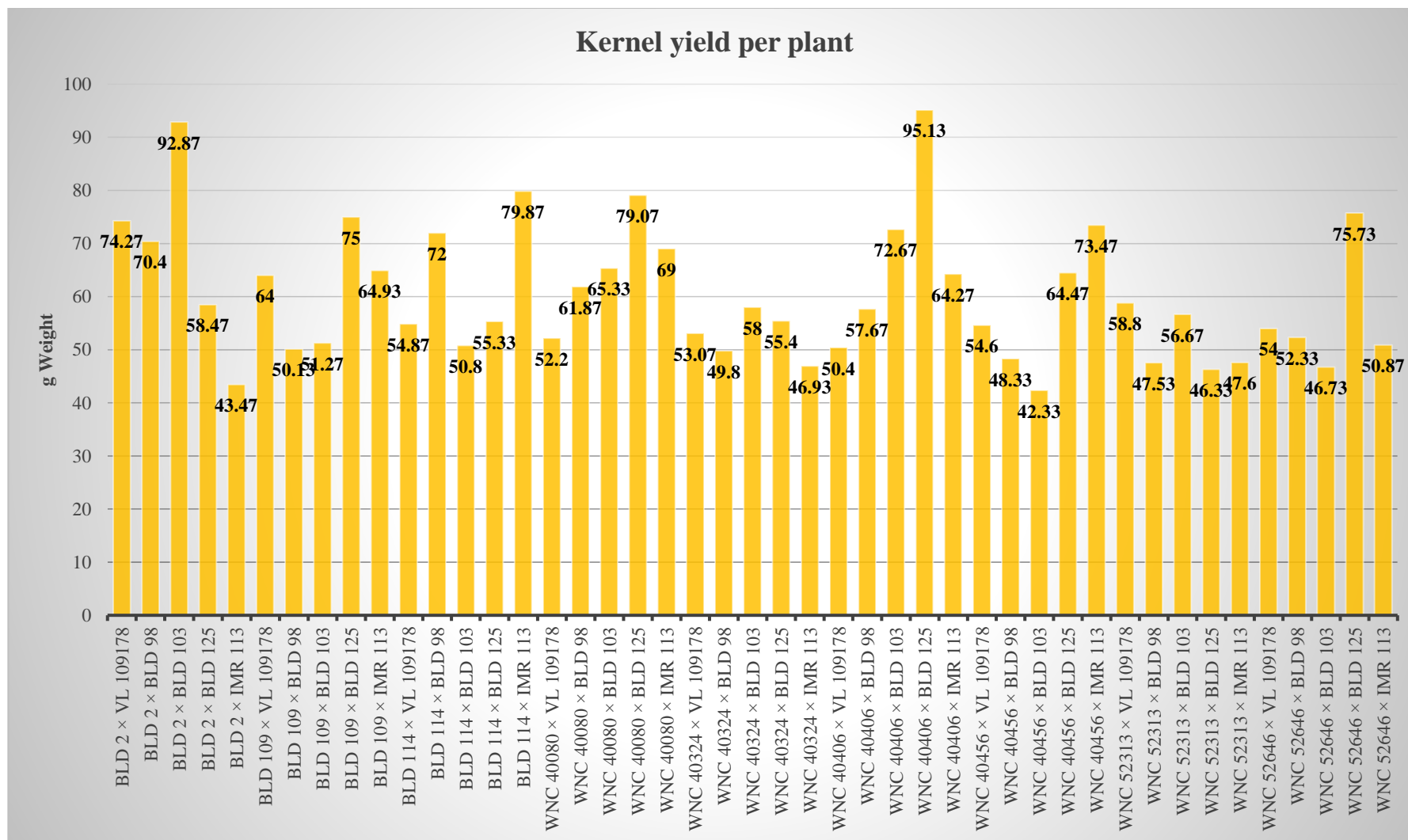


Fig 4.2 Per se Performance of hybrids for kernel yield per plant

over standard check (standard heterosis). In present study, the estimation of heterosis over better parent (BP) and over standard check (SC) was worked out. GAYMH 1 was the best check which was used for heterosis calculation. Heterosis was estimated for all the characters under study *viz.*, days to tasseling, days to silking, anthesis-silking interval, plant height (cm), ear height (cm), days to maturity, cob length (cm), cob girth (cm), kernels row per cob, kernels per row, 100 kernels weight (g), kernel yield per plant and shelling percentage (%) presented in the Table 4.2 to Table 4.8. Heterosis expressed as percentage may be either positive or negative depending on the magnitude.

While considering the result of heterosis, the high degree of heterosis were considered as favorable for the traits *viz.*, cob length (cm), cob girth (cm), kernel rows per cob, kernels per row, 100 kernels weight (g), kernel yield per plant (g) and shelling percentage (%). While the negative effects of heterosis were considered favorable for days to tasseling, days to silking, Anthesis-silking interval, days to maturity, plant height (cm) and ear height (cm). The character wise results of effect of heterosis are summarized and presented as under.

4.3.1 Days to tasseling

For this character, the parents of particular cross which flowered earlier was considered as better parent accordingly heterotic effects in negative direction was considered desirable for this trait. The spectrum of variation for heterobeltiosis ranged from -8.67 to 4.23 *per cent*. Out of 45 cross the number of crosses found significant and negative heterobeltiosis was 7 crosses. Among all the crosses, the cross BLD 109 × IMR 113 (-8.67 %) possessed lowest value of heterobeltiosis for days to tasseling followed by WNC 40324 × BLD 98 (-7.59 %) and WNC 40456 × VL 109178 (-5.44 %).

The magnitude of significant and negative standard heterosis was recorded by only 4 crosses over the standard check GAYMH 1. The standard heterosis for days to tasseling was ranged from -6.94 to 5.56 *per cent*. The lowest standard heterosis was observed in the cross WNC 40324 × BLD 98 (-6.94 %) followed by BLD 109 × IMR 113 (-4.86 %), WNC 40406 × BLD 103 (-4.86 %) and WNC 52646 × VL 109178 (-4.86 %). The results of days to tasseling matches with the result of Bekele *et al.* (2013), Mir *et al.* (2015) and Ram *et al.* (2015).

Table 4.2 : Magnitude of heterobeltiosis (better parent) and standard heterosis over GAYMH 1 for days to tasseling and days to silking

S.N.	Crosses	Days to tasseling		Days to silking	
		% Heterosis over			
		BP	SC	BP	SC
1.	BLD 2 × VL 109178	0.68	2.78	-0.63	2.60
2.	BLD 2 × BLD 98	-2.07	-1.39	-1.29	-0.65
3.	BLD 2 × BLD 103	4.11	5.56*	3.77	7.14**
4.	BLD 2 × BLD 125	-0.69	0.00	-2.55	-0.65
5.	BLD 2 × IMR 113	-4.67*	-0.69	-7.27**	-0.65
6.	BLD 109 × VL 109178	-2.04	0.00	-3.14	0.00
7.	BLD 109 × BLD 98	0.00	0.69	2.58	3.25
8.	BLD 109 × BLD 103	-4.79*	-3.47	-4.40	-1.30
9.	BLD 109 × BLD 125	-2.07	-1.39	0.00	1.95
10.	BLD 109 × IMR 113	-8.67**	-4.86*	-9.70**	-3.25
11.	BLD 114 × VL 109178	-0.68	1.39	-1.26	1.95
12.	BLD 114 × BLD 98	-1.38	-0.69	0.65	1.30
13.	BLD 114 × BLD 103	-1.37	0.00	-1.26	1.95
14.	BLD 114 × BLD 125	-2.07	-1.39	-0.64	1.30
15.	BLD 114 × IMR 113	-1.35	1.39	-0.62	3.25
16.	WNC 40080 × VL 109178	-3.40	-1.39	-2.52	0.65
17.	WNC 40080 × BLD 98	-1.38	-0.69	-0.00	0.65
18.	WNC 40080 × BLD 103	-1.37	0.00	-0.63	2.60
19.	WNC 40080 × BLD 125	4.14	4.86*	4.46	6.49**
20.	WNC 40080 × IMR 113	-5.33*	-1.39	-6.79**	-1.95
21.	WNC 40324 × VL 109178	-1.38	-0.69	0.64	1.95
22.	WNC 40324 × BLD 98	-7.59**	-6.94**	-7.10**	-6.49**
23.	WNC 40324 × BLD 103	-2.07	-1.39	-1.28	0.00
24.	WNC 40324 × BLD 125	0.00	0.69	1.28	2.60
25.	WNC 40324 × IMR 113	-4.14	-3.47	-3.85	-2.60
26.	WNC 40406 × VL 109178	-0.70	-1.39	-1.30	-1.30
27.	WNC 40406 × BLD 98	-1.40	-2.08	-1.95	-1.95
28.	WNC 40406 × BLD 103	-4.20	-4.86*	-3.90	-3.90
29.	WNC 40406 × BLD 125	-0.70	-1.39	-0.65	-0.65
30.	WNC 40406 × IMR 113	0.70	0.00	1.95	1.95
31.	WNC 40456 × VL 109178	-5.44*	-3.47	-4.40	-1.30
32.	WNC 40456 × BLD 98	0.69	1.39	1.29	1.95
33.	WNC 40456 × BLD 103	-2.05	-0.69	-3.14	0.00
34.	WNC 40456 × BLD 125	-2.07	-1.39	-3.18	-1.30
35.	WNC 40456 × IMR 113	-4.67*	-0.69	-6.06**	0.65
36.	WNC 52313 × VL 109178	0.70	-0.69	-1.28	0.00
37.	WNC 52313 × BLD 98	0.00	-1.39	-1.29	-0.65
38.	WNC 52313 × BLD 103	4.23	2.78	3.21	4.55*
39.	WNC 52313 × BLD 125	2.11	0.69	1.92	3.25
40.	WNC 52313 × IMR 113	-1.41	-2.78	-3.85	-2.60
41.	WNC 52646 × VL 109178	-2.84	-4.86*	-3.87	-3.25
42.	WNC 52646 × BLD 98	-1.42	-3.47	-0.65	0.00
43.	WNC 52646 × BLD 103	-2.13	-4.17	-2.58	-1.95

44	WNC 52646 × BLD 125	0.71	-1.39	0.65	1.30
45	WNC 52646 × IMR 113	0.00	-2.08	-1.94	-1.30
S.Em. ±		1.15	1.15	1.19	1.19
Range	Minimum	-8.67	-6.94	-9.70	-6.49
	Maximum	4.23	5.56	4.46	7.14
Total significant		7	6	5	4
Number of +ve significant		0	2	0	3
Number of -ve significant		7	4	5	1

Note : * and ** indicate level of significance at 5 % and 1 %, respectively

4.3.2 Days to silking

The estimates of heterosis over better parent for days to silking were ranged from -9.7 to 4.46 *per cent*. The number of crosses found significant and negative heterobeltiosis was 5. Among all the crosses under study, the cross BLD 109 × IMR 113 (-9.70 %) had least heterobeltiosis for days to silking followed by BLD 2 × IMR 113 (-7.27 %) and WNC 40324 × BLD 98 (-7.10%). The standard heterosis over GAYMH 1 was ranged from -6.49 to 7.14 *per cent*. Out of 45 crosses only one cross WNC 40324 × BLD 98 (-6.49 %) was recorded significant negative standard heterosis for days to silking. In present study, the crosses which exhibited significant and negative heterobeltiosis and significant and negative standard heterosis indicated that this trait might be improved through heterosis breeding. The results of days to silking are matches with the result of Bekele *et al.* (2013), Mir *et al.* (2015) and Ram *et al.* (2015).

4.3.3 Anthesis silking interval (ASI)

The estimates of significant and negative better parent heterosis were recorded by 3 crosses out of 45 crosses under study. The range of heterobeltiosis for anthesis silking interval were varies from -28.57 to 55.56 *per cent*. The crosses like BLD 2 × IMR 113 and WNC 52313 × IMR 113 (-28.57 %) was recorded lowest value for heterobeltiosis for this trait. None of the crosses were depicted significant and negative standard heterosis for anthesis silking interval. The range of standard heterosis was varied from -10 to 50 *per cent*. Out of 45 crosses only one cross WNC 40080 × IMR 113 found negative standard heterosis for this trait. The results are comparable with findings of Matin *et al.* (2016) and Nandhitha *et al.* (2018).

4.3.4 Plant height

Dwarfness is considered as desirable trait particularly in maize crop to avoid the losses due to lodging and advocated the importance of parent selection. None of the cross was registered heterobeltiosis in desired direction for plant height character.

Most of the hybrids were recorded significant positive heterosis over better parent. The cross WNC 52313 × BLD 98 (-1.83 %) recorded least value of heterosis over better parent for this trait. For plant height the magnitude of significant and negative standard heterosis was registered by 13 crosses over the standard check GAYMH 1. The range of heterosis over standard check for plant height is from -17.54 to 3.07 per cent. The cross BLD 2 x BLD 98 (-17.54 %) was found desirable for plant height as per the significant negative standard heterosis and it is followed by BLD 109 × VL 109178(-16.27 %) and BLD 109 × BLD 98 (-15.19 %). The present investigations are close agreement of Bekele *et al.* (2013), Rajitha *et al.* (2014), Mir *et al.* (2015), Reddy *et al.* (2015), Matin *et al.* (2016), Nandhitha *et al.* (2018) and Aswin *et al.*, (2020).

Table 4.3 : Magnitude of heterobeltiosis (better parent) and standard heterosis over GAYMH 1 for anthesis silking interval (ASI) and plant height

S.N.	Crosses	ASI		Plant height	
		% Heterosis over			
		BP	SC	BP	SC
1.	BLD 2 × VL 109178	-16.67	0.00	36.90**	-7.41
2.	BLD 2 × BLD 98	10.00	10.00	21.93*	-17.54**
3.	BLD 2 × BLD 103	-0.00	30.00	32.35**	-10.49
4.	BLD 2 × BLD 125	-16.67	0.00	35.83**	-8.14
5.	BLD 2 × IMR 113	-28.57**	0.00	38.77**	-6.15
6.	BLD 109 × VL 109178	0.00	0.00	46.52**	-16.27**
7.	BLD 109 × BLD 98	40.00**	40.00*	48.42**	-15.19**
8.	BLD 109 × BLD 103	30.00*	30.00	73.42**	-0.90
9.	BLD 109 × BLD 125	50.00**	50.00**	80.38**	3.07
10.	BLD 109 × IMR 113	20.00	20.00	77.53**	1.45
11.	BLD 114 × VL 109178	-8.33	10.00	13.73	-5.61
12.	BLD 114 × BLD 98	30.00*	30.00	5.31	-10.31
13.	BLD 114 × BLD 103	8.33	30.00	19.11**	1.45
14.	BLD 114 × BLD 125	16.67	40.00*	16.94*	-0.40
15.	BLD 114 × IMR 113	8.33	30.00	21.32**	-3.25
16.	WNC 40080 × VL 109178	44.44**	30.00	37.43**	-11.03*
17.	WNC 40080 × BLD 98	33.33*	20.00	39.94**	-9.40
18.	WNC 40080 × BLD 103	55.56**	40.00*	41.90**	-8.14
19.	WNC 40080 × BLD 125	44.44**	30.00	43.58**	-7.05
20.	WNC 40080 × IMR 113	0.00	-10.00	39.66**	-9.58
21.	WNC 40324 × VL 109178	27.27*	40.00*	14.45	-11.21*
22.	WNC 40324 × BLD 98	0.00	0.00	10.96	-13.92*
23.	WNC 40324 × BLD 103	9.09	20.00	24.48**	-3.44
24.	WNC 40324 × BLD 125	18.18	30.00	13.75	-11.75*
25.	WNC 40324 × IMR 113	-0.00	10.00	19.58**	-7.23
26.	WNC 40406 × VL 109178	-9.09	0.00	19.46*	-11.21*

27.	WNC 40406 × BLD 98	0.00	0.00	19.46*	-11.21*
28.	WNC 40406 × BLD 103	-0.00	10.00	19.71*	-11.03*
29.	WNC 40406 × BLD 125	-0.00	10.00	23.60**	-8.14
30.	WNC 40406 × IMR 113	18.18	30.00	23.36**	-8.32
31.	WNC 40456 × VL 109178	30.00*	30.00	5.23	-12.66*
32.	WNC 40456 × BLD 98	10.00	10.00	1.82	-8.86
33.	WNC 40456 × BLD 103	10.00	10.00	3.23	-7.59
34.	WNC 40456 × BLD 125	0.00	0.00	9.49	-1.99
35.	WNC 40456 × IMR 113	30.00*	30.00	21.54**	-3.07
36.	WNC 52313 × VL 109178	-8.33	10.00	5.66	-12.30*
37.	WNC 52313 × BLD 98	10.00	10.00	-1.83	-12.66*
38.	WNC 52313 × BLD 103	-0.00	30.00	2.24	-9.04
39.	WNC 52313 × BLD 125	16.67	40.00*	10.77	-1.45
40.	WNC 52313 × IMR 113	-28.57**	0.00	16.55*	-7.05
41.	WNC 52646 × VL 109178	0.00	20.00	10.24	-8.50
42.	WNC 52646 × BLD 98	50.00**	50.00**	6.24	-4.52
43.	WNC 52646 × BLD 103	-0.00	30.00	-0.99	-9.40
44.	WNC 52646 × BLD 125	16.67	40.00*	10.28	0.90
45.	WNC 52646 × IMR 113	-21.43*	10.00	21.54**	-3.07
S.Em. ±		0.50	0.50	10.82	10.82
Range	Minimum	-28.57	-10	-1.83	-17.54
	Maximum	55.56	50	80.38	3.07
Total significant		15	8	28	13
Number of +ve significant		12	8	28	0
Number of -ve significant		3	0	0	13

Note : * and ** indicate level of significance at 5 % and 1 %, respectively

4.3.5 Ear height

None of the cross was reported significant and negative better parent heterosis for ear height character. Most of the hybrids were recorded significant positive heterosis over better parent. Out of 45 crosses under study, 16 crosses reported significant and negative heterosis over standard check GAYMH 1 for ear height. Standard heterosis for ear height was varies between -25.59 to 9.09 *per cent*. The cross WNC 52313 × VL 109178 (-25.59 %) was found superior for this trait and followed by cross WNC 40324 × BLD 125 (-21.55 %) and WNC 40324 × BLD 98 (-21.21 %).

In the present investigation, heterosis over better parent for plant height and ear height was high in positive direction. None of the cross was found heterobeltiosis in desired (negative) direction for both traits. Where, the standard heterosis were found in desired (negative) direction for both plant height and ear height. Which indicated that this trait might be improved through exploitation of commercial heterosis. Similar results were reported by Bekele *et al.* (2013), Rajitha *et al.* (2014), Mir *et al.* (2015),

Reddy *et al.* (2015), Matin *et al.* (2016), Nandhitha *et al.* (2018) and Aswin *et al.* (2020).

4.3.6 Days to maturity

The magnitude of heterosis over better parent was varies between -5.20 to 6.67 *per cent*. Among all the crosses under study only 4 crosses reported significant and negative better parent heterosis. The cross *viz.*, BLD 109 × VL 109178 (-5.20 %), BLD 109 × BLD 103 (-4.76 %) and BLD 109 × IMR 113 (-3.56 %) were recorded three early maturing crosses based on the lowest *per cent* of significant and negative heterobeltiosis.

Out of 45 crosses, none of the cross were registered standard heterosis in desired direction. Most of the hybrids were recorded significant positive heterosis over standard check. The range of standard heterosis was varied from -1.66 to 7.05 *per cent*. The cross BLD 109 × VL 109178 (-1.66 %) had lowest value for standard heterosis. The results are in accordance with Rajitha *et al.* (2014), Mir *et al.* (2015), Ram *et al.* (2015) and Reddy *et al.*, (2015).

Table 4.4 : Magnitude of heterobeltiosis (better parent) and standard heterosis over GAYMH 1 for ear height and days to maturity

S.N.	Crosses	Ear height		Days to maturity	
		% Heterosis over			
		BP	SC	BP	SC
1.	BLD 2 × VL 109178	45.81**	-12.12	-0.80	2.90*
2.	BLD 2 × BLD 98	31.84**	-20.54**	-1.21	1.24
3.	BLD 2 × BLD 103	46.93**	-11.45	0.40	4.98**
4.	BLD 2 × BLD 125	43.02**	-13.80	5.83**	5.39**
5.	BLD 2 × IMR 113	56.98**	-5.39	0.79	5.81**
6.	BLD 109 × VL 109178	99.28**	-7.41	-5.20**	-1.66
7.	BLD 109 × BLD 98	71.74**	-20.20**	-0.40	2.07
8.	BLD 109 × BLD 103	122.46**	3.37	-4.76**	-0.41
9.	BLD 109 × BLD 125	134.78**	9.09	2.50	2.07
10.	BLD 109 × IMR 113	121.01**	2.69	-3.56**	1.24
11.	BLD 114 × VL 109178	20.41*	-20.54**	-1.60	2.07
12.	BLD 114 × BLD 98	15.91	-14.14	2.02	4.56**
13.	BLD 114 × BLD 103	36.82**	1.35	1.62	4.15**
14.	BLD 114 × BLD 125	33.64**	-1.01	6.67**	6.22**
15.	BLD 114 × IMR 113	16.82	-13.47	0.81	3.32*
16.	WNC 40080 × VL 109178	40.94**	-18.86*	-2.40	1.24
17.	WNC 40080 × BLD 98	56.73**	-9.76	-1.62	0.83
18.	WNC 40080 × BLD 103	49.71**	-13.80	-1.20	2.49
19.	WNC 40080 × BLD 125	48.54**	-14.48*	5.42**	4.98**
20.	WNC 40080 × IMR 113	49.12**	-14.14	-3.20*	0.41
21.	WNC 40324 × VL 109178	34.04**	-15.15*	0.41	2.07

22.	WNC 40324 × BLD 98	24.47*	-21.21**	-2.04	-0.41
23.	WNC 40324 × BLD 103	47.87**	-6.40	-0.82	0.83
24.	WNC 40324 × BLD 125	23.94*	-21.55**	2.92*	2.49
25.	WNC 40324 × IMR 113	51.06**	-4.38	-1.22	0.41
26.	WNC 40406 × VL 109178	25.00*	-17.51*	1.23	2.49
27.	WNC 40406 × BLD 98	15.38	-19.19*	0.41	1.66
28.	WNC 40406 × BLD 103	29.33**	-9.43	-0.00	1.24
29.	WNC 40406 × BLD 125	18.27*	-17.17*	5.83**	5.39**
30.	WNC 40406 × IMR 113	30.77**	-8.42	4.92**	6.22**
31.	WNC 40456 × VL 109178	23.98*	-18.18*	1.60	5.39**
32.	WNC 40456 × BLD 98	3.38	-17.51*	4.45**	7.05**
33.	WNC 40456 × BLD 103	5.49	-15.82*	1.19	5.81**
34.	WNC 40456 × BLD 125	16.03*	-7.41	4.17**	3.73**
35.	WNC 40456 × IMR 113	23.18**	-8.75	-2.37	2.49
36.	WNC 52313 × VL 109178	12.76	-25.59**	-1.21	1.24
37.	WNC 52313 × BLD 98	4.17	-15.82*	1.21	3.73**
38.	WNC 52313 × BLD 103	12.92	-8.75	-1.62	0.83
39.	WNC 52313 × BLD 125	15.00	-7.07	4.17**	3.73**
40.	WNC 52313 × IMR 113	27.27**	-5.72	-1.62	0.83
41.	WNC 52646 × VL 109178	35.71**	-10.44	0.82	2.07
42.	WNC 52646 × BLD 98	7.91	-8.08	4.92**	6.22**
43.	WNC 52646 × BLD 103	9.49	-6.73	5.33**	6.64**
44.	WNC 52646 × BLD 125	11.07	-5.39	3.75**	3.32*
45.	WNC 52646 × IMR 113	19.55*	-11.45	3.28*	4.56**
S.Em. ±		6.34	6.34	1.12	1.11
Range	Minimum	3.38	-25.59	-5.2	-1.66
	Maximum	134.78	9.09	6.67	7.05
Total significant		33	16	17	21
Number of +ve significant		33	0	13	21
Number of -ve significant		0	16	4	0

Note : * and ** indicate level of significance at 5 % and 1 %, respectively

4.3.7 Cob length

The hybrid with longer cob length is desirable in respect to heterobeltiosis, 33 crosses expressed significant positive heterotic effect. Heterobeltiosis is ranged from -11.91 % (WNC 40406 × BLD 98) to 16.53 % (WNC 40456 × BLD 125). The three most heterotic crosses were WNC 40456 × BLD 125 (16.53 %), BLD 2 × BLD 125 (9.21 %) and WNC 40324 × VL 109178 (9.07 %). With respect to standard heterosis out of forty five crosses only two crosses exhibited significant superior longer cob length over GAYMH 1. The longer cob length crosses were 9.01 % (WNC 40456 × BLD 125) and 6.01 % (WNC 40324 × VL 109178).

In the present investigation, heterobeltiosis and standard heterosis for cob length was found in positive direction. It indicates there may be chance of improvement of

this trait through heterosis breeding. The results are match with findings of Bekele *et al.* (2013), Rajitha *et al.* (2014), Reddy *et al.* (2015), Zeleke (2015), Matin *et al.* (2016), Nandhitha *et al.* (2018) and Aswin *et al.* (2020).

4.3.8 Cob girth

For the character cob girth the value of heterobeltiosis ranged from -8.78 % (WNC 52313 × BLD 103) to 6.89 % (BLD 109 × IMR 113). Among all the hybrids under study only 5 hybrids exhibit significant heterosis over better parent in desirable direction. Maximum value of heterobeltiosis was exhibited by the cross BLD 109 × IMR 113 (6.89 %) followed by WNC 40456 × BLD 125 (5.68 %) and BLD 2 × BLD 125 (5.63 %).

The value of standard heterosis ranged from -4.29 % (WNC 52313 × BLD 103) to 7.02 % (WNC 40324 × BLD 125) for this trait. Out of 45 hybrids 6 hybrids exhibit significant heterosis over standard check but none of the hybrids was reported standard heterosis in desirable direction. Similar results were in conformity with Bekele *et al.* (2013), Reddy *et al.* (2015), Zeleke (2015) and Matin *et al.* (2016).

Table 4.5 : Magnitude of heterobeltiosis (better parent) and standard heterosis over GAYMH 1 for cob length and cob girth

S.N.	Crosses	Cob length		Cob girth	
		% Heterosis over			
		BP	SC	BP	SC
1.	BLD 2 × VL 109178	7.73*	-0.56	2.68	2.77
2.	BLD 2 × BLD 98	0.53	-8.17**	-0.09	1.39
3.	BLD 2 × BLD 103	4.32	2.48	4.56	4.65
4.	BLD 2 × BLD 125	9.21**	2.16	5.63*	5.72*
5.	BLD 2 × IMR 113	1.53	1.12	-2.41	-2.33
6.	BLD 109 × VL 109178	1.56	-6.25*	4.84	3.62
7.	BLD 109 × BLD 98	-1.05	-9.62**	1.28	2.77
8.	BLD 109 × BLD 103	-5.51	-7.17*	3.87	2.01
9.	BLD 109 × BLD 125	-2.18	-8.49**	-1.83	-1.88
10.	BLD 109 × IMR 113	-3.22	-3.61	6.89*	6.13*
11.	BLD 114 × VL 109178	0.56	-7.17*	-2.40	-1.70
12.	BLD 114 × BLD 98	5.13	-3.13	0.04	1.52
13.	BLD 114 × BLD 103	-3.71	-5.41	-2.31	-1.61
14.	BLD 114 × BLD 125	-5.27	-11.38**	-0.89	-0.18
15.	BLD 114 × IMR 113	-2.65	-3.04	0.09	0.81
16.	WNC 40080 × VL 109178	-7.70*	-12.10**	4.16	2.95
17.	WNC 40080 × BLD 98	3.24	-1.68	2.73	4.25
18.	WNC 40080 × BLD 103	-5.06	-6.73*	1.14	-0.67
19.	WNC 40080 × BLD 125	-0.80	-5.53	1.66	1.61
20.	WNC 40080 × IMR 113	-4.14	-4.53	-0.27	-0.98
21.	WNC 40324 × VL 109178	9.07**	6.01*	2.15	3.89

22.	WNC 40324 × BLD 98	-4.86	-7.53*	-3.87	-2.24
23.	WNC 40324 × BLD 103	-4.32	-6.01*	-0.53	1.16
24.	WNC 40324 × BLD 125	-5.77	-8.41**	5.23*	7.02*
25.	WNC 40324 × IMR 113	-1.85	-2.24	4.49	6.26*
26.	WNC 40406 × VL 109178	-6.79*	-8.13**	1.90	3.35
27.	WNC 40406 × BLD 98	-11.91**	-13.18**	-1.81	-0.36
28.	WNC 40406 × BLD 103	-9.27**	-10.58**	2.12	3.58
29.	WNC 40406 × BLD 125	-1.14	-2.56	1.15	2.59
30.	WNC 40406 × IMR 113	-2.25	-2.64	3.70	5.19
31.	WNC 40456 × VL 109178	7.38*	-0.88	5.61*	4.38
32.	WNC 40456 × BLD 98	-3.20	-11.58**	-1.63	-0.18
33.	WNC 40456 × BLD 103	-4.28	-5.97*	2.00	0.18
34.	WNC 40456 × BLD 125	16.53**	9.01**	5.68*	5.64*
35.	WNC 40456 × IMR 113	-1.69	-2.08	2.34	1.61
36.	WNC 52313 × VL 109178	-3.00	-5.49	-4.31	0.40
37.	WNC 52313 × BLD 98	-10.03**	-12.34**	-6.14*	-1.52
38.	WNC 52313 × BLD 103	-3.71	-5.41	-8.78**	-4.29
39.	WNC 52313 × BLD 125	-3.37	-5.85*	-4.52	0.18
40.	WNC 52313 × IMR 113	-4.83	-5.21	0.68	5.64*
41.	WNC 52646 × VL 109178	3.82	-0.84	0.81	-0.18
42.	WNC 52646 × BLD 98	-4.36	-8.65**	-0.13	1.34
43.	WNC 52646 × BLD 103	0.24	-1.52	-2.08	-3.04
44.	WNC 52646 × BLD 125	4.03	-0.64	0.13	0.09
45.	WNC 52646 × IMR 113	-1.69	-2.08	2.12	1.39
S.Em. ±		0.52	0.48	0.40	0.40
Range	Minimum	-11.91	-13.18	-8.78	-4.29
	Maximum	16.53	9.01	6.89	7.02
Total significant		10	22	7	6
Number of +ve significant		5	2	5	0
Number of -ve significant		5	20	2	6

Note : * and ** indicate level of significance at 5 % and 1 %, respectively

4.3.9 Kernel rows per cob

For this character the magnitude of heterobeltiosis of kernel rows per cob was ranged from -12.75 % (WNC 52646 × IMR 113) to 17.02 % (WNC 40080 × BLD 125). Number of hybrids found significant and positive heterobeltiosis were four. The cross WNC 40080 × BLD 125 (17.02 %) was recorded maximum significant heterobeltiosis followed by WNC 40080 × BLD 98 (16.30 %).

For kernel rows per ear, only 8 hybrids were reported significant and positive standard heterosis over the standard check GAYMH 1. Standard heterosis for this trait is ranged from -9.47 % (WNC 40456 × BLD 98) to 15.79 % (WNC 40080 × BLD 125). The cross had maximum value with significant and positive standard heterosis was WNC 40080 × BLD 125 (15.79 %) followed by WNC 40080 × BLD 98 (12.63 %). The results are in

agreement with Bekele *et al.* (2013), Rajitha *et al.* (2014), Reddy *et al.* (2015), Nandhitha *et al.* (2018) and Aswin *et al.* (2020).

4.3.10 Kernels per row

Number of cross observed significant and positive heterosis over better parent were 5 for kernel per row. Range of heterobeltiosis for this trait is varied between -22.16 to 25.9 *per cent.* Based on positive and significant heterobeltiosis the crosses *viz.*, BLD 2 × VL 109178 (25.90 %), WNC 40456 × VL 109178 (16.55 %) and WNC 40406 × BLD 125 (15.34 %) were proved to be a best three crosses for this trait.

Out of 45 crosses, only 1 cross was found significant and positive standard heterosis over the check GAYMH 1 for this trait. The cross WNC 40406 × BLD 125 (12.91 %) was observed in significant and positive standard heterosis but most of crosses depicted standard heterosis in negative direction. Bekele *et al.*, (2013), Reddy *et al.*, (2015), Zeleke (2015), Nandhitha *et al.*, (2018), and Aswin *et al.*, (2020) recorded similar result.

4.3.11 100 kernels weight

In case 100 kernel weight the estimation of heterobeltiosis varies from -24.79 to 17.92 *per cent.* Among all the crosses under study 5 crosses were registered significant and positive heterobeltiosis. The cross BLD 109 × BLD 98 and BLD 114 × BLD 98 (17.92 %) both had maximum significant heterobeltiosis in desired direction followed by BLD 114 × VL 109178 (12.63 %) for this trait.

For 100 kernels weight, the number of crosses registered significant and positive standard heterosis over the standard check GAYMH 1 was 35. Among the desirable crosses, the cross *viz.*, BLD 109 × BLD 98 and BLD 114 × BLD 98 (32.98 %) both found with highest significant positive standard heterosis followed by the cross BLD 109 × BLD 103 (30.85 %). The earlier finding of Bekele *et al.* (2013), Rajitha *et al.* (2014), Reddy *et al.* (2015), Matin *et al.* (2016) and Aswin *et al.* (2020) were similar to the present results.

4.3.12 Kernel yield per plant

Kernel yield per plant is an attribute of economic importance which the breeders attempt to improve evolving new high yielding hybrids. The results indicated a wide range of heterobeltiosis varied from -36.33 % (BLD 2 × IMR 113) to 68.64 % (BLD 2 × BLD 103). 9 crosses exhibited highly significant positive heterobeltiosis the highest being cross by BLD 2 × BLD 103 (68.64 %), BLD 2 × BLD 98 (45.45 %) and WNC 40406 × BLD 125 (38.01 %). Whereas 24 hybrids manifested significant and

desired standard heterosis for kernel yield per plant over GAYMH 1. The standard heterosis ranged from -10.56 % to 100.99 %. The cross WNC 40406 × BLD – 125 (100.99 %) exhibited the highest standard heterosis over GAYMH 1.

These results confirm the findings of Bekele *et al.*, (2013), Rajitha *et al.*, (2014), Reddy *et al.*, (2015), Matin *et al.*, (2016), Patel *et al.*, (2016) and Nandhitha *et al.*, (2018).

Table 4.6 : Magnitude of heterobeltiosis (better parent) and standard heterosis over GAYMH 1 for kernels row per cob and kernels per row

S.N.	Crosses	Kernels row per cob		Kernels per row	
		% Heterosis over			
		BP	SC	BP	SC
1.	BLD 2 × VL 109178	1.01	5.26	25.90**	5.11
2.	BLD 2 × BLD 98	0.00	4.21	-5.26	-13.51**
3.	BLD 2 × BLD 103	2.02	6.32	-2.22	6.01
4.	BLD 2 × BLD 125	4.04	8.42*	-5.52	-7.51
5.	BLD 2 × IMR 113	-5.88	1.05	-7.39	-2.10
6.	BLD 109 × VL 109178	-9.28*	-7.37*	12.41*	-7.51
7.	BLD 109 × BLD 98	-1.03	1.05	-6.91	-15.02**
8.	BLD 109 × BLD 103	4.12	6.32	-22.16**	-15.62**
9.	BLD 109 × BLD 125	2.06	4.21	-9.51*	-11.41**
10.	BLD 109 × IMR 113	1.96	9.47**	-1.99	3.60
11.	BLD 114 × VL 109178	-4.30	-6.32	-0.93	-3.90
12.	BLD 114 × BLD 98	1.09	-2.11	-2.79	-5.71
13.	BLD 114 × BLD 103	0.00	-3.16	-13.02**	-5.71
14.	BLD 114 × BLD 125	-3.19	-4.21	-6.75	-8.71*
15.	BLD 114 × IMR 113	2.94	10.53**	-14.20**	-9.31*
16.	WNC 40080 × VL 109178	9.68*	7.37*	2.00	-8.11
17.	WNC 40080 × BLD 98	16.30**	12.63**	-3.29	-11.71**
18.	WNC 40080 × BLD 103	3.26	-0.00	-6.09	1.80
19.	WNC 40080 × BLD 125	17.02**	15.79**	-7.06	-9.01*
20.	WNC 40080 × IMR 113	-3.92	3.16	-6.53	-1.20
21.	WNC 40324 × VL 109178	6.12	9.47**	9.32*	2.10
22.	WNC 40324 × BLD 98	-7.14	-4.21	-9.32*	-15.32**
23.	WNC 40324 × BLD 103	-4.08	-1.05	-16.07**	-9.01*
24.	WNC 40324 × BLD 125	0.00	3.16	-12.88**	-14.71**
25.	WNC 40324 × IMR 113	0.00	7.37*	-9.09*	-3.90
26.	WNC 40406 × VL 109178	-5.38	-7.37*	-4.33	-7.21
27.	WNC 40406 × BLD 98	-2.17	5.26	-1.55	-4.50
28.	WNC 40406 × BLD 103	-1.09	-4.21	-16.34**	-9.31*
29.	WNC 40406 × BLD 125	-6.38	-7.37*	15.34**	12.91**
30.	WNC 40406 × IMR 113	-5.88	1.05	-3.98	1.50
31.	WNC 40456 × VL 109178	8.60*	6.32	16.55**	1.50
32.	WNC 40456 × BLD 98	-6.52	-9.47**	-4.28	-12.61**
33.	WNC 40456 × BLD 103	-1.09	-4.21	-10.53**	-3.00

34	WNC 40456 × BLD 125	-5.32	-6.32	7.36	5.11
35	WNC 40456 × IMR 113	-5.88	1.05	-2.84	2.70
36	WNC 52313 × VL 109178	-2.06	-0.00	3.77	-0.90
37	WNC 52313 × BLD 98	-6.19	-4.21	-7.23	-11.41**
38	WNC 52313 × BLD 103	-3.09	-1.05	-5.26	2.70
39	WNC 52313 × BLD 125	-7.22	-5.26	-3.99	-6.01
40	WNC 52313 × IMR 113	-4.90	2.11	-0.57	5.11
41	WNC 52646 × VL 109178	3.19	2.11	0.61	-0.30
42	WNC 52646 × BLD 98	-1.06	-2.11	2.12	1.20
43	WNC 52646 × BLD 103	-4.26	-5.26	-8.31*	-0.60
44	WNC 52646 × BLD 125	3.19	2.11	-1.21	-2.10
45	WNC 52646 × IMR 113	-12.75**	-6.32	-8.24*	-3.00
S.Em. ±		0.48	0.42	0.90	0.96
Range	Minimum	-12.75	-9.47	-22.16	-15.62
	Maximum	17.02	15.79	25.9	12.91
Total significant		6	12	17	15
Number of +ve significant		4	8	5	1
Number of -ve significant		2	4	12	14

Note : * and ** indicate level of significance at 5 % and 1 %, respectively

Table 4.7 : Magnitude of heterobeltiosis (better parent) and standard heterosis over GAYMH 1 for 100 kernels weight and kernel yield per plant

S.N.	Crosses	100 kernels weight		Kernel yield per plant	
		% Heterosis over			
		BP	SC	BP	SC
1.	BLD 2 × VL 109178	-0.00	23.40**	31.06**	56.90**
2.	BLD 2 × BLD 98	-0.86	22.34**	45.45**	48.73**
3.	BLD 2 × BLD 103	-13.22**	11.70**	68.64**	96.20**
4.	BLD 2 × BLD 125	2.59	26.60**	-2.01	23.52**
5.	BLD 2 × IMR 113	-4.31	18.09**	-36.33**	-8.17
6.	BLD 109 × VL 109178	8.00*	14.89**	8.60	35.21**
7.	BLD 109 × BLD 98	17.92**	32.98**	-14.93*	5.92
8.	BLD 109 × BLD 103	1.65	30.85**	-13.01	8.31
9.	BLD 109 × BLD 125	1.74	24.47**	25.70**	58.45**
10.	BLD 109 × IMR 113	0.00	21.28**	-4.88	37.18**
11.	BLD 114 × VL 109178	12.63**	13.83**	-25.99**	15.92
12.	BLD 114 × BLD 98	17.92**	32.98**	-2.88	52.11**
13.	BLD 114 × BLD 103	-6.61*	20.21**	-31.47**	7.32
14.	BLD 114 × BLD 125	-4.35	17.02**	-25.36**	16.90
15.	BLD 114 × IMR 113	-12.28**	6.38	7.73	68.73**
16.	WNC 40080 × VL 109178	-19.83**	3.19	-7.88	10.28
17.	WNC 40080 × BLD 98	-23.97**	-2.13	17.17*	30.70**
18.	WNC 40080 × BLD 103	-10.74**	14.89**	18.64*	38.03**
19.	WNC 40080 × BLD 125	-24.79**	-3.19	32.51**	67.04**
20.	WNC 40080 × IMR 113	-6.61*	20.21**	1.07	45.77**
21.	WNC 40324 × VL 109178	-9.09**	6.38	-6.35	12.11

22.	WNC 40324 × BLD 98	4.55	22.34**	-6.04	5.21
23.	WNC 40324 × BLD 103	-14.05**	10.64**	5.33	22.54*
24.	WNC 40324 × BLD 125	-13.91**	5.32	-7.15	17.04*
25.	WNC 40324 × IMR 113	-6.14	13.83**	-31.25**	-0.85
26.	WNC 40406 × VL 109178	-11.86**	10.64**	-26.89**	6.48
27.	WNC 40406 × BLD 98	-13.56**	8.51*	-16.34**	21.83*
28.	WNC 40406 × BLD 103	-8.26**	18.09**	5.42	53.52**
29.	WNC 40406 × BLD 125	-11.86**	10.64**	38.01**	100.99**
30.	WNC 40406 × IMR 113	-14.41**	7.45	-6.77	35.77**
31.	WNC 40456 × VL 109178	11.46**	13.83**	-3.65	15.35
32.	WNC 40456 × BLD 98	-15.09**	-4.26	-0.14	2.11
33.	WNC 40456 × BLD 103	-19.01**	4.26	-23.12**	-10.56
34.	WNC 40456 × BLD 125	-10.43**	9.57*	8.04	36.20**
35.	WNC 40456 × IMR 113	-6.14	13.83**	7.62	55.21**
36.	WNC 52313 × VL 109178	0.00	5.32	-13.53*	24.23**
37.	WNC 52313 × BLD 98	1.89	14.89**	-30.10**	0.42
38.	WNC 52313 × BLD 103	-12.40**	12.77**	-16.67**	19.72*
39.	WNC 52313 × BLD 125	-5.22	15.96**	-31.86**	-2.11
40.	WNC 52313 × IMR 113	-7.02*	12.77**	-30.27**	0.56
41.	WNC 52646 × VL 109178	-0.00	23.40**	-10.20	14.08
42.	WNC 52646 × BLD 98	-0.00	23.40**	-12.97	10.56
43.	WNC 52646 × BLD 103	-11.57**	13.83**	-22.28**	-1.27
44.	WNC 52646 × BLD 125	-11.21**	9.57*	25.94**	60.00**
45.	WNC 52646 × IMR 113	-1.72	21.28**	-25.49**	7.46
S.Em. ±		1.24	1.20	20.72	20.31
Range	Minimum	-24.79	-4.26	-36.33	-10.56
	Maximum	17.92	32.98	68.64	100.99
Total significant		28	35	25	24
Number of +ve significant		5	0	9	24
Number of -ve significant		23	35	16	0

Note : * and ** indicate level of significance at 5 % and 1 %, respectively

4.3.13 Shelling percentage

The extent of heterobeltiosis for shelling percentage was varied from -10.86 to 6.31 *per cent*. The number of cross depicted significant and positive heterobeltiosis was 3. Among all the crosses, the cross BLD 2 × BLD 103 (6.33 %) possessed maximum significant and positive heterobeltiosis followed by the cross BLD 114 × IMR 113 (5.55 %) and WNC 40080 × BLD 103 (4.81 %).

For shelling percentage out of 45 crosses under study, 4 crosses were recorded significant and positive standard heterosis over the standard check GAYMH 1. The range of standard heterosis was varied from -7.86 to 8.98 *per cent*. The cross BLD 114 × IMR 113 (8.98 %) was reported maximum standard heterosis followed by the cross BLD 2 × BLD 103 (7.29 %) and WNC 52646 × BLD 125 (5.59%).

Table 4.8 : Magnitude of heterobeltiosis (better parent) and standard heterosis over GAYMH 1 for shelling percentage

S.N.	Crosses	Shelling percentage	
		% Heterosis over	
		BP	SC
1.	BLD 2 × VL 109178	-1.90	0.78
2.	BLD 2 × BLD 98	-0.73	0.18
3.	BLD 2 × BLD 103	6.31**	7.29**
4.	BLD 2 × BLD 125	2.50	3.44
5.	BLD 2 × IMR 113	-2.13	0.21
6.	BLD 109 × VL 109178	-1.69	1.62
7.	BLD 109 × BLD 98	-2.96	0.31
8.	BLD 109 × BLD 103	-6.17**	-3.01
9.	BLD 109 × BLD 125	-10.86**	-7.86**
10.	BLD 109 × IMR 113	-6.98**	-3.84
11.	BLD 114 × VL 109178	-4.72*	-1.63
12.	BLD 114 × BLD 98	-0.27	2.97
13.	BLD 114 × BLD 103	-1.85	1.33
14.	BLD 114 × BLD 125	-5.02*	-1.93
15.	BLD 114 × IMR 113	5.55*	8.98**
16.	WNC 40080 × VL 109178	1.17	3.93
17.	WNC 40080 × BLD 98	-0.21	-2.36
18.	WNC 40080 × BLD 103	4.81*	3.12
19.	WNC 40080 × BLD 125	3.79	4.55
20.	WNC 40080 × IMR 113	-0.52	1.86
21.	WNC 40324 × VL 109178	1.45	4.68
22.	WNC 40324 × BLD 98	-7.81**	-4.88
23.	WNC 40324 × BLD 103	1.01	4.22
24.	WNC 40324 × BLD 125	-5.19*	-2.18
25.	WNC 40324 × IMR 113	-5.50*	-2.50
26.	WNC 40406 × VL 109178	-1.41	1.28
27.	WNC 40406 × BLD 98	0.52	-1.83
28.	WNC 40406 × BLD 103	2.35	0.70
29.	WNC 40406 × BLD 125	2.19	2.94
30.	WNC 40406 × IMR 113	-0.91	1.46
31.	WNC 40456 × VL 109178	-1.05	1.65
32.	WNC 40456 × BLD 98	4.31	1.36
33.	WNC 40456 × BLD 103	-0.26	-1.87
34.	WNC 40456 × BLD 125	0.56	1.29
35.	WNC 40456 × IMR 113	-2.13	0.21
36.	WNC 52313 × VL 109178	1.73	5.48*
37.	WNC 52313 × BLD 98	-2.81	0.78
38.	WNC 52313 × BLD 103	0.41	4.11
39.	WNC 52313 × BLD 125	-9.60**	-6.26*
40.	WNC 52313 × IMR 113	-2.50	1.10
41.	WNC 52646 × VL 109178	-3.19	0.06
42.	WNC 52646 × BLD 98	-2.24	1.04
43.	WNC 52646 × BLD 103	-10.55**	-7.54**

44	WNC 52646 × BLD 125	2.16	5.59*
45	WNC 52646 × IMR 113	-1.99	1.30
S.Em. ±		1.77	1.91
Range	Minimum	-10.86	-7.86
	Maximum	6.31	8.98
Total significant		13	7
Number of +ve significant		3	4
Number of -ve significant		10	3

Note : * and ** indicate level of significance at 5 % and 1 %, respectively

Earlier workers *viz.*, Nandhitha *et al.*, (2018) and Reddy *et al.*, (2018) also reported similar result.

The aim of this experiment was to estimate hybrid vigor to know genetic makeup of the parents and create mendelian variability through segregation or recombination in advanced generations of crosses. In plant breeding, the heterosis measured over a better parent and popular cultivar is more realistic and is of more practical importance than heterosis over mid parents. The results revealed that the extent of heterosis varied from the cross to cross for all the traits. For any one trait, certain hybrids expressed considerable high heterosis, while it was low in other hybrids, suggesting that the selection of parents has an important for the performance of any hybrid. The superiority of hybrids over better parents indicates the parental combinations ability to throw high levels of transgressive segregation (Fonseca and Patterson, 1968). Such hybrids might be exploited as a basic material for breeding purposes. According to Mather and Jinks (1982), heterobeltiosis could be linked to one or two situations like (I) The accumulated action of favourable dominant genes dispersed amongst two parents, (II) The complementary interaction of additive dominant on recessive genes at different loci, (III) Favourable intra or inter locus interaction referred to as over dominance evidently, a manifestation of heterobeltiosis might be due to the non-additive gene effects in the parent. Thus, for all traits studied, hybrid vigour depends on the choice of genotypes. Thereby it is necessary to cross the potentially complementary parents. Aldaji *et al.* 2015 and Gami *et al.* 2020.

The overall results of heterosis revealed that, among all 45 crosses under study the crosses *viz.*, WNC 40406 × BLD 125 and BLD 2 × BLD 103 were found significant in desired direction for both heterobeltiosis (38.01 % and 68.64%) as well as standard heterosis (100.99 % and 96.20 %) while the cross BLD 114 × IMR 113 was found significant for standard heterosis (68.73 %) in desired direction for kernel yield per plant. These crosses were also registered heterosis over better parent in desirable

direction for component traits *viz.*, cob girth and shelling percentage. The crosses like WNC 40406 \times BLD 125 and BLD 114 \times IMR 113 show heterobeltiosis in desirable direction for days to tasseling and days to silking traits. Desirable heterobeltiosis for kernel row per cob was reported by BLD 2 \times BLD 103 and BLD 114 \times IMR 113.

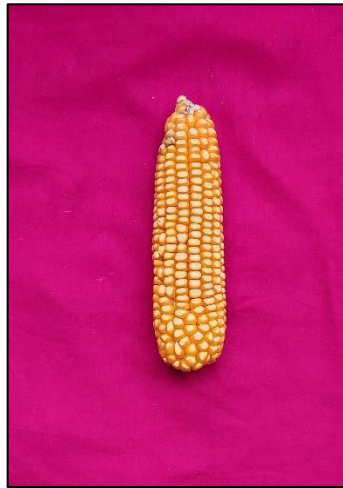
For the standard heterosis the crosses *viz.*, WNC 40406 \times BLD 125, BLD 2 \times BLD 103 and BLD 114 \times IMR 113 were also reported standard heterosis in desirable direction for component traits like plant height, ear height, 100 kernels weight and shelling percentage. Two crosses WNC 40406 \times BLD 125 and BLD 114 \times IMR 113 possessed desirable standard heterosis for cob girth and crosses WNC 40406 \times BLD 125 and BLD 2 \times BLD 103 found with desirable standard heterosis for kernels per row. Desirable standard heterosis for kernel row per cob was reported by BLD 2 \times BLD 103 and BLD 114 \times IMR 113.

4.3.14 Number of desirable hybrids

Exact figure of hybrids exhibiting significant heterosis in desirable direction for all the thirteen traits are presented in Table no 4.9. The perusal of data showed that the most important trait kernel yield per plant out of 45 hybrids tested 9 hybrids observed with significant heterobeltiotic effect while 24 hybrids exhibited significant positive heterosis over standard check GAYMH 1. It is an evident from the perusal of the data that high heterosis in kernel yield per plant was due to concomitant heterosis in over or more major components of kernel yield per plant. For days to tasseling 7 hybrids heterobeltiotic effect while 4 hybrids manifested significant negative standard heterosis, over GAYMH 1. For days to silking 5 hybrids heterobeltiotic effect while 1 hybrid manifested significant negative standard heterosis, over GAYMH 1. The character like plant height and ear height, none of the hybrid show significant heterosis over better parent while 13 and 16 hybrids recorded significant heterosis over GAYMH 1 for plant height and ear height respectively. Four hybrids were observed with significant heterobeltiosis for days to maturity. For cob length and cob girth trait, 5 parent were recorded significant heterobeltiosis. For kernels per row and 100 kernels weight 5 hybrids were observed with significant heterobeltiosis. For kernel yield per plant 9 hybrid observed with significant heterobeltiotic effect while 24 hybrids manifested significant positive standard heterosis, over GAYMH 1.



WNC 40406 × BLD 125



BLD 2 × BLD 103



BLD 114 × IMR 113



WNC 40080 × BLD 125



WNC 52646 × BLD 125



GAYMH 1 (Check)

Plate 2: Pictorial observation for cob of top five most promising heterotic hybrids and check (GAYMH 1) for kernel yield per plant

Table 4.9 : Hybrids with significant heterosis in desirable direction for different traits in maize

Sr. No.	Characters	Over BP	Over SC
1	Days to tasseling	7	4
2	Days to silking	5	1
3	ASI	3	0
4	Plant height (cm)	0	13
5	Ear height (cm)	0	16
6	Days to maturity	4	0
7	Cob length (cm)	5	2
8	Cob girth (cm)	5	0
9	Kernels row per cob	4	8
10	Kernels per row	5	1
11	100 kernels weight (g)	5	0
12	Kernel yield per plant	9	24
13	Shelling (%)	3	4

4.3.15 Manifested heterobeltiosis for other characters in top five ranking crosses for kernel yield per plant

A comparative data of top five hybrids *viz.*, BLD 2 × BLD 103, BLD 2 × BLD 98, WNC 40406 × BLD 125, WNC 40080 × BLD 125 and BLD 2 × VL 109178 showed high heterobeltiosis for kernel yield per plant in table no 4.10.

The highest yielding cross BLD 2 × BLD 103 recorded 68.64 % higher kernel yield per plant than their better parent. This cross had also desired heterobeltiosis for shelling percentage.

The next superior hybrid BLD 2 × BLD 98 had higher heterobeltiosis for kernel yield per plant (45.45 %) with four yield attributing character *viz.*, days to tasseling, days to silking, days to maturity and cob length.

The third cross WNC 40406 × BLD 125 with significant better parent heterosis for kernel yield per plant (38.01 %) had also exhibited desired heterobeltiosis for five character like days to tasseling, days to silking, cob girth, kernels per row and shelling percentage.

The hybrid, WNC 40080 × BLD 125 which ranked fourth with significant better parent heterosis for kernel yield per plant (32.51 %) was found in desirable direction for the characters cob girth, kernels row per cob and shelling percentage.

The fifth hybrid BLD 2 × VL 109178 with significant heterobeltiosis for kernel yield per plant (31.06 %). Also manifested desirable heterobeltiosis for days to silking, anthesis silking interval, days to maturity, cob length, cob girth, kernels row per cob and kernels per row.

4.4 COMBINING ABILITY ANALYSIS AND GENE ACTION

Constant efforts are being made to improve yield and yield attributing characters in maize through hybridization. Selection of appropriate parents is very crucial in any planned hybridization programme. Eventually the lines which produced good progeny on crossing are of immense value for the plant breeder. In a crop improvement programme, much of the success depends upon isolation of valuable gene combinations as determined in the form of line with high combining ability.

A line by tester analysis of 45 hybrids developed by 9 females with 5 males along with parents and check was carried for yield and its components. The variation existing in the hybrids was partitioned in to portion attributed females, males, female \times male and error sources.

Further, using appropriate expectation of observed mean square as describes in the material methods. The component of variances attributed to male and female were used as a measure of general combining ability (σ^2_{gca}) of male and female parent, respectively. While the variances due to females \times males interaction were used as a measure of specific combining ability variances (σ^2_{sca})

For the development of elite hybrids, it is necessary to select parents with good general combining ability for yield and its components traits. The success of any crop improvement programme is depending upon the selection of parents with superior combining ability and breeding procedure adopted. The knowledge of combining ability is prerequisite to isolate the parents with diverse genetic background and the best specific combination. At the same time, it also elucidates the nature of gene action (additive - related to GCA and non-additive gene effect - related to SCA) involved in the inheritance of various traits.

The analysis of variance for combining ability and estimation of variance components for various traits were done as per line \times tester analysis following the procedure suggested by Kempthorne (1957). The results are presented in subsequent paragraph.

Table 4.10 : Manifested of heterobeltiosis (HB) for other characters in five top ranking crosses for kernel yield per plant

Sr. No.	Cross	Character												
		KY/P	DT	DS	ASI	PH	EH	DM	CL	CG	KR/C	K/R	SI	Shelling (%)
1	BLD 2 × BLD 103	68.64**	4.11	3.77	-0.00	32.35**	46.93**	0.40	4.32	4.56	2.02	-2.22	-13.22**	6.31**
2	BLD 2 × BLD 98	45.45**	-2.07	-1.29	10.00	21.93*	31.84**	-1.21	0.53	-0.09	0.00	-5.26	-0.86	-0.73
3	WNC 40406 × BLD 125	38.01**	-0.70	-0.65	-0.00	23.60**	18.27*	5.83**	-1.14	1.15	-6.38	15.34**	-11.86**	2.19
4	WNC 40080 × BLD 125	32.51**	4.14	4.46	44.44**	43.58**	48.54**	5.42**	-0.80	1.66	17.02**	-7.06	-24.79**	3.79
5	BLD 2 × VL 109178	31.06**	0.68	-0.63	-16.67	36.90**	45.81**	-0.80	7.73*	2.68	1.01	25.90**	-0.00	-1.90

Note : * and ** indicate level of significance at 5 % and 1 %, respectively

DT = Days to tasseling, DS = Days to silking, ASI = Anthesis silking interval, PH = Plant height, EH = Ear height, DM = Days to maturity, CL = Cob length, CG = Cob girth, KR/C = Kernels row per cob, K/R = Kernels per row, SI = 100 kernels weight, KY/P = Kernel yield per plant, Shelling (%) = Shelling percentage.

:

4.4.1 Analysis of variance for combining ability and gene action

The analysis of variance for combining ability and estimates of variance components for thirteen traits are furnished in Table 4.11. It is calculated by partitioning the total genetic variance into general combining ability representing additive type of gene action and specific combining ability representing non additive type of gene action. The analysis of variance for combining ability revealed that mean square due female were significant for all the characters under study. While, mean square observed due to male were also significant for all the characters except days to tasseling and shelling percentage. Mean square due to line x tester interaction was found significant for most of the traits except plant height and ear height.

The estimates of mean square due to females, males and females x males were significant. The value of variances due to male was larger than the females for most of the character. Which revealed that the males contributed largely for the total parental variances. The interaction mean square due to females and male was highly significant. Which suggested that female might have performed differently in a cross combination and/or vice versa depending up on the genetic makeup of females/males.

The ratio of $\sigma_{gca}^2/\sigma_{sca}^2$ was less than unity for majority of the characters except plant height and ear height. If the ratio of $\sigma_{gca}^2/\sigma_{sca}^2$ was less than unity than it indicates non-additive component genetic variance was predominantly involved in expression of character. In this study for plant height and ear height, the ratio of $\sigma_{gca}^2/\sigma_{sca}^2$ was found more than unity, suggesting a greater role of additive genetic variance in the inheritance of this trait.

In present study, the magnitude of specific combining ability (SCA) variance was higher than general combining ability (GCA) variance for the majority of traits *viz.*, days to tasseling, days to silking, anthesis silking interval (ASI), days to maturity, cob length (cm), cob girth (cm), kernels row per cob, kernels per row, 100 kernels weight (g), kernel yield per plant, and shelling percentage (%). It indicates that non-additive gene effect is important for inheritance of these traits. This result was in accordance with the findings of Lahane *et al.* (2015), Zeleke *et al.* (2015), Patel *et al.* (2016), Kuselan *et al.* (2017), Gami *et al.* (2018), Rajesh *et al.* (2018), Nandhitha *et al.* (2018) and Kumar *et al.* (2019). So, exploitation of these traits for improvement of yield through heterosis breeding is beneficial.

Table 4.11 : Analysis of variance (mean sum of square) for combining ability, estimates of components of variance and their ratio for various characters in maize

Source of variation	d.f.	DT	DS	ASI	PH	EH	DM	CL	CG	KR/C	K/R	SI	KY/P	Shelling (%)
Replications	2	21.65**	25.62**	1.09	1905.64**	390.99**	5.34	5.7**	5.44**	5.1**	27.48**	21.09**	589.86**	4.6
Hybrid (Crosses)	44	4.07**	5.45**	0.83**	247.01*	160.95**	9.22**	1.87**	0.52**	1.79**	6.77**	22.88**	474.63**	22.17**
Female in hybrid	8	7.22**	5.98**	1.03*	289.24	222.54**	23.59**	2.53**	0.62*	3.99**	7.75**	56.5**	601.03**	20.05**
Male in hybrid	4	2.67	6.34*	1.06*	1052.45**	547.07**	10.42**	3.75**	0.67*	1.3**	16.17**	7.72**	473.03**	12.77
Females × Males (L × T)	32	3.45**	5.2**	0.76*	135.77	97.29	5.47**	1.47**	0.48**	1.3**	5.35**	16.37**	443.24**	23.87**
Error	88	1.74	2.08	0.4	145.97	68.27	1.87	0.34	0.24	0.27	1.35	2.12	25.26	5.38
COMPONENTS OF VARIANCE														
σ^2 Females		0.25	0.05	0.02	10.23	8.35*	1.21**	0.07	0.01	0.18*	0.16	2.67**	10.52	-0.25
σ^2 Males		-0.03	0.04	0.01	33.95**	16.66**	0.18	0.08	0.01	-0.001	0.40*	-0.32	1.10	-0.41
σ^2_{gca}		0.07	0.05	0.01	25.48**	13.69**	0.55**	0.08*	0.01	0.06	0.31*	0.75	4.47	-0.36
σ^2_{sca}		0.57**	1.04**	0.12*	-3.4	9.67	1.20**	0.37**	0.08**	0.34**	1.33**	4.75**	139.33**	6.16**
$\sigma^2_{gca} / \sigma^2_{sca}$		0.12	0.04	0.12	-7.49	1.41	0.46	0.21	0.10	0.19	0.24	0.16	0.03	-0.06

Note : * and ** indicate level of significance at 5 % and 1 %, respectively

DT = Days to tasseling, DS = Days to silking, ASI = Anthesis silking interval, PH = Plant height, EH = Ear height, DM = Days to maturity, CL = Cob length, CG = Cob girth, KR/C = Kernels row per cob, K/R = Kernels per row, SI = 100 kernels weight, KY/P = Kernel yield per plant, Shelling (%) = Shelling percentage.

The overall character wise *per cent* contribution of females (lines), male (testers) and their interactions (hybrids) toward total variance are presented in Table 4.12. The study of parental *per cent* contribution, revealed that the female parent contributed more to total variance for all traits except plant height and ear height. For these traits, male parent was dominant to the total variance.

Looking at comparative study of *per cent* contribution of parents and hybrids to total variance indicates, the hybrids contributed majority of character like days to tasseling, days to silking, ASI, days to maturity, cob length (cm), cob girth (cm), kernels row per cob, kernels per row, 100 kernels weight (g), kernel yield per plant, and shelling percentage (%). Whereas, parental contribution is more than the hybrid to the total variance for character *viz.*, plant height, ear height and days to maturity.

Table 4.12 : Percent contribution of lines, testers and their interactions to total variance

Percent contribution	Days to tasseling	Days to silking	ASI	Plant height (cm)	Ear height (cm)	Days to maturity	Cob length (cm)
Female	32.29	19.97	22.55	21.29	25.14	46.54	24.64
Male	5.98	10.58	11.52	38.73	30.90	10.28	18.25
L × T (Hybrid)	61.74	69.45	65.94	39.98	43.96	43.18	57.11

Table 4.12 Cont....

Percent contribution	Cob girth (cm)	Kernels row per cob	Kernels per row	100 kernels weight (g)	Kernel yield per plant	Shelling (%)
Female	21.63	40.48	20.81	44.90	23.02	16.44
Male	11.74	6.59	21.71	3.07	9.06	5.24
L × T (Hybrid)	66.63	52.93	57.48	52.03	67.92	78.32

4.4.2 Estimation of general combining ability and specific combining ability effects

The estimates of general combining ability (*gca*) and specific combining ability (*sca*) effects of hybrids for thirteen traits are presented in Table 4.13 and Table 4.14. The results with respect to general and specific combining ability effects for various characters are summarized and presented as under.

4.4.2.1 Days to tasseling

For days to tasseling negative value of *gca* and *sca* effects to be considered as desirable for parents and crosses, respectively. Among all the parents, six parents depicted in desirable direction for this trait. Out of six desirable parents only one genotype WNC 52646 (-1.06) was found with significant negative *gca* effect and proved to be a good general combiner. Whereas rest of the five parents *viz.*,

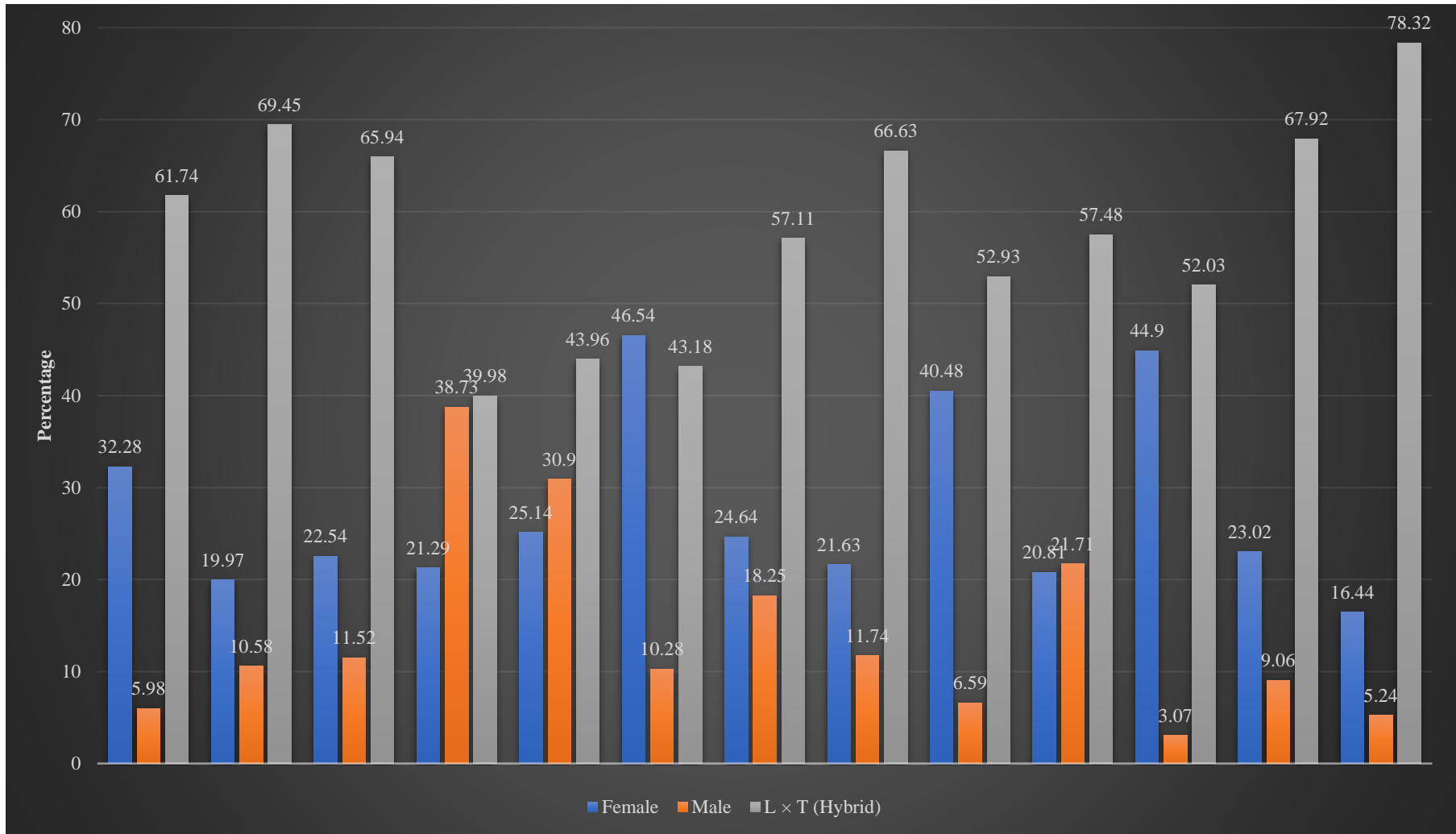


Fig. 4.3 Percent contribution of lines, testers and their interactions to total variance

WNC 40324 (-0.66), WNC 40406 (-0.46), BLD 109 (-0.39), BLD 98 (-0.30), IMR 113 (-0.30) were considered as average general combiners.

Out of 45 crosses, only 2 crosses *viz.*, WNC 40324 × BLD 98 (-1.90) and WNC 40406 × BLD 103 (-1.54) were reported good specific combiner for days to tasseling due to significant and negative *sca* effects. The results of days to tasseling matches with the result of Amiruzzaman *et al.* (2013), Ram *et al.* (2015), Kumar *et al.* (2016), Reddy *et al.* (2016), Rajesh *et al.* (2018) and Aswin *et al.* (2020).

4.4.2.2 Days to silking

Earliness is desirable for days to silking trait. So, parents having negative *gca* effect and hybrids with negative *sca* effect are considered as best for this trait. Out of 14 parents 8 genotypes reported *gca* effect in desirable direction. But only one parent WNC 40406 (-0.78) was found significant and negative *gca* effect and it was considered as good general combiner for days to silking. The parental genotype *viz.*, WNC 52646 (-0.71), WNC 40324(-0.64), IMR 113 (-0.55), BLD 98 (-0.33), WNC 40456 (-0.18), BLD 109 (-0.11), VL 109178 (-0.10), were considered as average general combiners.

For days to silking, only 3 crosses were found with significant and negative *sca* effects. The crosses *viz.*, WNC 40324 × BLD 98 (-2.54), BLD 2 × BLD 98 (-1.77) and WNC 40406 × BLD 103 (-1.74) were recognized as good specific combiner. The results of days to silking matches with the result of Amiruzzaman *et al.* (2013), Ram *et al.* (2015), Kumar *et al.* (2016), Reddy *et al.* (2016), Rajesh *et al.* (2018) and Aswin *et al.* (2020).

4.4.2.3 Anthesis silking interval (ASI)

Negative value of *gca* and *sca* effect was considered as desirable for anthesis silking interval (ASI). Total 6 parental genotype had *gca* effect in desirable direction. Among them 2 genotypes were found with significant and negative *gca* effect. The parents BLD 2 (-0.40) and WNC 40406 (-0.33) was registered as good general combiner for this trait and rest of the parental genotypes depicted as average general combiners.

Among all crosses, 3 crosses were exhibited significant *sca* effects in desired direction and proved to be good specific combiners. The cross WNC 40080 × IMR 113 (-0.84) considered good specific combiner followed by BLD 109 × VL 109178 (-0.79) and WNC 40456 × BLD 125 (-0.76). The results are comparable with findings of Reddy *et al.* (2016) and Patel *et al.* (2019).

4.4.2.4 Plant height

Among the parents under study, only 2 genotypes *viz.*, BLD 98 (-7.31), VL 109178 (-5.79) and were exhibited significant and negative *gca* effect. Negative value of GCA is desirable therefore, these two genotypes were proved to be good general combiners. Besides these 5 parents had desirable *gca* effect which were reported as average general combiners.

An examination of specific combining ability effects of hybrids elucidated that only one cross BLD 109 \times VL 109178 (-13.94) was reported with significant and negative *sca* effects. The present investigations are close agreement of Amiruzzaman *et al.* (2013), Kumar *et al.* (2016), Reddy *et al.* (2016), Rajesh *et al.* (2018) and Aswin *et al.* (2020).

4.4.2.5 Ear height

Parental genotypes like BLD 98 (-4.94) and VL 109178 (-4.87) were exhibited significant and negative *gca* effects, hence considered to be good general combiners for ear height. While the parents *viz.*, WNC 40406 (-3.03), WNC 40080 (-2.90), WNC 40324 (-2.43), WNC 40456 (-2.23), BLD 2 (-1.36), WNC 52313 (-1.30) were average general combiners. The combination BLD 109 \times BLD 98 (-12.59) was recorded highest significant general combining ability effect in a desirable direction followed by WNC 40324 \times BLD 125 (-10.24), considered good specific combiners for this trait. Similar results were reported by Amiruzzaman *et al.* (2013), Kumar *et al.* (2016) and Rajesh *et al.* (2018).

4.4.2.6 Days to maturity

Out of 14 parents, 7 parents exhibited *gca* effects in desirable direction. Among them 5 genotypes had significant and negative value of *gca* effects. The parental genotype *viz.*, BLD 109 (-1.86), WNC 40324 (-1.53), WNC 40080 (-0.79), WNC 52313 (-0.73) among lines and BLD 125 (0.94), and VL 109178 (-0.80) among testers were considered to be good general combiners.

With respect to *sca* effects of days to maturity, only 5 crosses out of 45 *viz.*, BLD 2 \times BLD 98 (-2.28), WNC 52646 \times BLD 125 (-1.94), WNC 40456 \times BLD 125 (-1.87), WNC 40456 \times IMR 113 (-1.80), WNC 40406 \times BLD 103 (-1.71) and WNC 40324 \times VL 109178 (1.60) were found with significant and negative *sca* effects. The results are in accordance with Habtamu zelege *et al.* (2015), Ram *et al.* (2015), Kumar *et al.* (2016), Reddy *et al.* (2016) and Rajesh *et al.* (2018).

Table 4.13 : The estimates of general combining ability (*gca*) effects of the parents for various characters in maize

Parents	Days to tasseling	Days to silking	ASI	Plant height (cm)	Ear height (cm)	Days to maturity	Cob length (cm)	Cob girth (cm)	Kernels row per cob	Kernels per row	100 kernels weight (g)	Kernel yield per plant	Shelling (%)
FEMALE PARENTS (Lines)													
BLD 2	1.07**	0.62	-0.40*	-4.42	-1.36	0.87*	0.69**	0.12	0.55**	0.40	1.84**	7.71**	1.26*
BLD 109	-0.39	-0.11	0.27	3.65	8.70**	-1.86**	-0.38*	0.14	0.25	-1.11**	3.24**	0.88	-2.48**
BLD 114	0.54	0.82*	0.27	7.23*	1.70	0.87*	-0.21	-0.28*	-0.23	-0.55	1.11**	2.39	0.93
WNC 40080	0.61	0.69	0.07	-2.75	-2.90	-0.79*	-0.23	-0.03	0.89**	-0.32	-2.49**	5.31**	1.14
WNC 40324	-0.66	-0.64	0.00	-3.62	-2.43	-1.53**	0.18	0.24	0.28*	-0.88**	-0.89*	-7.54**	-0.64
WNC 40406	-0.46	-0.78*	-0.33*	-4.49	-3.03	0.34	-0.44**	0.19	-0.68**	0.64*	-1.09**	7.84**	0.15
WNC 40456	0.01	-0.18	-0.13	1.31	-2.23	1.54**	0.41**	0.11	-0.41**	0.65*	-2.22**	-3.54**	-0.14
WNC 52313	0.34	0.29	-0.07	-1.75	-1.30	-0.73*	-0.35*	-0.23	-0.31*	0.46	-0.69	-8.80**	0.25
WNC 52646	-1.06**	-0.71	0.33*	4.85	2.84	1.27**	0.33*	-0.25*	-0.33*	0.72*	1.18	-4.25**	-0.48
S.Em. ±	0.34	0.37	0.16	3.12	2.13	0.35	0.15	0.12	0.13	0.30	0.37	1.31	0.60
MALE PARENTS (Testers)													
VL 109178	0.03	-0.10	-0.15	-5.79*	-4.87**	-0.80**	0.14	0.08	0.04	0.46*	-0.56*	-2.83**	0.97*
BLD 98	-0.30	-0.33	-0.04	-7.31**	-4.94**	0.01	-0.61**	-0.13	-0.23*	-1.25**	0.70*	-3.51**	-0.75
BLD 103	0.14	0.34	0.19	1.91	3.73*	-0.02	-0.07	-0.21*	-0.18	0.12	0.22	-0.55	0.16
BLD 125	0.44	0.64*	0.22	6.76**	2.50	0.94**	0.20	0.10	0.05	-0.09	-0.52	7.03**	-0.58
IMR 113	-0.30	-0.55	-0.22	4.43	3.58*	-0.13	0.34**	0.15	0.32**	0.77**	0.15	-0.14	0.20
S.Em. ±	0.25	0.28	0.12	2.32	1.59	0.26	0.11	0.09	0.10	0.22	0.28	0.98	0.45

Note : * and ** indicate level of significance at 5 % and 1 %, respectively

4.4.2.7 Cob length

For cob length character, positive and significant value of *gca* effect for parents and *sca* effect for crosses had to be considered as desirable. Out of 14 parents, 4 genotypes reported with significant and positive value of *gca* effect. Among 4 desirable genotypes, 3 female parents like BLD 2 (0.69), WNC 40456 (0.41), WNC 52646 (0.33) and one male parent IMR 113 (0.34) were best general combiner.

The estimates of *sca* effect for cob length revealed that 4 crosses out of 45 crosses having significant SCA value in desirable (positive) direction. Therefore, the combinations *viz.*, WNC 40456 × BLD 125 (1.68), WNC 40324 × VL 109178 (1.47), WNC 40080 × BLD 98 (1.35) and BLD 114 × BLD 98 (1.10) were found best specific combiners for cob length. The results are match with findings of Habtamu zeleke *et al.* (2015), Kumar *et al.* (2016), Reddy *et al.* (2016), Rajesh *et al.* (2018) and Aswin *et al.* (2020).

4.4.2.8 Cob girth

Out of 14 parental genotypes, none of the genotype exhibited significant and positive *gca* effects for this trait. On the other hand, the estimates of *sca* effect shows only one cross out of 45 crosses *i.e.*, WNC 52313 × IMR 113 (0.68) had significant and positive *sca* effects. Therefore, it was considered as good specific combiners for cob girth. Similar results were in conformity with Habtamu zeleke *et al.* (2015), Kumar *et al.* (2016), Reddy *et al.* (2016) and Rajesh *et al.* (2018).

4.4.2.9 Kernel rows per cob

For the character like Kernel rows per cob, the *gca* and *sca* effects of the parents and hybrids in in positive direction was considered as desirable in maize. From all the parental genotype under study, WNC 40080 (0.89) and BLD 2 (0.55) among the lines and IMR 113 (0.32) among the testers were found significant in desirable direction for the trait Kernel rows per cob.

The estimation of *sca* effects for Kernel rows per cob, shows that among all the crosses under study, 6 crosses possessed significant and positive *sca* effect. The cross BLD 114 × IMR 113 (1.15) had highest value of significant and positive *sca* effects followed by WNC 40456 × VL 109178 (1.08) and WNC 40080 × BLD 125 (0.96). The results are in agreement with Kumar *et al.* (2016), Reddy *et al.* (2016) and Rajesh *et al.* (2018).

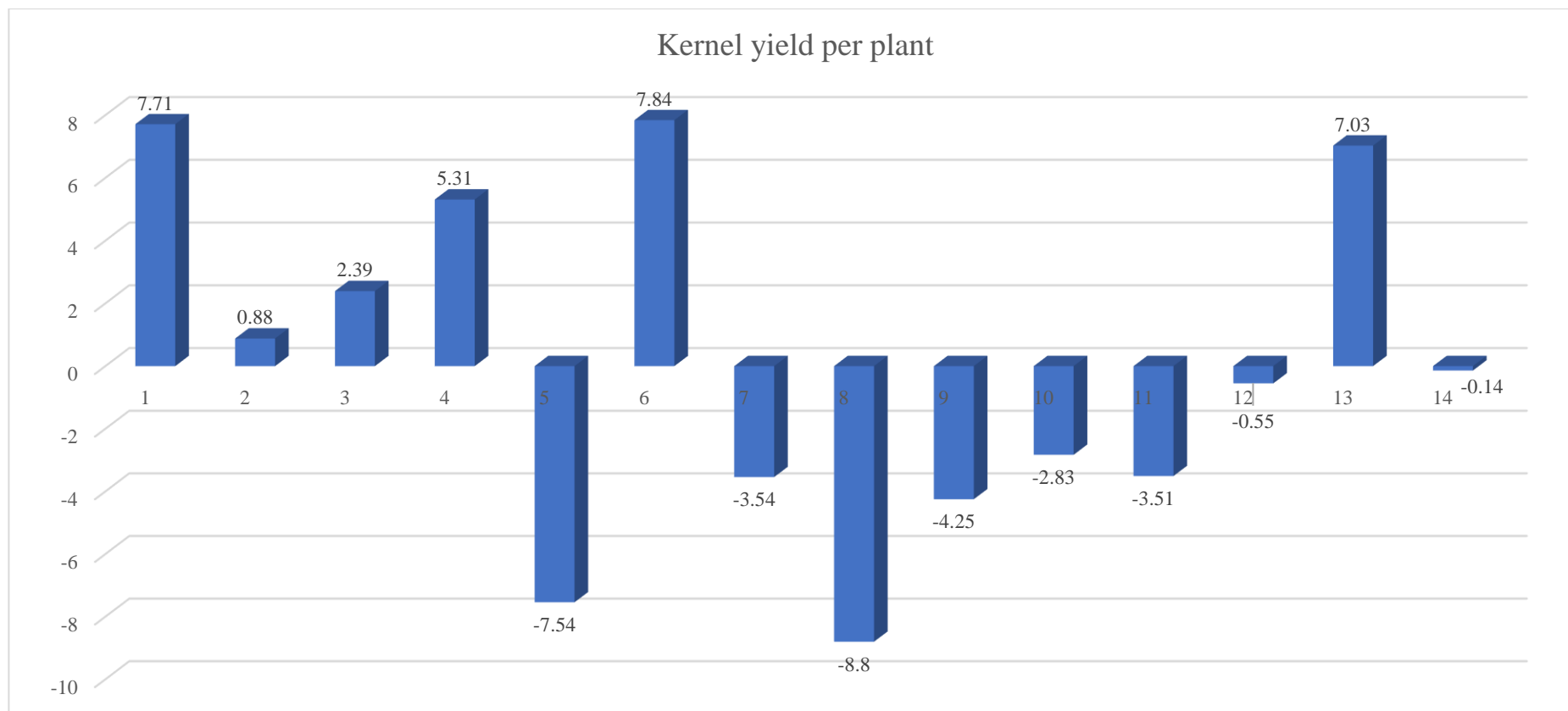


Fig 4.4 General combining ability effect of parents in maize for kernel yield per plant

1	BLD 2	3	BLD 114	5	WNC 40324	7	WNC 40456	9	WNC 52646	11	BLD 98	13	BLD 125
2	BLD 109	4	WNC 40080	6	WNC 40406	8	WNC 52313	10	VL 109178	12	BLD 103	14	IMR 113

4.4.2.10 Kernels per row

Among the parents 3 lines WNC 52646 (0.72), WNC 40456 (0.65), WNC 40406 (0.64) and 2 testers IMR 113 (0.77) and VL 109178 (0.46) exhibited *gca* effects significant in positive direction. Therefore, out of 14 parents 5 prenatal genotypes were proved to be good general combiners.

The estimates of *sca* effects implied that 8 out of 45 hybrids exhibited significant and positive *sca* effects for this trait. Top three high significant and positive SCA value expressed by the combination WNC 40406 \times BLD 125 (3.25) followed by BLD 109 \times IMR 113 (2.07) and WNC 40324 \times VL 109178 (1.82). Habtamu zelege *et al.* (2015), Kumar *et al.* (2016), Reddy *et al.* (2016), Rajesh *et al.* (2018) and Aswin *et al.* (2020) recorded similar result.

4.4.2.11 100 kernel weight

The female parent *viz.*, BLD 109 (3.24), BLD 2 (1.84), BLD 114 (1.11) and male parent BLD 98 (0.70) were reported significant *gca* effects in the positive direction and therefore these parents were good general combiners for 100 kernel weight.

Out of total crosses, 9 crosses expressed significant *sca* effects in the positive direction. Among the desirable combination the cross, WNC 40080 \times IMR 113 (4.12) possessed high significant and positive *sca* effects followed by BLD 114 \times BLD 98 (3.96) and WNC 40456 \times VL 109178 (2.56). these 3 combinations were good specific combiners for this trait. The earlier findings of Kumar *et al.* (2016), Reddy *et al.* (2016) and Rajesh *et al.* (2018) were similar to the present result.

4.4.2.12 Kernel yield per plant

Among all the parental genotypes under study, 4 genotypes *viz.*, WNC 40406 (7.84), BLD 2 (7.71), BLD 125 (7.03) and WNC 40080 (5.31) found significant *gca* effects in the positive direction and therefore these parents were good general combiners for kernel yield per plant.

Estimates of *sca* effects implied that 14 out of 45 hybrids exhibited significant and positive *sca* effects for this trait. The cross BLD 2 \times BLD 103 (25.53) had maximum significant and positive *sca* effects followed by WNC 40406 \times BLD 125 (20.08) and BLD 114 \times IMR 113 (17.43). These results confirm the findings of Amiruzzaman *et al.* (2013), Habtamu zelege *et al.* (2015), Ram *et al.* (2015), Kumar *et al.* (2016), Reddy *et al.* (2016), Reddy *et al.* (2016) and Rajesh *et al.* (2018).

Table 4.14 : The estimates of specific combining ability (*sca*) effects of the crosses for various characters in maize

Sr. No.	Crosses	Days to tasseling	Days to silking	ASI	Plant height (cm)	Ear height (cm)	Days to maturity	Cob length (cm)
1.	BLD 2 × VL 109178	0.70	0.64	-0.12	10.46	5.40	-0.13	-0.13
2.	BLD 2 × BLD 98	-0.96	-0.81	0.10	-6.69	-2.86	-2.28**	-0.65
3.	BLD 2 × BLD 103	1.93*	2.53**	0.55	-2.91	-2.53	0.76	0.58
4.	BLD 2 × BLD 125	-1.04	-1.77*	-0.49	-3.42	-3.64	0.13	0.25
5.	BLD 2 × IMR 113	-0.63	-0.59	-0.04	2.57	3.62	1.53	-0.05
6.	BLD 109 × VL 109178	0.84	0.04	-0.79*	-13.94*	-0.00	-1.07	-0.01
7.	BLD 109 × BLD 98	1.50	1.93*	0.44	-10.42	-12.59**	1.12	0.18
8.	BLD 109 × BLD 103	-0.94	-1.07	-0.12	6.69	2.07	-0.84	0.04
9.	BLD 109 × BLD 125	-0.24	0.30	0.51	9.18	8.96	0.19	-0.45
10.	BLD 109 × IMR 113	-1.16	-1.19	-0.04	8.50	1.56	0.60	0.23
11.	BLD 114 × VL 109178	0.57	0.10	-0.45	2.14	-6.00	-0.80	-0.33
12.	BLD 114 × BLD 98	-0.10	-0.01	0.10	-5.01	0.41	0.39	1.10**
13.	BLD 114 × BLD 103	-0.21	-0.34	-0.12	7.43	7.07	0.09	0.17
14.	BLD 114 × BLD 125	-1.17	-0.97	0.18	-0.81	5.96	0.79	-1.09**
15.	BLD 114 × IMR 113	0.90	1.21	0.29	-3.75	-7.44	-0.47	0.16
16.	WNC 40080 × VL 109178	-0.83	-0.43	0.41	2.12	0.27	0.20	-1.13**
17.	WNC 40080 × BLD 98	-0.16	-0.21	-0.03	6.64	9.34	-0.95	1.35**
18.	WNC 40080 × BLD 103	-0.27	0.13	0.41	-0.25	-3.33	0.42	-0.04
19.	WNC 40080 × BLD 125	1.76*	1.83*	0.04	-3.09	-2.77	1.46	-0.11
20.	WNC 40080 × IMR 113	-0.50	-1.32	-0.84*	-5.43	-3.51	-1.13	-0.08
21.	WNC 40324 × VL 109178	0.77	1.57	0.81*	2.66	3.47	1.60*	1.47**
22.	WNC 40324 × BLD 98	-1.90*	-2.54**	-0.63	-0.82	-2.46	-1.21	-0.03
23.	WNC 40324 × BLD 103	0.33	0.13	-0.19	9.29	3.54	-0.18	-0.33
24.	WNC 40324 × BLD 125	1.03	1.16	0.11	-10.89	-10.24*	0.19	-1.00**

25.	WNC 40324 × IMR 113	-0.23	-0.32	-0.11	-0.23	5.69	-0.40	-0.11
26.	WNC 40406 × VL 109178	0.24	0.04	-0.19	3.52	1.73	0.07	-0.25
27.	WNC 40406 × BLD 98	0.24	-0.07	-0.30	5.04	0.14	-1.41	-0.35
28.	WNC 40406 × BLD 103	-1.54*	-1.74*	-0.19	-3.85	1.14	-1.71*	-0.46
29.	WNC 40406 × BLD 125	-0.17	-0.37	-0.22	-3.36	-5.30	0.66	0.60
30.	WNC 40406 × IMR 113	1.24	2.15*	0.89*	-1.36	2.29	2.40**	0.45
31.	WNC 40456 × VL 109178	-1.23	-0.56	0.61	-4.94	0.27	1.20	0.10
32.	WNC 40456 × BLD 98	1.44	1.33	-0.16	3.58	1.01	1.72*	-0.93**
33.	WNC 40456 × BLD 103	-0.01	-0.34	-0.39	-3.31	-5.99	0.76	-0.54
34.	WNC 40456 × BLD 125	-0.64	-1.30	-0.76*	2.18	3.56	-1.87*	1.68**
35.	WNC 40456 × IMR 113	0.44	0.88	0.69	2.50	1.16	-1.80*	-0.30
36.	WNC 52313 × VL 109178	-0.23	-0.36	-0.12	-1.21	-8.00	0.13	0.09
37.	WNC 52313 × BLD 98	-0.23	-0.47	-0.23	-0.36	1.74	1.32	-0.30
38.	WNC 52313 × BLD 103	1.33	1.53	0.21	-2.91	0.07	-0.98	0.31
39.	WNC 52313 × BLD 125	0.03	0.56	0.51	6.24	2.96	0.39	-0.04
40.	WNC 52313 × IMR 113	-0.90	-1.25	-0.38	-1.76	3.22	-0.87	-0.07
41.	WNC 52646 × VL 109178	-0.83	-1.03	-0.19	-0.81	2.87	-1.20	0.18
42.	WNC 52646 × BLD 98	0.17	0.86	0.70	8.04	5.27	1.32	-0.37
43.	WNC 52646 × BLD 103	-0.61	-0.81	-0.19	-10.18	-2.06	1.69*	0.27
44.	WNC 52646 × BLD 125	0.43	0.56	0.11	3.98	0.50	-1.94*	0.15
45.	WNC 52646 × IMR 113	0.84	0.41	-0.44	-1.03	-6.58	0.13	-0.23
S.Em. ±		0.76	0.83	0.36	6.97	4.77	0.78	0.34
Range	Minimum	-1.9	-2.54	-0.84	-13.94	-12.59	-2.28	-1.13
	Maximum	1.93	2.53	0.89	10.46	9.34	2.4	1.68
Total significant		4	7	5	1	2	9	8
Number of +ve significant		2	4	3	0	0	4	4
Number of -ve significant		2	3	2	1	2	5	4

Note : * and ** indicate level of significance at 5 % and 1 %, respectively

Table 4.14 cont....

S.N.	Crosses	Cob girth (cm)	Kernels row per cob	Kernels per row	100 kernels weight (g)	Kernel yield per plant	Shelling (%)
1.	BLD 2 × VL 109178	-0.03	-0.01	1.21	1.49	9.20**	-2.18
2.	BLD 2 × BLD 98	-0.03	0.12	-1.21	-0.10	6.02*	-0.92
3.	BLD 2 × BLD 103	0.54	0.34	1.74*	-2.96**	25.53**	3.57**
4.	BLD 2 × BLD 125	0.39	0.37	-1.04	2.45**	-16.46**	1.38
5.	BLD 2 × IMR 113	-0.86**	-0.83**	-0.70	-0.88	-24.29**	-1.84
6.	BLD 109 × VL 109178	0.08	-1.32**	-0.08	-2.58**	5.76*	2.21
7.	BLD 109 × BLD 98	0.16	0.01	-0.04	1.83*	-7.42*	2.93*
8.	BLD 109 × BLD 103	0.13	0.64*	-1.55*	1.64	-9.25**	-0.51
9.	BLD 109 × BLD 125	-0.76**	0.13	-0.40	0.39	6.90*	-3.45*
10.	BLD 109 × IMR 113	0.39	0.53	2.07**	-1.28	4.01	-1.17
11.	BLD 114 × VL 109178	-0.30	-0.71*	0.16	-0.78	-4.88	-3.68**
12.	BLD 114 × BLD 98	0.39	0.09	1.47*	3.96**	12.94**	1.53
13.	BLD 114 × BLD 103	0.00	-0.08	0.09	0.44	-11.22**	-0.63
14.	BLD 114 × BLD 125	-0.09	-0.45	-0.36	0.19	-14.27**	-2.37
15.	BLD 114 × IMR 113	0.00	1.15**	-1.35*	-3.81**	17.43**	5.15**
16.	WNC 40080 × VL 109178	0.15	-0.09	-1.00	-0.51	-10.47**	0.34
17.	WNC 40080 × BLD 98	0.55	0.84**	-0.09	-3.44**	-0.12	-2.74*
18.	WNC 40080 × BLD 103	-0.10	-0.80**	1.53*	2.38**	0.39	0.52
19.	WNC 40080 × BLD 125	-0.08	0.96**	-0.65	-2.55**	6.54*	2.35
20.	WNC 40080 × IMR 113	-0.51	-0.91**	0.22	4.12**	3.65	-0.47
21.	WNC 40324 × VL 109178	0.02	0.79*	1.82**	-1.11	3.25	2.69*
22.	WNC 40324 × BLD 98	-0.69*	-0.68*	-0.33	2.63	0.67	-2.86*
23.	WNC 40324 × BLD 103	-0.10	-0.32	-0.31	-0.56	5.91*	3.15*
24.	WNC 40324 × BLD 125	0.46	-0.03	-1.36*	-1.48	-4.27	-0.98
25.	WNC 40324 × IMR 113	0.30	0.24	0.18	0.52	-5.57	-2.00

26.	WNC 40406 × VL 109178	-0.01	-0.39	-1.76*	0.42	-14.80**	-0.68
27.	WNC 40406 × BLD 98	-0.36	0.15	0.55	-1.50	-6.85*	-1.33
28.	WNC 40406 × BLD 103	0.31	0.24	-1.90**	1.98*	5.19	-0.32
29.	WNC 40406 × BLD 125	-0.14	-0.40	3.25**	0.39	20.08**	2.12
30.	WNC 40406 × IMR 113	0.19	0.40	-0.14	-1.28	-3.62	0.22
31.	WNC 40456 × VL 109178	0.23	1.08**	0.16	2.56**	0.79	-0.11
32.	WNC 40456 × BLD 98	-0.25	-0.65*	-1.27	-4.37**	-4.80	1.38
33.	WNC 40456 × BLD 103	-0.11	-0.03	-0.51	-1.22	-13.75**	-1.99
34.	WNC 40456 × BLD 125	0.39	-0.53	1.51*	1.19	0.80	1.16
35.	WNC 40456 × IMR 113	-0.26	0.13	0.11	1.85*	16.97**	-0.44
36.	WNC 52313 × VL 109178	-0.03	0.17	-0.19	-1.64	10.24**	2.41
37.	WNC 52313 × BLD 98	-0.11	-0.09	-0.81	0.10	-0.34	0.55
38.	WNC 52313 × BLD 103	-0.44	0.26	0.94	-0.09	5.83*	2.17
39.	WNC 52313 × BLD 125	-0.09	-0.51	-0.77	1.65	-12.08**	-4.97**
40.	WNC 52313 × IMR 113	0.68*	0.16	0.83	-0.01	-3.65	-0.16
41.	WNC 52646 × VL 109178	-0.10	0.47	-0.31	2.16*	0.89	-0.99
42.	WNC 52646 × BLD 98	0.34	0.20	1.73*	0.90	-0.09	1.47
43.	WNC 52646 × BLD 103	-0.23	-0.24	-0.04	-1.62	-8.65**	-5.96**
44.	WNC 52646 × BLD 125	-0.08	0.45	-0.16	-2.21**	12.77**	4.76**
45.	WNC 52646 × IMR 113	0.07	-0.88**	-1.22	0.79	-4.93	0.72
	S.Em. ±	0.28	0.30	0.67	0.84	2.93	1.34
Range	Minimum	-0.86	-1.32	-1.9	-4.37	-24.29	-5.96
	Maximum	0.68	1.15	3.25	4.12	25.53	5.15
	Total significant	4	14	13	16	26	12
	Number of +ve significant	1	6	8	9	14	6
	Number of -ve significant	3	8	5	7	12	6

Note : * and ** indicate level of significance at 5 % and 1 %, respectively

4.4.2.13 Shelling percentage

The data of *gca* effect for shelling percentage showed that only 2 parents BLD 2 (1.26) from lines and VL 109178 (0.97) from testers had observed with significant *gca* effects in the positive direction. Hence these genotypes were good general combiners for shelling percentage.

The data on *sca* effects showed that 6 hybrids out of 45 hybrids exhibited significant *sca* effects in the positive direction. Top 3 significant and positive SCA reported by BLD 114 × IMR 113 (5.15), WNC 52646 × BLD 125 (4.76) and BLD 2 × BLD 103 (3.57). Earlier workers *viz.*, Reddy *et al.* (2016), Sandesh *et al.* (2018), Chandel *et al.* (2019) and Patel *et al.* (2019) also reported similar result.

Overall, the results of *gca* effects of the parents were classified as good, average and poor combiners for different traits presented in Table 4.16. Among all the parents under study, the genotype *viz.*, BLD 2, WNC 40080, WNC 40406, BLD 125 were good general combiner for kernel yield per plant. Among them, BLD 2 was also found promising for other traits like anthesis silking interval (ASI), cob length, kernels row per cob, 100 kernels weight, kernel yield per plant, shelling percentage. While parent WNC 40406 was also found good general combiner for days to silking, anthesis silking interval (ASI) and Kernels per row. For days to tasseling only one parent (WNC 52646) is found good general combiner. For 100 kernels weight the parental genotypes BLD 2, BLD 109, BLD 114, and BLD 98 were reported as good general combiner. The parents like VL 109178 and BLD 98 both are found promising for plant height and ear height character. Among the parents, BLD 109, WNC 40080, WNC 40324, WNC 52313, VL 109178 were found good general combiner for early maturity characters. This suggested that these parental genotypes could be utilized in future breeding programmes for exploitation of hybrid vigor and also to generate a greater number of desirable segregants for kernel yield per plant and yield attributing characters.

For comparative study most promising hybrids, having high specific combining ability effects for kernel yield per plant with various characters under study are presented in Table 4.17. The crosses *viz.*, BLD 2 × BLD 103 (25.53), WNC 40406 × BLD 125 (20.08), BLD 114 × IMR 113 (17.43), WNC 40456 × IMR 113 (16.97) and BLD 114 × BLD 98 (12.94) were reported with high and significant specific combining ability effects for kernel yield per plant. The crosses like WNC 40406 × BLD 125 (3.25), BLD 2 × BLD 103 (1.74), and BLD 114 × BLD 98 (1.47) possessed

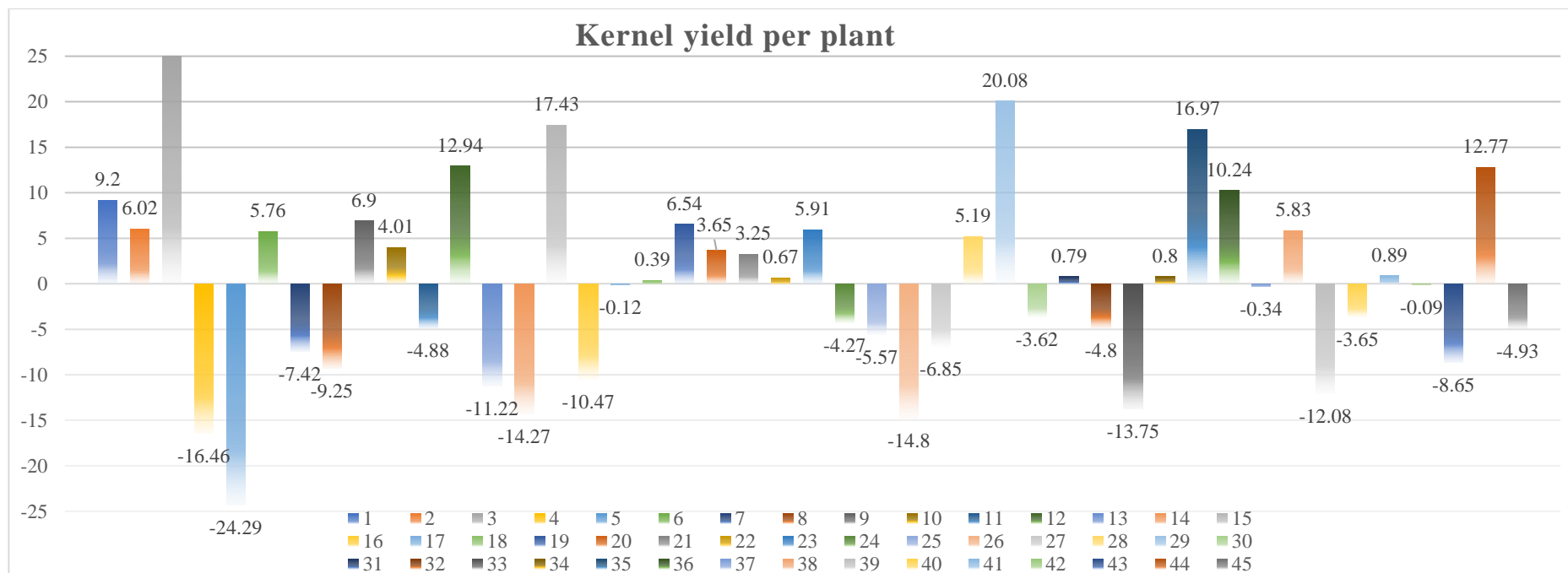


Fig 4.5 Specific combining ability effect of hybrids in maize for kernel yield per plant

1	BLD 2 × VL 109178	13	BLD 114 × BLD 103	25	WNC 40324 × IMR 113	37	WNC 52313 × BLD 98
2	BLD 2 × BLD 98	14	BLD 114 × BLD 125	26	WNC 40406 × VL 109178	38	WNC 52313 × BLD 103
3	BLD 2 × BLD 103	15	BLD 114 × IMR 113	27	WNC 40406 × BLD 98	39	WNC 52313 × BLD 125
4	BLD 2 × BLD 125	16	WNC 40080 × VL 109178	28	WNC 40406 × BLD 103	40	WNC 52313 × IMR 113
5	BLD 2 × IMR 113	17	WNC 40080 × BLD 98	29	WNC 40406 × BLD 125	41	WNC 52646 × VL 109178
6	BLD 109 × VL 109178	18	WNC 40080 × BLD 103	30	WNC 40406 × IMR 113	42	WNC 52646 × BLD 98
7	BLD 109 × BLD 98	19	WNC 40080 × BLD 125	31	WNC 40456 × VL 109178	43	WNC 52646 × BLD 103
8	BLD 109 × BLD 103	20	WNC 40080 × IMR 113	32	WNC 40456 × BLD 98	44	WNC 52646 × BLD 125
9	BLD 109 × BLD 125	21	WNC 40324 × VL 109178	33	WNC 40456 × BLD 103	45	WNC 52646 × IMR 113
10	BLD 109 × IMR 113	22	WNC 40324 × BLD 98	34	WNC 40456 × BLD 125		
11	BLD 114 × VL 109178	23	WNC 40324 × BLD 103	35	WNC 40456 × IMR 113		
12	BLD 114 × BLD 98	24	WNC 40324 × BLD 125	36	WNC 52313 × VL 109178		

high significant and positive *sca* effects for kernels per row. While the combination like BLD 114 × BLD 98 (3.96) and WNC 40456 × IMR 113 (1.85) had highest value of significant and positive *sca* effects for 100 kernels weight. Which indicated that these crosses could be utilize for future crop improvement program.

Table 4.15 : Variance for general combining ability and specific combining ability along with gene action for different traits in maize

Sr. No.	Traits	σ^2_{gca}	σ^2_{sca}	$\sigma^2_{gca} / \sigma^2_{sca}$	Gene action
1	Days to tasseling	0.07	0.57**	0.12	Non additive gene action
2	Days to silking	0.05	1.04**	0.04	Non additive gene action
3	ASI	0.01	0.12*	0.12	Non additive gene action
4	Plant height (cm)	25.48**	-3.40	-7.50	Additive gene action
5	Ear height (cm)	13.69**	9.67	1.41	Additive gene action
6	Days to maturity	0.55**	1.20**	0.46	Non additive gene action
7	Cob length (cm)	0.08*	0.37**	0.21	Non additive gene action
8	Cob girth (cm)	0.01	0.08**	0.10	Non additive gene action
9	Kernels row per cob	0.06	0.34*	0.19	Non additive gene action
10	Kernels per row	0.31*	1.33	0.24	Non additive gene action
11	100 kernels weight (g)	0.75	4.75**	0.16	Non additive gene action
12	Kernel yield per plant	4.47	139.33**	0.03	Non additive gene action
13	Shelling (%)	-0.35	6.16**	-0.06	Non additive gene action

Note : * and ** indicate level of significance at 5 % and 1 %, respectively

Table 4.16 : Classification of parents with respect to general combining ability for different characters in maize

S.N.	Parents	DT	DS	ASI	PH	EH	DM	CL	CG	KR/C	K/R	SI	KY/P	Shelling (%)
FEMALE PARENTS (Lines)														
1	BLD 2	P	A	G	A	A	P	G	A	G	A	G	G	G
2	BLD 109	A	A	A	A	P	G	P	A	A	P	G	A	P
3	BLD 114	A	P	A	P	A	P	A	P	A	A	G	A	A
4	WNC 40080	A	A	A	A	A	G	A	A	G	A	P	G	A
5	WNC 40324	A	A	A	A	A	G	A	A	G	P	P	P	A
6	WNC 40406	A	G	G	A	A	A	P	A	P	G	P	G	A
7	WNC 40456	A	A	A	A	A	P	G	A	P	G	P	P	A
8	WNC 52313	A	A	A	A	A	G	P	A	P	A	A	P	A
9	WNC 52646	G	A	P	A	A	P	G	P	P	G	A	P	A
MALE PARENTS (Testers)														
1	VL 109178	A	A	A	G	G	G	A	A	A	G	P	P	G
2	BLD 98	A	A	A	G	G	P	P	A	P	P	G	P	A
3	BLD 103	A	A	A	A	P	P	A	P	A	A	A	A	A
4	BLD 125	A	P	A	P	A	P	A	A	A	A	A	G	A
5	IMR 113	A	A	A	A	P	A	G	A	G	G	A	A	A

DT = Days to tasseling, DS = Days to silking, ASI = Anthesis silking interval, PH = Plant height, EH = Ear height, DM = Days to maturity, CL = Cob length, CG = Cob girth, KR/C = Kernels row per cob, K/R = Kernels per row, SI = 100 kernels weight, KY/P = Kernel yield per plant, Shelling (%) = Shelling percentage.

Table 4.17 : Comparative study of most promising hybrids showing high specific combining ability (*sca*) effects for kernel yield per plant with various characters

Hybrids	DT	DS	ASI	PH	EH	DM	CL	CG	KR/C	K/R	SI	KY/P	Shelling (%)
BLD - 2 × BLD - 103	25.53**	1.93*	2.53**	0.55	-2.91	-2.53	0.76	0.58	0.54	0.34	1.74*	-2.96**	3.57**
WNC - 40406 × BLD - 125	20.08**	-0.17	-0.37	-0.22	-3.36	-5.30	0.66	0.60	-0.14	-0.40	3.25**	0.39	2.12
BLD - 114 × IMR - 113	17.43**	0.90	1.21	0.29	-3.75	-7.44	-0.47	0.16	0.00	1.15**	-1.35*	-3.81**	5.15**
WNC - 40456 × IMR - 113	16.97**	0.44	0.88	0.69	2.50	1.16	-1.80*	-0.30	-0.26	0.13	0.11	1.85*	-0.44
BLD - 114 × BLD - 98	12.94**	-0.10	-0.01	0.10	-5.01	0.41	0.39	1.10**	0.39	0.09	1.47*	3.96**	1.53

Note: * and ** indicate level of significance at 5 % and 1 %, respectively

DT = Days to tasseling, DS = Days to silking, ASI = Anthesis silking interval, PH = Plant height, EH = Ear height, DM = Days to maturity, CL = Cob length, CG = Cob girth, KR/C = Kernels row per cob, K/R = Kernels per row, SI = 100 kernels weight, KY/P = Kernel yield per plant, Shelling (%) = Shelling percentage.

Table 4.18 : Best performing parents and crosses on the basis of combining ability effects and mean performance for kernel yield per plant

Sr. No.	Parents	<i>gca</i> effects	Mean	Other traits found with desirable direction	Crosses	<i>sca</i> effects	Mean	Other traits found with desirable direction
1	WNC 40406	7.84**	68.93	DT, DS, ASI, PH, EH, CG, K/R, KY/P, Shelling %	BLD 2 × BLD 103	25.53**	92.87	PH, EH, CL, CG, KR/C, K/R, KY/P, Shelling %
2	BLD 2	7.71**	47.00	ASI, PH, EH, DM, CL, CG, KR/C	WNC 40406 × BLD 125	20.08**	95.13	DT, DS, ASI, PH, EH, CL, K/R, SI, KY/P, Shelling %
3	WNC 40080	5.31**	52.80	PH, EH, DM, KR/C, KY/P, Shelling %	BLD 114 × IMR 113	17.43**	79.87	PH, EH, DM, CL, KR/C, KY/P, Shelling %
4	BLD 125	7.03**	59.67	CL, CG, KR/C, KY/P	WNC 40456 × IMR 113	16.97**	73.47	DM, KR/C, K/R, SI, KY/P,
5					BLD 114 × BLD 98	12.94**	72.00	DT, DS, PH, CL, CG, KR/C, K/R, SI, KY/P, Shelling %

Note : * and ** indicate level of significance at 5 % and 1 %, respectively

DT = Days to tasseling, DS = Days to silking, ASI = Anthesis silking interval, PH = Plant height, EH = Ear height, DM = Days to maturity, CL = Cob length, CG = Cob girth, KR/C = Kernels row per cob, K/R = Kernels per row, SI = 100 kernels weight, KY/P = Kernel yield per plant, Shelling (%) = Shelling percentage.

4.4.2.14 Performance of top five hybrids with *sca* effects

For successful exploitation of heterosis on commercial scale, production of hybrid seed on large scale and high heterotic response are essential. While possibility of hybrid seed production in maize do exist, there is a need to identify heterotic hybrids. A comparative data of yield of top five hybrids *viz.*, BLD 2 × BLD 103, WNC 40406 × BLD 125, BLD 114 × IMR 113, WNC 40456 × IMR 113 and BLD 114 × BLD 98 are presented in Table no 4.18. These hybrids have higher *per se* performance, high *sca* effects and high standard heterosis over check GAYMH 1 for kernel yield per plant with other yield attributing component. The hybrid BLD 2 × BLD 103 with highest *per se* performance 92.87 g exhibited significant positive *sca* effect 25.53 *per cent* for kernel yield per plant with the desirable *sca* effects for plant height, ear height, cob length, cob girth, kernels row per cob, kernels per row, kernel yield per plant and Shelling percentage.

The next superior hybrid, WNC 40406 × BLD 125 recorded significant positive *sca* effect 20.08 percent and *per se* performance 95.13 g for kernel yield per plant with desirable *sca* effect for days to tasseling, days to silking, anthesis silking interval, plant height, ear height, cob length, kernels per row, 100 kernels weight, kernel yield per plant and Shelling percentage.

The third crosses BLD 114 × IMR 113 had mean performance 79.87 g and significant positive *sca* effect 17.43 percent for kernel yield per plant. This cross exhibited desirable *sca* effect for plant height, ear height, days to maturity, cob length, kernels row per cob, kernel yield per plant and Shelling percentage.

The hybrid WNC 40456 × IMR 113 which ranked fourth with significant positive *sca* effect 16.97 percent with mean performance 73.47 g for kernel yield per plant. This cross exhibited desirable *sca* effect for days to maturity, kernels row per cob, kernels per row, 100 kernels weight and kernel yield per plant.

The fifth hybrid BLD 114 × BLD 98 recorded significant positive *sca* effects 12.94 percent with mean performance 72.00 g for kernel yield per plant associated with desirable *sca* effect like days to tasseling, days to silking, plant height, cob length, cob girth, kernels row per cob, kernels per row, 100 kernels weight, kernel yield per plant and Shelling percentage.

4.4.2.15 Breeding methodology

The breeding methodology to be followed depends primarily upon the nature and magnitude of gene action. For successful exploitation of heterosis, existence of

significant amount of dominance variance as measured by SCA variance is the prerequisite. In the present investigation potency and predictable ratio is less than one and less than 0.5, respectively and the characters are governed by the non-additive gene action. Five top heterotic hybrids had high *sca* effects. All of these 5 involved good × good and good × poor / poor × good combiners as parents. High *sca* effects of the cross *viz.*, BLD 2 × BLD 103, WNC 40406 × BLD 125, BLD 114 × IMR 113, WNC 40456 × IMR 113 and BLD 114 × BLD 98 suggested that they could be directly utilized for heterosis breeding.

High *gca* effects of their parents, good × good involved interaction between additive × additive alleles revealed that it could be fixable in subsequent generation if no repulsion phase linkage are involved and thus may be exploited for selection of homozygous pure lines through pedigree method of breeding. In order to exploit high *sca* effects simultaneously reciprocal recurrent selection method may be adopted.

The cross BLD 2 × BLD 103 manifested high *sca* effects and higher *per se* performance involving good × average general combiners as parents, could best be exploited for isolation of higher yielding inbred lines by pedigree method.

The high yielding potential of the hybrids BLD 2 × BLD 103, WNC 40406 × BLD 125, BLD 114 × IMR 113, WNC 40456 × IMR 113 and BLD 114 × BLD 98 involving good × good, average × average or poor combiners was attributed to interaction of additive × non-additive alleles which would be unfixable in subsequent generation and hence can be grown directly as commercial hybrids.

Improved lines can also be identified from these crosses as they involved male parent's *viz.*, BLD 103, BLD 125, IMR 113 and BLD 98. Likewise, female parental lines BLD 2, WNC 40406, BLD 114 and WNC 40456 could be exploited fully in future maize breeding programme by appropriate breeding techniques in order to evolve high yielding hybrids or varieties.

Since, the experiment was carried out only for one season over single location, it is expected that the estimation of genetic variances would be biased upward due to genotype × environment interaction and this would lead to test the material over the environments or locations for precise estimation of combining ability to draw any inference regarding gene action involved in the inheritance of different traits.

SUMMARY AND CONCLUSIONS

V. SUMMARY AND CONCLUSIONS

The present investigation entitled "Estimation of Heterosis and combining ability in maize (*Zea mays* L.)" was carried to achieve information on the range of heterosis, *i.e.*, heterobeltiosis and standard heterosis, combining ability and genetic components of variation involved in the expression of yield and its attributing traits. The experimental materials comprised of 14 (9 + 5) parents, 45 crosses generated through line \times tester mating design and one standard check GAYMH 1. The experiment was conducted at the Maize Research Station, Sardarkrushinagar Dantiwada Agricultural University, Bhiloda. Experimental materials were evaluated in a randomized block design with three replications during *kharif* 2020. In this investigation the observations were recorded for 13 different traits including days to tasseling, days to silking, anthesis silking interval (ASI), plant height, ear height, days to maturity, cob length, cob girth, kernel rows per cob, kernels per row, 100 kernel weight, kernel yield per plant and shelling percentage.

5.1 Analysis of variance

The analysis of variance depicted significant difference among all the genotypes for all the characters under study. Further partitioning of analysis of variance reported that, parents were found highly significant for all the characters which means presence of sufficient amount of genetic variability and parents were differed significantly for all the characters. The analysis of variance due to hybrids were indicated the highly significant difference for all the traits under study except plant height. The variance due to lines *vs.* testers were significant for days to tasseling, days to silking, plant height, ear height and kernels row per cob. The variance due to parents *vs.* hybrids found significant for the trait *viz.*, days to tasseling, days to silking, plant height, ear height, cob length, cob girth, kernels row per cob, 100 kernels weight and shelling percentage. This suggested the existence of differences between parents and hybrids for the characters under study.

5.2 *per se* performance of parents and hybrids.

The *per se* performance hybrids were higher than parents in desirable direction for the traits like plant height, ear height, cob length, cob girth, kernels row per cob, kernels per row and kernel yield per plant, which suggested the possibility, for

existence of heterotic effects. In this trial, in respect to *per se* performance of parents, female parent BLD 114 and male parent IMR 113 were found to be superior for kernel yield per plant. Among the hybrids, WNC 40406 × BLD 125 and BLD 2 × BLD 103 manifested higher *per se* performance.

5.3 Magnitude of heterosis

The degree and magnitude of various heterotic effects were varied from cross to cross. It indicates, the degree of heterosis varied from cross to cross for all the characters. In this experiment, out 45 crosses the crosses *viz.*, BLD 2 × BLD 103, BLD 2 × BLD 98 and WNC 40406 × BLD 125 were registered best three crosses based on significant heterobeltiosis for kernel yield per plant. While best three crosses based on standard heterosis were WNC 40406 × BLD 125, BLD 2 × BLD 103 and BLD 114 × IMR 113. Among the best three crosses for kernel yield per plant based on standard heterosis, WNC 40406 × BLD 125, BLD 2 × BLD 103 were found significant with respect to standard heterosis as well as heterobeltiosis. The importance of standard heterosis is higher than heterobeltiosis therefore these three crosses were considered as best three crosses for kernel yield per plant. The crosses which possess higher magnitude of heterosis for kernel yield per plant also had significant heterosis for 100 kernel weight in positive direction. The results of heterosis analysis revealed that the crosses WNC 40406 × BLD 125, BLD 2 × BLD 103 and BLD 114 × IMR 113 were found as promising and need to be included for further evaluation.

5.4 Combining ability analysis

The analysis of variance for combining ability revealed that specific combining ability variance for hybrids was highly significant for all the characters under study. Mean square due female also found significant for all the characters. Mean square due to line × tester interaction was found significant for most of the traits except plant height and ear height. It signified the contribution of hybrids for specific combining ability variance components.

Both GCA and SCA variances were important for inheritance of various traits under study. In present study, the magnitude of SCA variances was higher than the GCA variances and the ratio of $\sigma^2_{gca}/\sigma^2_{sca}$ was less than unity for all the characters except ear height. Which indicated non-additive gene action in the inheritance of these traits.

The per cent contribution to total variance revealed that female parents contributed more to total variance for all traits except plant height and ear height. In comparison, the comparative study of per cent contribution of parents and hybrids to total variance revealed that hybrids contributed more in the majority of traits *viz.*, days to tasseling, days to silking, anthesis silking interval (ASI), cob length (cm), cob girth (cm), kernels row per cob, kernels per row, 100 kernels weight (g), kernel yield per plant, and shelling percentage (%).

Based on estimates of *gca* effects the parent, WNC 40406 was good general combiner for days to silking, anthesis silking interval (ASI), kernels per row and kernel yield per plant; BLD 2 was good general combiner for anthesis silking interval (ASI), cob length, kernels row per cob, 100 kernels weight, kernel yield per plant and shelling percentage. WNC 40080 was good general combiner for days to maturity, kernels row per cob and kernel yield per plant; BLD 125 was good general combiner for kernel yield per plant.

The estimates of specific combining ability varied from cross to cross. Considering the *sca* performance of the hybrids, fourteen hybrids manifested desirable and significant *sca* effects for kernel yield per plant. The estimates of *sca* effects showed that top five hybrids *viz.*, BLD 2 × BLD 103, WNC 40406 × BLD 125 and BLD 114 × IMR 113, WNC 40456 × IMR 113 and BLD 114 × BLD 98 were exhibited maximum positive significant *sca* effect for kernel yield per plant and other contributing traits.

Based on the *gca* effect's overall performance, it can be concluded that the parental genotypes BLD 2, WNC 40080, WNC 40406, BLD 125 were good general combiner for kernel yield per plant. Considering all the aspects *i.e.*, *per se* performance, heterosis and combining ability effects, the hybrids BLD 2 × BLD 103, WNC 40406 × BLD 125 and BLD 114 × IMR 113 for kernel yield per plant were found potential to generate desirable segregants for selection of superior plant. These crosses may be exploited commercially after testing in wide range of environments. These crosses can also be used to throw off transgressive segregant in segregating generations for the improvement of yield and specific attributing traits.

5.5 Conclusion

Based on the results obtained, the following conclusion can be drawn.

- (1) The *per se* performance of the hybrids were higher than parents in for the traits like plant height, ear height, cob length, cob girth, kernels row per cob, kernels per row and kernel yield per plant.
- (2) The degree and magnitude of various heterotic effects were varied from cross to cross and character to character. However, greater amount of heterobeltiosis and standard heterosis were observed for kernel yield per plant and its components characters like plant height, ear height, cob length, cob girth, kernels row per cob, kernels per row, kernel yield per plant and shelling percentage.
- (3) Among the parents, female WNC 40406, BLD 2 and male parent BLD 125 were found to be good general combiners for kernel yield per plant and some component traits, hence these parents could be largely utilized to develop high yield genotypes/hybrids.
- (4) A perusal of *sca* effects of hybrids revealed that, hybrids BLD 2 × BLD 103, WNC 40406 × BLD 125 and BLD 114 × IMR 113 ranked top for all aspects of kernel yield per plant and some of its component traits.
- (5) Hybrids BLD 2 × BLD 103 and WNC 40406 × BLD 125 were leading for depicted higher *per se* performance, standard heterosis and *sca* effects for kernel yield per plant and some of its component characters, so these crosses can be exploited for commercial cultivation with due consideration of quality character of grains.

REFERENCES

REFERENCES

- Abdel-Moneam, M. A.; Sultan, M. S.; Sadek, S. E. and Shalof, M. S. (2014). Estimation of heterosis and genetic parameters for yield and yield components in maize using the diallel cross method. *Asian Journal of Crop Science*, **6**(2): 101-111.
- Abuali, A. I.; Abdelmulla, A. A.; Khalafalla, M. M.; Idris, A. E. and Osman, A. M. (2012). Combining ability and heterosis for yield and yield components in maize (*Zea mays* L.). *Australian Journal of Basic and Applied Sciences*, **6**(10): 36-41.
- Alam, A. K. M. M.; Ahmed, S.; Begum, M. and Sultan, M. K. (2008). Heterosis and Combining ability for grain yield and its contributing characters in maize. *Bangladesh Journal of Agricultural Research*, **33**(3): 375-379.
- Aldaji, A. M. M. I.; Noubissie, T. J. B.; Njintang, Y. N.; Nguimbou, R. M. and Bell, J. M. (2015). Diallel analysis of seed oil content in sesame. *Journal of Global Bioscience*, **4**(3): 1735-1746.
- Amiruzzaman, M.; Islam, Md. A.; Hasan, Lutful; Kadir M. and Rohman, Md. M. (2013). Heterosis and combining ability in a diallel among elite inbred lines of maize (*Zea mays* L.). *Emirates Journal of Food and Agriculture*, **25**(2): 132-137.
- Anilkumar, C. and Lohithaswa, H. C. (2018). Heterotic hybrid frequency in relation to combining ability and parental genetic divergence in maize. *Electronic Journal of Plant Breeding*, **9**(4): 1322-1334.
- Anonymous (2019-20). Ministry of agriculture and farmer welfare, Department of Agriculture, Cooperation and farmer welfare Directorate of Economics and Statistics, New Delhi, India.
- Anonymous (2020-21^a). United States Department of Agriculture.
- Anonymous (2020-21^b). Directorate of Agriculture - Agriculture, Farmer's Welfare and Cooperation Department, Government of Gujarat.
- Arunachalam, V.C. (1974). The fallacy behind the use of the modified line \times tester design. *Indian Journal of Genetics*, **34**: 280-287.
- Aswin, R. C.; Sudha, M., Senthil, A.; Sivakumar, S. and Senthil, N. (2020). Identification of superior drought tolerant maize hybrids based on combining ability and heterosis with Line \times Tester mating design. *Electronic Journal of Plant Breeding*, **11**(2):566-573.
- Bekele, A. and Rao, T. N. (2013). Heterosis study for grain yield, protein and oil improvement in selected genotypes of maize (*Zea mays* L.). *Journal of Plant Sciences*, **1**(4): 57-63.
- Bharti, B.; Dubey, R.B.; Kumar, A.; Bind, H.N. and Jat, B.S. (2017). Combining ability analysis for grain yield and its contributing traits in maize (*Zea mays* L.) over environments. *Electronic Journal of Plant Breeding*, **8**(4): 1069-1076.
- Chandel, Uttam; Kumar, Deep and Guleria, Guleria, Satish Kumar (2019). Combining ability effects and heterotic grouping in newly developed early maturing yellow maize (*Zea mays* L.) inbreds under sub-tropical conditions. *Electronic Journal of Plant Breeding*, **10**(3): 1049-1059.

- Darshan, S. S. and Marker, S. (2019). Heterosis and combining ability for grain yield and its component characters in quality protein maize (*Zea mays* L.) hybrids. *Electronic Journal of Plant Breeding*, **10**(1): 111-118.
- Doebley, J. F.; Gaut, B. S. and Smith, B. D. 2006. *Cell*, **127**: 1309.
- *East, E. M. (1916). Studies on the size of inheritance in *Nicotiana*. *Genetics*, **1**:164– 176.
- *Fonseca, S. and Patterson, F. L. (1968). Hybrid vigour in a seven-parent diallel cross in common winter wheat (*Triticum aestivum* L.). *Crop Science*, **8**(1): 85-88.
- Gami, R. A.; Chauhan, B. B. and Patel, R. N. (2020). Hayman's diallel analysis for yield and attributing traits in sesame (*Sesamum indicum* L.). *Electronic Journal of Plant Breeding*, **11**(2): 359-366.
- Gami, R. A.; Soni, N. V.; Chaudhary, S. M.; Solanki, S. D. and Patel P. C. (2018). Genetic Studies of the Kernel Yield and Attributing Traits of Single Cross Hybrid in Yellow Maize (*Zea mays* L.). *International Journal of Plant and Soil Science*, **22**(4): 40890.
- *Griffing, B. (1956^a). Concept of general and specific combining ability in relation to diallel crossing systems. *Australian Journal of Biological Sciences*, **9**: 463- 493.
- *Griffing, B. (1956^b). A generalized treatment of the use of diallel crosses in quantitative inheritance. *Heridity*, **10**: 31-50.
- *Henderson, C.R. (1952). Specific and general combining ability in "heterosis" [Edited by Johan, W. Gowen, DWA State College Press Ames Iowa, U.S.A (199-217)].
- *Jenkins, M. T. and Brunson, A. M. (1932). Methods of testing inbred lines of maize in crossbred combinations. *Journal of the American Society of Agronomy*, **24**: 523-530.
- Kage, U.K.; Wali, M.C.; Madalageri, D.; Natikar, P. and Gangashetty, P. (2013). Gene action and heterosis study in hybrids derived from new inbred lines in maize (*Zea mays* L.). *Molecular Plant Breeding*, **4**(18): 146-149.
- *Kempthorne, O. (1957). An Introduction to Genetic Statistics, *New York, John Wiley and Sons, 1st Edn.*, pp: 456-471.
- Kumar, S.; Chandel, U.; Guleria, S. K. and Devlash, R. (2019). Combining ability and heterosis for yield contributing and quality traits in medium maturing inbred lines of maize (*Zea mays* L.) using line × tester. *International Journal of Chemical Studies*, **7**(1): 2027-2034.
- Kumar, V.; Singh, S. K.; Singh, N. P. and Mahajan, V. (2016). Combining ability studies for grain yield other agronomic traits in maize (*Zea mays* L.). *Electronic Journal of Plant Breeding*, **7**(3): 544-554.
- Kuselan, K.; Manivannan, N.; Ravikesavan, R. and Paranidharan, V. (2017). Combining ability analysis for yield and its component characters in maize (*Zea mays* L.). *Electronic Journal of Plant Breeding*, **8**(2): 591-600.
- Lahane, G. R.; Patel, J. M. and Chauhan, R. M. (2015). Estimation of combining ability and heterosis for quantitative traits in maize (*Zea mays* L.) using diallel approach. *Agricultural Research Communication Centre*, **35**(4) 2015: 269-274.
- *Mathar, K. and Jinks, J. L. (1971). Components of mean, additive and dominance effects in Biometrical Genetics. Chapman and Hall Ltd. London, 65-67.

- *Mather, K. and Jinks, J. L. (1982). Biometrical genetics. 3rd ed. Chapman and Hall, London. Maydica, **37**: 217-223.
- Matin, M. Q. I.; Rasul, Md. G.; Islam, A. K. M. A.; Mian, M. A. K.; Akter Ivy, N. and Ahmed, J. U. (2016). Combining Ability and Heterosis in Maize (*Zea mays* L.). *American Journal of BioScience*, **4**(6): 84-90.
- *Meredith, W. R. and Bridge R. R. (1972) Heterosis and gene action in cotton (*Gossypium hirsutum* L.). *Crop Science*, **12**: 304-310.
- Mir, S. D.; Ahmad Mushtaq; Parray, G.A.; Zaffar Gul and Dar, S.H. (2015). Heterosis studies in single crosses of inbred lines in maize (*Zea mays* L.). *Electronic Journal of Plant Breeding*, **6**(4): 1073-1077.
- Murtadha, M. A.; Ariyo, O. J. and Alghamdi, S. S. (2018). Analysis of combining ability over environments in diallel crosses of maize (*Zea mays* L.). *Journal of Saudi Society of Agricultural Sciences*, **17**: 68-78.
- Nandhitha, G.; Ganesan, K. N.; and Ravikesavan R. (2018). Heterosis and combining ability studies in single cross hybrids synthesized with diverse inbred lines of maize (*Zea mays* L.). *Electronic Journal of Plant Breeding*, **9**(4): 1503-1511.
- Panase, V. G. and Sukhatme, P. V. (1985). Statistical methods for agricultural workers. 4th ed. ICAR, New Delhi, pp. 97-156.
- Patel, K.; Gami, R. A.; Kugashiya, K.G.; Chauhan, R. M.; Patel, R. N. and Patel, R. M. (2019). Gene action and combining ability analysis for kernel yield and its attributing traits in maize (*Zea mays* L.). *Electronic Journal of Plant Breeding*, **10**(2): 370-376.
- Patel, P. C. and Kathiria, K. B. (2016). Heterosis and combining ability for yield and quality traits in quality protein maize (*Zea mays* L.). *Electronic Journal of Plant Breeding*, **7**(4): 960-966.
- Rajesh, V.; Kumar, S. S.; Reddy, V. Narsimha and Sankar, A. Siva (2018). Combining ability and genetic action studies for yield and its related traits in maize (*Zea mays* L.). *International Journal of Current Microbiology and Applied Sciences*, **7**(6): 2645-2652.
- Rajesh, V.; Kumar, S. S.; Reddy, V. Narsimha and Sankar, A. Siva. (2014). Heterosis studies for grain yield and its component traits in single cross hybrids of maize (*Zea mays* L.). *International Journal of Plant, Animal and Environmental Sciences*, **4**(1): 304-306.
- Rajitha, A.; Ratna Babu D.; M, Lal Ahamed and Rao, V. Srinivasa. (2014). Heterosis and combining ability for grain yield and yield component traits in maize (*Zea mays* L.). *Electronic Journal of Plant Breeding*, **5**(3): 378-384.
- Ram, L.; Singh, R.; Singh, S. K. and Srivastava R. P. (2015). Heterosis and combining ability studies for quality protein maize. *Ekin Journal of Crop Breeding and Genetics*, **1-2**: 8-25.
- Reddy, V. R.; Jabeen, Farzana; and Sudarshan M.R. (2015). Heterosis studies in diallel crosses of maize for yield and yield attributing traits in maize (*Zea mays* L.) over locations. *International Journal of Agriculture, Environment and Biotechnology*, **8**(2): 271-283.
- Reddy, Y. S.; Krishnan, V.; Vengadessan, V.; Paramasivam, K. and Narayanan, A. L. (2018). Heterosis analysis for grain yield traits in Maize (*Zea mays* L.). *Electronic Journal of Plant Breeding*, **9**(2): 518-527.

- Sandesh, G.M.; Karthikeyan A.; Kavithamani, D.; Thangaraj, K.; Ganesan, K.N.; Ravikesavan, R. and Senthil, N. (2018). Heterosis and combining ability studies for yield and its component traits in Maize (*Zea mays* L.). *Electronic Journal of Plant Breeding*, **9**(3): 1012 – 1023.
- Senthil Kumar, P. and Bharathi, P. (2009). Studies on relationship between *gca* and *sca* effects in maize (*Zea mays* L.). *Electronic Journal of Plant Breeding*, **1**: 24-27.
- Shah, T. R.; Prasad, K. and Kumar, P. (2016). Maize-A potential source of human nutrition and health: A review. *Cogent Food and Agriculture*, **2**: 1166995.
- Shrestha, jiban; Gurung, D. B. and Rijal T. R. (2018) Standard heterosis for grain yield in maize hybrids. *Farming and Management*, **3**(1): 30-36.
- *Shull, G. H. (1914). Duplicate genes for capsule form in *Bursa bursapastoris*. *Zeitscher. Indust. Abstamm, U. verebungol*, **12**: 97-149.
- Snedecor, G. W. and Cochran, W. G. (1967). Statistical methods. 6th edition. Ames, The Iowa State University Press, Ames, Iowa.
- Snedecor, G. W. and W. G. Cochran. (1967). Statistical methods. 6thed. Ames, The Iowa State University Press, Ames, Iowa.
- *Sprague, G. F. and Tatum, L. A. (1942). General and specific combining ability in single crosses of corn. *Journal of American Society of Agronomy*, **34**: 923-932.
- Suthamathi, P. and Nallathambi, G. (2015). Combining ability for yield and yield attributing traits under moisture stress environments in maize (*Zea mays* L.). *Electronic Journal of Plant Breeding*, **6**(4): 918-927.
- Yerva, S. R.; Sekhar, T.C.; Allam, C.R. and Krishnan, V. (2016). Combining ability studies in maize (*Zea mays* L.) for yield and its attributing traits using Griffing's diallel approach. *Electronic Journal of Plant Breeding*, **7**(4): 1046-1055.
- Zelege, Habtamu (2015). Heterosis and Combining Ability for Grain Yield and Yield Component of Maize in Eastern Ethiopia. *Science, Technology and Arts Research Journal*, **4**(3): 32-37.
- *Original was not seen

APPENDICES

APPENDICES

Appendix A

Weekly meteorological data recorded during the crop season (October-2019 to February-2020 and June-2020 to October-2020)

Month	Standard Week	Temperature (°C)		Relative humidity (%)	Rainfall (mm)
		Maximum	Minimum		
1	2	3	4	5	6
October	44	33.1	16.2	82.6	00
November	45	34.3	18.4	87.0	00
	46	37.7	18.1	92.4	00
	47	37.7	19.0	92.3	00
	48	34.1	19.0	88.0	00
	49	34.0	18.2	89.5	00
December	50	32.7	14.2	86.5	00
	51	37.5	16.6	88.4	00
	52	31.7	16.5	89.1	00
	1	30.6	16.0	86.0	00
January	2	30.7	17.4	86.4	00
	3	32.9	17.4	88.2	00
	4	32.1	18.1	87.2	00
	5	33.9	18.8	89.4	00
	6	34.0	20.3	87.3	00
February	7	34.1	18.2	89.7	00
	8	35.4	19.3	88.7	00
	9	34.5	17.9	87.8	00
	10	37.8	21.0	87.7	00
March	11	37.6	23.2	83.4	00
	12	42.8	25.4	85.2	00
	13	38.3	26.7	84.4	00
	23	39.2	28.6	88	11.5
June	24	37.8	26.6	89.8	52.0
	25	40.8	26.7	89.7	00
	26	39.7	26.9	90.8	17.2
	27	37.9	28.3	86.8	60.7
July	28	37.3	28.6	86.8	51.1
	29	33.5	26.7	87.4	9.5
	30	32.2	25.4	84.7	48.9
	31	33.8	27.8	87.1	2.6
August	32	30.5	26.0	89.1	77.9
	33	30.3	25.7	91.4	257.3
	34	30.9	25.5	88.8	670
	35	31.2	26.0	87.5	101.2
	36	31.7	28.4	88.7	64.4
September	37	33.5	25.6	89.5	37.6
	38	35.5	24.7	92.5	20.8
	39	35.4	24.1	90.8	00
	40	34.0	25.5	87.5	00
October	41	34.7	26.5	89.4	00
	42	34.1	24.0	88.4	00
	43	36.0	25.5	87.5	00

Appendix B

Mean performance of parents and hybrids for various characters in maize

Sr. No.	Genotypes	Days to tasseling	Days to silking	ASI	Plant height (cm)	Ear height (cm)	Days to maturity	Cob length (cm)
Parents								
Female								
1	BLD 2	51.67	56.33	4.67	124.67	59.67	84.67	14.70
2	BLD 109	52.00	55.33	3.33	105.33	46.00	84.33	13.33
3	BLD 114	49.33	53.33	4.00	157.00	73.33	82.33	15.33
4	WNC 40080	51.00	54.00	3.00	119.33	57.00	83.33	15.85
5	WNC 40324	48.33	52.00	3.67	143.00	62.67	81.67	16.17
6	WNC 40406	47.67	51.33	3.67	137.00	69.33	81.33	16.40
7	WNC 40456	57.33	60.67	3.33	165.00	79.00	88.33	14.93
8	WNC 52313	47.33	52.00	4.67	164.00	80.00	82.33	16.21
9	WNC 52646	47.00	51.67	4.67	170.67	84.33	81.33	15.89
Male								
10	VL 109178	49.00	53.00	4.00	153.00	65.33	83.33	15.36
11	BLD 98	48.33	51.67	3.33	165.67	87.67	82.33	15.20
12	BLD 103	48.67	53.00	4.33	168.67	85.33	84.00	16.35
13	BLD 125	48.33	52.33	4.00	168.67	88.33	80.00	15.57
14	IMR 113	50.00	55.00	5.00	147.00	73.33	84.33	16.57
Hybrids								
15	BLD 2 × VL 109178	49.33	52.67	3.33	170.67	87.00	82.67	16.55
16	BLD 2 × BLD 98	47.33	51.00	3.67	152.00	78.67	81.33	15.28
17	BLD 2 × BLD 103	50.67	55.00	4.33	165.00	87.67	84.33	17.05
18	BLD 2 × BLD 125	48.00	51.00	3.33	169.33	85.33	84.67	17.00
19	BLD 2 × IMR 113	47.67	51.00	3.33	173.00	93.67	85.00	16.83
20	BLD 109 × VL 109178	48.00	51.33	3.33	154.33	91.67	79.00	15.60
21	BLD 109 × BLD 98	48.33	53.00	4.67	156.33	79.00	82.00	15.04
22	BLD 109 × BLD 103	46.33	50.67	4.33	182.67	102.33	80.00	15.45
23	BLD 109 × BLD 125	47.33	52.33	5.00	190.00	108.00	82.00	15.23
24	BLD 109 × IMR 113	45.67	49.67	4.00	187.00	101.67	81.33	16.04
25	BLD 114 × VL 109178	48.67	52.33	3.67	174.00	78.67	82.00	15.45
26	BLD 114 × BLD 98	47.67	52.00	4.33	165.33	85.00	84.00	16.12
27	BLD 114 × BLD 103	48.00	52.33	4.33	187.00	100.33	83.67	15.74
28	BLD 114 × BLD 125	47.33	52.00	4.67	183.60	98.00	85.33	14.75
29	BLD 114 × IMR 113	48.67	53.00	4.33	178.33	85.67	83.00	16.13
30	WNC 40080 × VL 109178	47.33	51.67	4.33	164.00	80.33	81.33	14.63
31	WNC 40080 × BLD 98	47.67	51.67	4.00	167.00	89.33	81.00	16.36
32	WNC 40080 × BLD 103	48.00	52.67	4.67	169.33	85.33	82.33	15.52
33	WNC 40080 × BLD 125	50.33	54.67	4.33	171.33	84.67	84.33	15.72
34	WNC 40080 × IMR 113	47.33	50.33	3.00	166.67	85.00	80.67	15.89
35	WNC 40324 × VL 109178	47.67	52.33	4.67	163.67	84.00	82.00	17.64
36	WNC 40324 × BLD 98	44.67	48.00	3.33	158.67	78.00	80.00	15.39
37	WNC 40324 × BLD 103	47.33	51.33	4.00	178.00	92.67	81.00	15.64
38	WNC 40324 × BLD 125	48.33	52.67	4.33	162.67	77.67	82.33	15.24
39	WNC 40324 × IMR 113	46.33	50.00	3.67	171.00	94.67	80.67	16.27
40	WNC 40406 × VL 109178	47.33	50.67	3.33	163.67	81.67	82.33	15.29
41	WNC 40406 × BLD 98	47.00	50.33	3.33	163.67	80.00	81.67	14.45
42	WNC 40406 × BLD 103	45.67	49.33	3.67	164.00	89.67	81.33	14.88
43	WNC 40406 × BLD 125	47.33	51.00	3.67	169.33	82.00	84.67	16.21
44	WNC 40406 × IMR 113	48.00	52.33	4.33	169.00	90.67	85.33	16.20
45	WNC 40456 × VL 109178	46.33	50.67	4.33	161.00	81.00	84.67	16.49
46	WNC 40456 × BLD 98	48.67	52.33	3.67	168.00	81.67	86.00	14.71
47	WNC 40456 × BLD 103	47.67	51.33	3.67	170.33	83.33	85.00	15.65
48	WNC 40456 × BLD 125	47.33	50.67	3.33	180.67	91.67	83.33	18.14

Sr. No.	Genotypes		Days to tasseling	Days to silking	ASI	Plant height (cm)	Ear height (cm)	Days to maturity	Cob length (cm)
49	WNC 40456 × IMR 113		47.67	51.67	4.33	178.67	90.33	82.33	16.29
50	WNC 52313 × VL 109178		47.67	51.33	3.67	161.67	73.67	81.33	15.73
51	WNC 52313 × BLD 98		47.33	51.00	3.67	161.00	83.33	83.33	14.59
52	WNC 52313 × BLD 103		49.33	53.67	4.33	167.67	90.33	81.00	15.74
53	WNC 52313 × BLD 125		48.33	53.00	4.67	181.67	92.00	83.33	15.67
54	WNC 52313 × IMR 113		46.67	50.00	3.33	171.33	93.33	81.00	15.77
55	WNC 52646 × VL 109178		45.67	49.67	4.00	168.67	88.67	82.00	16.50
56	WNC 52646 × BLD 98		46.33	51.33	5.00	176.00	91.00	85.33	15.20
57	WNC 52646 × BLD 103		46.00	50.33	4.33	167.00	92.33	85.67	16.39
58	WNC 52646 × BLD 125		47.33	52.00	4.67	186.00	93.67	83.00	16.53
59	WNC 52646 × IMR 113		47.00	50.67	3.67	178.67	87.67	84.00	16.29
60	GAYMH 1 (Check)		48.00	51.33	3.33	184.33	99.00	80.33	16.64
Mean	Parents	Female	50.18	54.07	3.89	142.89	67.93	83.29	15.42
		Male	48.87	53.00	4.13	160.60	79.99	82.79	15.81
	Hybrids		47.53	51.51	4.00	170.42	87.83	82.73	15.85
General mean			48.04	52.03	3.98	165.7	84.38	82.78	15.8
Range	Female	Min.	47.00	51.33	3.00	105.33	46.00	81.33	13.33
		Max.	57.33	60.67	4.67	170.67	84.33	88.33	16.40
	Male	Min.	48.33	51.67	3.33	147.00	65.33	80.00	15.20
		Max.	50.00	55.00	5.00	168.67	88.33	84.33	16.57
	Hybrids	Min.	44.67	48.00	3.00	152.00	73.67	79.00	14.45
		Max.	50.67	55.00	5.00	190.00	108.00	86.00	18.14
S.Em. ±			0.81	0.84	0.35	7.65	4.77	0.79	0.37
CD at 5%			2.26	2.36	0.98	21.43	13.35	2.21	1.03
C.V. %			2.90	2.80	15.25	8.00	9.79	1.65	4.03

Appendix B cont....

Sr. No.	Genotypes	Cob girth (cm)	Kernels row per cob	Kernels per row	100 kernels weight (g)	Kernel yield per plant	Shelling (%)
Parents							
Female							
1	BLD 2	14.92	13.20	18.53	38.67	47.00	76.69
2	BLD 109	13.96	12.93	17.87	33.33	58.93	78.56
3	BLD 114	15.01	12.27	21.53	30.33	74.13	78.46
4	WNC 40080	14.39	11.33	20.00	40.33	52.80	74.35
5	WNC 40324	15.16	13.07	20.73	36.67	53.00	78.41
6	WNC 40406	15.12	11.73	21.53	39.33	68.93	74.21
7	WNC 40456	14.07	12.00	19.33	32.00	44.33	73.84
8	WNC 52313	15.64	12.93	21.20	33.00	68.00	78.79
9	WNC 52646	14.76	12.53	22.00	38.67	60.13	78.54
Male							
10	VL 109178	14.73	12.40	18.27	31.67	56.67	78.07
11	BLD 98	15.13	12.27	20.27	35.33	48.40	72.62
12	BLD 103	14.64	12.27	24.07	40.33	55.07	74.77
13	BLD 125	14.90	12.53	21.73	38.33	59.67	76.55
14	IMR 113	14.80	13.60	23.47	38.00	68.27	77.81
Hybrids							
15	BLD 2 × VL 109178	15.32	13.33	23.33	38.67	74.27	76.58
16	BLD 2 × BLD 98	15.11	13.20	19.20	38.33	70.40	76.12
17	BLD 2 × BLD 103	15.60	13.47	23.53	35.00	92.87	81.53
18	BLD 2 × BLD 125	15.76	13.73	20.53	39.67	58.47	78.60
19	BLD 2 × IMR 113	14.56	12.80	21.73	37.00	43.47	76.15
20	BLD 109 × VL 109178	15.45	11.73	20.53	36.00	64.00	77.22
21	BLD 109 × BLD 98	15.32	12.80	18.87	41.67	50.13	76.22
22	BLD 109 × BLD 103	15.21	13.47	18.73	41.00	51.27	73.70
23	BLD 109 × BLD 125	14.63	13.20	19.67	39.00	75.00	70.02
24	BLD 109 × IMR 113	15.82	13.87	23.00	38.00	64.93	73.07
25	BLD 114 × VL 109178	14.65	11.87	21.33	35.67	54.87	74.75
26	BLD 114 × BLD 98	15.13	12.40	20.93	41.67	72.00	78.25
27	BLD 114 × BLD 103	14.67	12.27	20.93	37.67	50.80	77.00
28	BLD 114 × BLD 125	14.88	12.13	20.27	36.67	55.33	74.52
29	BLD 114 × IMR 113	15.03	14.00	20.13	33.33	79.87	82.81
30	WNC 40080 × VL 109178	15.35	13.60	20.40	32.33	52.20	78.98
31	WNC 40080 × BLD 98	15.54	14.27	19.60	30.67	61.87	74.19
32	WNC 40080 × BLD 103	14.81	12.67	22.60	36.00	65.33	78.37
33	WNC 40080 × BLD 125	15.15	14.67	20.20	30.33	79.07	79.45
34	WNC 40080 × IMR 113	14.76	13.07	21.93	37.67	69.00	77.40
35	WNC 40324 × VL 109178	15.49	13.87	22.67	33.33	53.07	79.54
36	WNC 40324 × BLD 98	14.57	12.13	18.80	38.33	49.80	72.28
37	WNC 40324 × BLD 103	15.08	12.53	20.20	34.67	58.00	79.20
38	WNC 40324 × BLD 125	15.95	13.07	18.93	33.00	55.40	74.34
39	WNC 40324 × IMR 113	15.84	13.60	21.33	35.67	46.93	74.09
40	WNC 40406 × VL 109178	15.41	11.73	20.60	34.67	50.40	76.96
41	WNC 40406 × BLD 98	14.85	12.00	21.20	34.00	57.67	74.60
42	WNC 40406 × BLD 103	15.44	12.13	20.13	37.00	72.67	76.52
43	WNC 40406 × BLD 125	15.29	11.73	25.07	34.67	95.13	78.23
44	WNC 40406 × IMR 113	15.68	12.80	22.53	33.67	64.27	77.10
45	WNC 40456 × VL 109178	15.56	13.47	22.53	35.67	54.60	77.25
46	WNC 40456 × BLD 98	14.88	11.47	19.40	30.00	48.33	77.02
47	WNC 40456 × BLD 103	14.93	12.13	21.53	32.67	42.33	74.57

Sr. No.	Genotypes	Cob girth (cm)	Kernels row per cob	Kernels per row	100 kernels weight (g)	Kernel yield per plant	Shelling (%)	
48	WNC 40456 × BLD 125	15.75	11.87	23.33	34.33	64.47	76.97	
49	WNC 40456 × IMR 113	15.15	12.80	22.80	35.67	73.47	76.15	
50	WNC 52313 × VL 109178	14.97	12.67	22.00	33.00	58.80	80.16	
51	WNC 52313 × BLD 98	14.68	12.13	19.67	36.00	47.53	76.58	
52	WNC 52313 × BLD 103	14.27	12.53	22.80	35.33	56.67	79.12	
53	WNC 52313 × BLD 125	14.93	12.00	20.87	36.33	46.33	71.23	
54	WNC 52313 × IMR 113	15.75	12.93	23.33	35.33	47.60	76.82	
55	WNC 52646 × VL 109178	14.88	12.93	22.13	38.67	54.00	76.04	
56	WNC 52646 × BLD 98	15.11	12.40	22.47	38.67	52.33	76.78	
57	WNC 52646 × BLD 103	14.45	12.00	22.07	35.67	46.73	70.26	
58	WNC 52646 × BLD 125	14.92	12.93	21.73	34.33	75.73	80.24	
59	WNC 52646 × IMR 113	15.11	11.87	21.53	38.00	50.87	76.98	
60	GAYMH 1 (Check)	14.91	12.67	22.20	31.33	47.33	75.99	
Mean	Parents	Female	14.78	12.44	20.30	35.81	58.58	76.81
		Male	14.84	12.61	21.56	36.73	57.61	75.96
	Hybrids		15.15	12.76	21.27	35.89	60.68	76.53
General mean		15.06	12.70	21.16	35.87	59.52	76.53	
Range	Female	Min.	13.96	11.33	17.87	30.33	44.33	74.21
		Max.	15.64	13.20	22.00	40.33	74.13	78.79
	Male	Min.	14.64	12.27	18.27	31.67	48.40	72.62
		Max.	15.13	13.60	24.07	40.33	68.27	78.07
	Hybrids	Min.	14.27	11.47	18.73	30.00	42.33	70.02
		Max.	15.95	14.67	25.07	41.67	95.13	82.81
S.Em. ±		0.29	0.34	0.64	0.88	2.91	1.27	
CD at 5%		0.81	0.95	1.79	2.48	8.14	3.54	
C.V. %		3.33	4.63	5.24	4.27	8.46	2.86	

CERTIFICATE

This is to certify that I have no objection for supplying to any scientist only one copy or any part of this thesis at a time through reprographic process, if necessary for rendering reference service in a library or documentation centre.

Revi D Patel,

Place : SARDARKRUSHINAGAR.

Date : 14th SEPTEMBER, 2021

(PATEL RAVIKUMAR D.)