HETEROSIS AND COMBINING ABILITY ANALYSIS OF SUB-TROPICAL MAIZE (*Zea mays* L.) INBRED LINES

THESIS

By

Ambika

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Submitted to

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CERTIFICATE-I

This is to certify that the thesis entitled, **"Heterosis and combining ability analysis of sub-tropical maize (*Zea mays* L.) inbred lines"** submitted in partial fulfillment of the requirements for the award of the degree of **Master of Science (Agriculture)** in the discipline of **Genetics and Plant Breeding** of Chaudhary Sarwan Kumar Himachal Pradesh Krishi Vishvavidyalaya, Palampur is a bonafide research work carried out by **Miss. Ambika** daughter of **Smt. Jaram Dei** and **Shri. Lal Pat** under my supervision and that no part of this thesis has been submitted for any other degree or diploma.

The assistance and help received during the course of this investigation have been fully acknowledged.

Place: Palampur
Dated: 07 September, 2022

Dr. Uttam Chand
Major Advisor

CERTIFICATE-II

This is to certify that the thesis entitled, **"Heterosis and combining ability analysis of sub-tropical maize (*Zea mays* L.) inbred lines"** submitted by **Miss Ambika (A-2020-30-036)** daughter of **Smt. Jaram Dei** and **Shri. Lal Pat** to the Chaudhary Sarwan Kumar Himachal Pradesh Krishi Vishvavidyalaya, Palampur in partial fulfillment of the requirements for the degree of **Master of Science (Agriculture)** in the discipline of **Genetics and Plant Breeding** has been approved by the Advisory Committee after an oral examination of the student in collaboration with an External Examiner.

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Needless to mention, all omissions and errors are solely my responsibility.

Place: Palampur
Dated:07 September,2022 ***(Ambika)***

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LIST OF ABBREVIATIONS USED

S. No.	Abbreviation	Meaning
1	^{0}N	Degree North
2	^{0}S	Degree South
3	^{0}E	Degree East
4	et al.,	et alii (and others)
5	%	per cent
6	GCA	General combining ability
7	SCA	Specific combining ability
8	&	And
9	/	Per
10	SPDA	Soli Plant Analysis Development
11	BLSB	Banded Leaf and Sheath blight
12	TLB	Turcicum Leaf Blight
13	MLB	Maydis Leaf Blight
14	QPM	Quality protein maize
15	df	degree of freedom
16	ANOVA	Analysis of variance
17	pH	Puissance de hydrogen (ion conc.)
18	SAREC	Shivalik Agricultural Research and Extension Center
19	P.S.M.-2	Palam Sankar Makka-2
20	cm	Centimeter
21	m^2	Square meter
22	cm^2	Square centimeter
23	Q	Quintal
24	Ha	Hectare
25	*viz.,*	Vi delicet (namely)
26	CD	Critical difference

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ABSTRACT

The present investigation entitled “Heterosis and combining ability analysis of sub-tropical maize (*Zea mays* L.) inbred lines” was carried out to assess the nature and magnitude of gene action, estimation of heterosis and combining ability effects for grain yield and its component traits. The experimental material consisted of 7 inbreds, 21 crosses and 3 checks *viz.,* Palam Sankar Makka-2, Bio 9544 and Bio 605 were evaluated in RBD with two replications at Shivalik Agricultural Research and Extension Centre, Kangra during *kharif*, 2021. Analysis of variance revealed significant differences among genotypes except number of kernel rows per ear suggesting thereby sufficient amount of genetic variability in the experimental material. Analysis of variance for combining ability revealed significant GCA and SCA effects for most of the traits except GCA for days to 50% silking and shelling (%) indicated the preponderance of both additive and non-additive gene action for inheritance of the studied traits. The ratio of GCA variance to SCA variance was less than unity for all traits indicated preponderance of non-additive gene action. P_1 (KGI-109) and P_3 (DMEL-143) inbred lines were good general combiner for grain yield and may be used as parents for the development of high yielding single cross maize hybrids. The promising cross combinations *viz.,* $P_1 \times P_4$ (KGI-109 × DMEL-156), $P_1 \times P_3$ (KGI-109 × DMEL-143), $P_2 \times P_3$ (LM-18 × DMEL-143), $P_6 \times P_7$ (DMR139 × KGI-110), $P_3 \times P_7$ (DMEL-143 × KGI-110) and $P_2 \times P_5$ (LM-18 × CML139) were identified on the basis of mean performance, SCA effects and significant standard heterosis for grain yield. In addition, these crosses also exhibited resistance to Turcicum leaf blight and moderate resistance to Banded leaf and sheath blight and Maydis leaf blight. These promising hybrids may be commercially exploited after evaluation in multi-location trials over the years to assess their suitability in different agro-climatic zones of the state.

(Ambika) Student Date: 07 September, 2022	(Dr. Uttam Chand) Major Advisor Date: 07 September, 2022

Head of the Department

1. INTRODUCTION

Maize (*Zea mays* L.) is the world's leading crop and is widely cultivated as cereal grain that was originated in Mexico and Central America. Maize (2n=20) belongs to the tribe *Maydae,* family *Poaceae*. It is one of the most versatile emerging crops having wider adaptability. Globally, maize is known as "queen of cereals" because of it has highest genetic yield potential. Maize is the only food cereal crop that can be grown in diverse seasons, ecologies and uses. Its growing versatility worldwide ranges from latitudes 58' N and 40' S, at elevations varying from sea level to above 3000 m with rainfall ranging from 250 to 5000 mm (Dowswell et al. 1996).

Maize is a strategically important crop for millions of poor farmers because of its multiple applications as food, feed and raw material for industry. Maize produced in the developed world is mostly utilized as livestock feed (70%), food (5%) and industrial and seed purposes (25%). Because of its high quality, maize is known as a "Poor Man's Nutricerea", with about 10% protein, 4% oil, 70% carbohydrate, 2.3% crude fiber, 10.4% albuminoides, 80% saturated fatty acids and 1.4% ash as well as sufficient amounts of vitamin A, nicotinic acid, riboflavin and vitamin E. Maize is used as a basic raw material in hundreds of industrial goods, including starch, oil, protein, alcoholic beverages, food sweeteners, medicines, cosmetics, textile, gum, packaging and paper industries.

Maize is grown on 206.74 million hectares area all over world, yielding 58.90 quintal per hectare with the production 1217.87 million metric tons (USDA/FAS 2022). India is the sixth-largest maize producer in the world. Maize is cultivated on 9.90 million hectare in India, yielding 27.06 quintal per hectare during *kharif* with the production of 33.00 million metric tons (USDA/FAS, 2022). Due to availability of photo and thermo insensitive varieties, maize is grown throughout India. It is generally grown as a *kharif* crop and occupies with 85 % of area under cultivation at this time of year.

Maize is one of the most important *kharif* season crop of Himachal Pradesh covering 0.27 million hectare area with the production of 0.73 million tonnes and productivity of 26.3 quintal per hectare (Anonymous 2021).

Maize hybrid development involves a number of phases, beginning with the development of inbred lines, their evaluation, the crossing selected inbred lines and hybrid production. The production of superior hybrids will result from the selection of the right inbred line. For this a detailed evaluation of existing germplasm or newly developed elite lines for their potential use in breeding programmes is required.

Combining ability analysis is of special importance in cross pollinated crops like maize as it helps in identifying potential parents that can be used for producing hybrids/synthetics. The nature and magnitude of gene action is an important factor in developing an effective breeding programme which can be understood through combining ability analysis. GCA for an inbred line is defined as the average performance of lines in a series of hybrid combination, whereas, SCA as those cases in which certain hybrid combination perform better or poorer than would be expected on the basis of the average performance of the parental inbred lines (Sprague and Tatum, 1942). The nature of the gene action involved may be additive and additive × additive which is due to general combining ability or it may be non-additive (additive × dominance, dominance × dominance) which is due to specific combining ability. The nature of gene action is important factor in determining effective breeding programme and in hybrid development non-additive gene action is of utmost importance.

Breeders have utilized different mating designs to aid in the production of hybrids. Among them diallel crossing technique given by Jinks (1954) and Hayman (1954) provides the information about inheritance pattern of gene action in F_1 generations (Hayman, 1954; Jinks, 1954). Diallel mating design is also helpful for obtaining the genetic information about the traits of interest through random and fixed selection sets of parental lines in short time (Hayman 1954; Griffing 1956b) and relative importance of both additive and non-additive type of gene actions.

Heterosis and combining ability are pre-requisites for developing a good maize variety/hybrid. Information on heterotic patterns and combining ability among maize germplasm is essential in maximizing the effectiveness of hybrid development. The phenomenon of heterosis has been exploited in crop breeding leading to significant increase in yield. Exploitation of heterosis is one of the main reasons for the success of hybrid development in maize by both public and private sectors (Stuber, 1994). Heterosis is used to describe the phenomenon when the parents are taken from the different populations of the same species. Diallel crosses have been widely used in genetic research to determine the general and specific combining abilities and nature of gene action for many traits in maize.

Since no information is available on heterosis, combining ability and gene action in the newly developed and locally adapted maize inbreds. Therefore, half diallel analysis was attempted for identification of superior inbreds on the basis of combining ability, development of suitable hybrids and estimation of heterosis using standard commercial checks.

Keeping the aforementioned consideration in view, the present study was undertaken with the following objectives:

1 Assess the nature and magnitude of gene action
2 Estimate heterosis and combining ability effects for grain yield and its component traits in sub-tropical maize

2. REVIEW OF LITRATURE

Combining ability and heterosis provides genetic information for variety development. Various approaches for determining combining ability exist. Diallel analysis is one of the most essential methods for determining the GCA and SCA effects.

Review of the literature relevant to the present maize study is presented under the following heading:

2.1 Combining ability and gene action

2.2 Heterosis

2.3 Diseases reaction

2.1 Combining ability and gene action

Sprague and Tatum (1942) provided the first specific demonstration of combining abilities. GCA (general combining ability) and SCA (specific combining ability) are two types of combining abilities. The general combining ability is the average performance of a genotype in a series of hybrid combinations, whereas, specific combining ability is the case in which some combinations perform significantly better or worse than the expectations which are based on the average performance of the lines involved. According to them GCA is a measure of additive gene action, while SCA is a measure of non-additive gene action.

Various biometrical techniques can be used to estimate combining ability *viz.,* top cross technique was first proposed by Davis (1927) and elaborated by Jenkins and Brunson (1932), diallel cross analysis in 1956b by Griffing, modified top cross (line × tester mating design) by Kempthorne (1957), partial diallel analysis by Kempthorne and Curnow (1961) and triallel by Rawlings and Cockerham (1962).

Martin and Hallauern (1976) examined certain traits *viz.,* ear circumference, ear length, number of grain rows, 100-grain weight and yield and found that epistasis was more common for all traits except 100-grain weight. Epistasis was least prevalent in terms of yield but most common in terms of ear length and number of grain rows.

Dhillon and Singh (1977) observed the inheritable pattern of the days to 50% silking, plant height, ear length, ear height, ear circumference, number of kernel rows per cob, grain moisture and concluded that GCA was more essential than SCA for inheritance except for the grain yield.

Singh et al. (1979) observed that additive gene action for ear weight and non-additive gene action for days to silking, ear length and plant height, whereas, for days to maturity, 100-kernel weight and yield per plant both the additive and non-additive gene action were present.

Sanghi et al. (1983) reported that additive gene action have a larger role in the expression of grain yield, dry matter yield, days to maturity and days to silking in maize.

Melchinger et al. (1987) observed the ratio of general to specific combining ability to eatimate hybrid performance and indicated the significance of variances owing to GCA and SCA.

Muthiah (1989) observed that the proportion of general combining ability variance was more than the proportion of SCA variance indicating that additive gene action was prevalent across all of the traits under study.

Debnath and Sarkar (1990) reported that non-additive gene action for ear diameter, 1000-kernal weight and grain yield, whereas, both additive and non-additive gene action was observed for ear length, kernel rows per ear and kernels per row.

Mahajan et al. (1991) studied combining ability among twenty-eight maize hybrids, eight inbred lines evaluated in eight environments and two seasons and reported that additive gene action was predominant for days to silking and days to dry husk.

Vasal et al. (1993) reported that extremely significant general combining ability and non-significant specific combining ability for days to silking, plant height, endosperm hardness and grain yield indicated that additive gene action is important for the inheritance of these traits.

Pal and Pradhan (1994) reported non-additive gene action for number of rows per ear, grain yield, number of grains per row, oil content and ear length, whereas, additive gene action play a significant role in ear diameter, maturity, embryo size and 1000-grain weight.

Rastogi and Rastogi (1995) determined combining ability in ten early and five late maturing inbred lines crossed with Chandan Safed-2, a genetically broad base extra early composite (H-62). H-16 and H-15 were the best general combiners for 1000-kernel weight, ear weight, early maturity and grain yield, whereas, at both crop densities H-1681 (late maturing) was good general combiner for 1000-kernel weight, number of kernel rows per ear and grain yield.

Petrovic et al. (1998) studied combining ability analysis using seven lines, three testers and their twenty-one F_1s in line × tester mating system and observed that combination of lines with positive GCA and SCA values produced promising hybrids.

Joshi et al. (1998) observed non-additive gene action in the expression of yield per plant, starch content, protein content and 1000-grain weight, as well as additive gene effects in the expression of oil content.

Zelleke (2000) studied both general and specific combining ability effects of six maize parents using half-diallel mating design for ear length, plant height, days to maturity, test weight and grain yield. He observed that the GCA × year interaction was significant for grain yield, plant height and days to maturity, while the SCA × year interaction was significant only for days to maturity.

Kara (2001) observed significant GCA effects for kernels per row, ear length, kernel rows per cob and 1000-grain weight, whereas, significant SCA effects for grain yield per unit area, ear height and ear diameter.

Mahto and Ganguly (2001) observed additive and non-additive effects for 100-grain weight and shelling percentage.

Aguiar et al. (2003) reported ear height, grain yield, plant height, ear prolificacy and ear placement showed significant general combining ability. Specific combining ability was non-significant for ear placement. Grain yield showed both additive and non-additive gene effects, whereas, other traits showed additive gene action.

Malik et al. (2004) observed high significant general combining ability for plant height, days to pollen shedding, ears per plant, ear height, leaf area, grain moisture at harvest, kernel rows per ear, kernels per row, seed index and grain yield indicating predominance of additive gene action.

Iqbal et al. (2007) reported that inbred lines KDM347, KDM342 and KDM334 are good general combiners for test weight, ear diameter, grain yield per plot, ear length and number of kernel rows per ear. Among hybrids, KDM336 × KDM346, KDM331 × super-1, KDM331 × KDM346, KDM333 × KDM-34 and KDM342 × C6 showed significant specific combining ability effect for studied characters.

Dadheech and Joshi (2007) and Gudeta (2007) reported combining ability and significant mean squares due to genotypes for days to tasseling, days to silking, days to maturity, plant height, test weight, ear height, number of kernels per row, number of kernel rows per ear, ear diameter, ear length and grain yield. They discovered significant GCA and SCA mean squares for all of the attributes investigated and showing non-additive gene action for the inheritance of these traits.

Uddin et al. (2008) reported that significant GCA and SCA variance for 100-kernel weight, number of kernels per row and yield per plant which indicated importance of additive gene effect in their expression. Also σ^2GCA/σ^2SCA ratio was high for number of kernels per row, 100-kernel weight, ear diameter, ear length and grain yield per plant indicated non-additive gene effect. Crosses exhibited significant specific combining ability effect were having high × high, high × low, low × high, average × low and low × low general combining parents.

Fan et al. (2008) estimated combining abilities for grain yield and yield contributing traits such as ear length, 1000-kernel weight, cob diameter, kernel rows per ear and grains per row. They observed that CIMMYT lines had greater GCA effects for ear diameter and number of kernel rows per ear than local lines.

Shenawy et al. (2009) evaluated the combining ability effects of nine white maize inbred lines succeeding diallel crosses for traits such as grain yield, plant height, ear height and days to silking at three locations and for all of these traits both negative and positive significant GCA and SCA effects were reported. Additive and non-additive gene action for control of these traits was also reported by them.

Kanagarasu et al. (2010) reported less GCA variance than SCA for traits like 100-grain weight, leaf length, grain yield per plant, cob circumference, cob length, number of kernel rows per ear, number of kernels per row, plant height, ear height, days to 50% silking and days to 50% tasseling indicating non-additive gene action for the control of these traits.

Kumar et al. (2012) studied combining ability, gene action and heterosis found that non-additive gene action predominated in the expression of traits like days to 50% pollen shed, days to 50% silking, ear length, plant height, ear circumference, 100-grain weight, number of kernel rows per cob, grains per row and grain yield per plant.

Krupakar et al. (2013) studied combining ability for oil content (%), starch content (%), grain yield per plant and protein content (%) over three environments and observed ratio of GCA/SCA less than unity indicated the predominance of non-additive gene effects for most of the traits.

Kumar et al. (2013) reported significant mean squares for ear length, ear girth, days to 50% pollen shed, days to 50% silking, 100-grain weight, grain yield per plant and harvest index in E1, E2 and pooled over environment.

Kapoor et al. (2014) observed the importance of both additive and dominant gene action for cob height, plant height, leaves per plant, inter nodal length, flag leaf area, days to tasseling, silking, maturity, grains per cob, harvest index and grain yield per plant. Additive gene action predominated for cob length, cob circumference and kernel rows per cob.

Chandel and Mankotia (2014) observed that variance component of GCA was greater than variance component of SCA indicated additive gene action for grain yield and ear length, whereas, non-additive gene action was reported for plant height, ear diameter, ear height and number of kernel rows per ear.

Khan et al. (2014) reported non-additive gene action for all of the parameters, parent P_6 was a good general combiner for days to 50% silking, grain yield per plant, 100-grain weight and protein content, parent P_7 and P_8 for oil content as well as protein content, whereas, F_1 ($P_2 \times P_5$) revealed positive significant specific combining ability effects for grain yield per plant.

Niyonzima et al. (2015) studied combining ability using 60 F_1s, fifty lines and four testers. For shelling percentage, days to 50% silking, ear length, days to 50% pollen shed, ear height, ear diameter, kernels per row, fodder yield per plot, plant height, kernel rows per ear, 100-kernel weight, days to brown husk and grain yield per plant non-additive gene action was observed. Best crosses involved good × poor and poor × poor general combining parents.

Dar et al. (2015) observed significant mean squares for days to 50% pollen shed, days to 50% silking, kernel rows per cob, kernels per row, plant height, ear height, 100-grain weight, protein content (%) and grain yield per plant across the environments and reported non-additive gene action for number of kernel rows per cob, number of kernels per row, 100-grain weight, protein content and grain yield per plant.

Haydar and Paul (2015) reported that for plant height, cob diameter, cob length and number of kernel rows per cob all traits exhibited non-additive gene action. Three crosses showed significant positive specific combining ability effects for cob diameter, grain yield, number of kernels per cob and number of kernel rows per cob.

Kumar et al. (2017) reported more σ^2SCA than σ^2GCA for all the traits *viz.,* ear circumference, ear length, number of grain rows per ear, harvest index, 100-grain weight and grain yield per plant in both the environments revealed preponderance of non-additive gene action. The estimates of GCA effects for grain yield per plant identified three inbred lines *viz.,* EIQ-112, EIQ-109 and EIQ-106 as good combiners in E1 and two inbreds *viz.,* EIQ-109 and EIQ-112 in E2. Positive significant specific combining ability effects for grain yield per plant also observed by twenty and seventeen hybrids in E1 and E2 environments, respectively.

Amadabade (2017) reported significant GCA and SCA variances for majority of the characters indicated preponderance of additive and non-additive gene action for expression of traits. For all the traits σ^2SCA was found greater than the σ^2GCA predominance of non-additive variance.

Wani et al. (2017) reported combining ability analysis in early maturing maize inbred lines under temperate conditions and found that the magnitude of dominance variance was higher in range in individual environments as well as pooled across environments for all traits indicating non-additive gene action.

Karim et al. (2018) observed additive gene action for 1000-kernel weight, ear height, plant height, days to tasseling, days to silking and grain yield per hectare.

Negi et al. (2018) reported that non-additive gene action for days to 50% silking, plant height, kernel rows per cob, grain yield, days to 50% tasseling and kernels per row.

El Hosary et al. (2018) observed combining ability for different traits *viz.*, ear length, ear diameter, plant height, ear height, number of rows per ear, number of kernels per row, 100-kernel weight, ear weight per plant, grain yield per plant and shelling (%). They reported significant GCA and SCA mean squares for all the studied traits, except GCA for ear diameter and number of rows per ear in L1 across two locations, whereas, specific combining ability for number of rows per ear and shelling (%) in L_2. Parent P_3 and P_8 showed significant positive general combining ability effects for grain yield and ear weight, whereas, $P_1 \times P_7$, $P_3 \times P_5$ and $P_4 \times P_8$ showed significant specific combining ability effects for grain yield.

Hosamani et al. (2018) observed that all genotypes showed highly significant mean sums of squares due to genotypes and a large range of variability except number of kernels per row.

Chandel et al. (2019) reported preponderance of non-additive gene action in newly developed maize inbreds for plant height, shelling percentage, grain yield per plant, ear height, ear length, kernel rows per cob, kernels per row, days to 50% silking, ear circumference, days to 50% tasseling and test weight.

Kumar et al. (2019) reported that the mean square due to parents, crosses and parents v/s crosses were significant for all the traits except days to 75% brown husk. The ratio of GCA and SCA variance was less than unity for all the traits except plant height. This showed that the predominance of non-additive gene effects in inheritance of these traits. Among female inbred lines, L_{28} was observed good general combiner for cob length, biological yield, grain yield and protein content. They reported that tester T_1 was good general combiner for test weight, biological yield and protein content, whereas, tester T_2 for cob circumference, harvest index, grain yield, plant height and cob placement.

Ali et al. (2019) reported that the significant general combining ability variances for plant height, cob length, number of kernel rows per cob, number of kernels per cob, cob weight, 1000-grain weight and grain yield per plant. The GCA/SCA ratio was less than one for all studied traits. Based on GCA estimates it could be concluded that the best combiners were ML10, ML14 and ML15 inbred lines for most of the studied traits.

Kumar and Mandal (2020) studied fourteen quantitative characters in *rabi* maize high SCA variance was observed for most of the traits except for kernels per row, ear length and harvest index indicating non-additive gene action for the inheritance of most of the traits.

Chaurasia et al. (2020) studied combining ability using seven parental inbred lines and their twenty-one crosses and reported that σ^2GCA/σ^2SCA ratio was less than one for days to 50% silking, grain yield per plant, plant height, ear height, days to 50% pollen shed, test weight, anthesis-silking interval, ear length, kernel rows per ear, ear diameter, kernels per row, grains per plant, days to 50% physiological maturity and shelling (%) indicated predominance of non-additive gene action for these traits.

Tello and Zelleke (2020) studied sixty-four test-crosses and reported that mean squares due to both lines and testers were significant for grain yield and the majority of its traits indicating that both additive and non-additive gene action were important in the inheritance of these traits.

Mousa et al. (2021) studied combining ability in twenty-one crosses generated by crossing seven inbred lines to three testers. They found significant mean squares due to crosses for any and all traits studied except lines and lines × testers for ears per plant and testers for kernel rows per cob.

kumar et al. (2022) studied combining ability and gene action in full diallel mating design in maize (*Zea mays* L.). The results of the analysis of variance showed except of ASI, ear circumference and shelling (%) there were significant differences among the hybrids, parents vs. hybrids and straight crosses for all of the traits.

Aly et al. (2022) estimated combining ability and gene action by half diallel (9 x 9) analysis approach. The σ^2GCA and σ^2SCA were significant or highly significant for most of the studied traits, indicating that the importance of additive as well as non-additive types of gene action in the inheritance of these traits. For earliness, cob placement and shorter plant the inbred line-Sd-14 was the best general combiner, while the inbred lines Sk-12 and Sk-9 were the best general combiners for high grain yield and longer ear length.

2.2 Heterosis

Shull introduced the idea of heterosis in 1908. According to Shull, heterosis refers to the superiority of a first-generation hybrid of genetically distinct parents over the average value for the character under consideration. Mid parent heterosis refers to estimation based on the average value, whereas, better parent heterosis refers to estimation based on the superior/average. However, from a commercial stand point, heterosis can also be defined as the degree of hybrid performance as compared with the best variety available is referred as standard heterosis. Standard heterosis is the ability of F_1 to outperform the best commercial check variety. For grain yield and other economic traits a newly produced maize hybrid must outperform established cultivars. As a result, significant conventional heterosis is required for hybrid development.

Heterosis is vital in maize breeding and is influenced by dominance and gene frequency differences. The genetic divergence of the two paternal varieties determines how heterosis manifests (Hallauer and Miranda, 1988). As a result, evaluating the level of genetic variation has been assisted by the magnitude of heterosis among lines or populations. It also serves as a foundation for selecting germplasm for use as parents in the development of segregating populations and for use as reciprocal recurrent selection plant breeding programme (Ortiz et al., 2008). Various plant breeders have employed heterosis extensively in maize crop.

Shull (1908) coined the term heterosis to define the phenomenon but it did not involve a description of genetic mechanism involved in its expression.

Bruce (1910) and Keeble and Pellow (1910) were the first to postulate dominance hypothesis, which proposed that increase in vigour after crossing were resulted from the combination of various dominance alleles by each parent.

Griffing and Zsiros (1971) proposed that heterosis is the outcome of the combination of genetic and environmental stimuli and reported that the environment is a crucial component in the expression of heterosis.

Ganguli et al. (1989) studied that heterosis out performed the better parent in terms of ear height, grain yield, days to silking and plant height.

Netaji et al. (2000) reported significant positive standard heterosis and better parent heterosis for grain yield. The better parent heterosis was found in grain yield per plot, followed by ear length, plant height, 1000-grain weight and number of grain rows per ear.

Geetha (2001) reported the highest standard heterosis for number of kernel rows per cob and grain yield per plant as well as the highest better parent heterosis (97.45%) for grain yield per plant.

Bassey (2002) calculated heterosis for grain yield and its component in maize and found that fresh weight of the plant had the highest mid parent heterosis (28.15%), while dried weight of maize ears had the lowest mid parent heterosis (3.45%).

Mohammadi et al. (2002) studied that the degree of heterosis for yield was more than its components indicating the role of overdominant gene action in expression of heterosis for these traits in maize.

Saleh et al. (2002) observed high estimates of standard heterosis for ear weight, grain weight and grain yield, whereas, moderate estimates for ear height, number of rows per ear, number of kernels per row, shelling (%), ear circumference and grain weight.

Ricardo et al. (2003) reported that for grain yield mid parent heterosis ranged from -4.3 per cent to 17.3 per cent.

Mosa (2003) evaluated half-diallel crosses in eight inbred lines of maize for the presence of heterotic effect on grain yield in two locations. Mid parent and better parent heterosis were significantly high for grain yield varied from 58.33 per cent to 751.98 per cent and 24.08 per cent to 709.88 per cent, respectively.

Malik et al. (2004) reported high heterotic effects for ear weight, number of kernel rows per ear, plant height, 100-kernel weight and grain yield. The mid parent heterosis and better parent heterosis recorded for grain yield was 17.2 per cent and 2.8 per cent, respectively.

Muraya et al. (2006) recorded significant positive mid parent heterosis for cob length, cob diameter, number of kernel rows per cob, number of kernels per row and plant height, whereas, negative significant mid parent heterosis for days to 50 % tasseling.

Mahantesh. (2006) reported that significant standard heterosis for days to anthesis, days to sillking, plant height, days to brown husk, ear height, ear length, ear circumference, number of kernels per row, number of kernel rows per cob, shelling (%), 100-seed weight and grain yield per plant, whereas, mid parent heterosis for grain yield ranged from -43.2 per cent to 66.9 per cent.

Iqbal et al. (2009) reported heterosis in grain yield ranged from 19% to 40% over the best check on single cross maize hybrids and concluded that top producing hybrids had ideal plant height in the 132 cm -166 cm range and were similar in maturity to local check hybrids (97-100 days).

Saidaiah et al. (2008) studied heterosis for yield and its contributing traits in forty crosses developed by crossing ten inbred lines with four testers and reported that twenty-three crosses significantly out yielded over the better parent.

Amiruzzaman et al. (2010) observed that standard heterosis ranged for yield per plant (-17.60% - 9.71%), length of ear (-13.89% - 7.54%), number of kernels per cob (-20.41% - 8.04%), 1000-grain weight (-6.17% - 14.48%) and also reported that kernel weight revealed maximum heterotic contribution to high yield.

Sundarajan and Kumar (2011) reported significant standard heterosis in the number of grains per cob, days to 50% tasseling, cob circumference, grain yield per plant (19.63%), 100-grain weight, plant height, cob length and days to 50% silking.

Kumar et al. (2012) reported better parent heterosis for grain yield per plant (20.40% - 268.76%), number of branches per tassel (-12.00% - 119.23%), leaf area index (-10.00% - 68.68%) and SPAD chlorophyll (23.09% -29.19%).

Dhairyashil et al. (2013) studied ten parents and their ninety F_1 hybrids to calculate better parent heterosis. For grain yield better parent heterosis ranged from 30.79 per cent to 242.73 per cent in *rabi* and from -14.84 per cent to 300 per cent in the *kharif* season.

Elmyhum (2013) estimated better parent heterosis and combining ability using six inbred lines and their F_1 hybrids. Hybrids *viz.,* HN7 (89.56%) and HN8 (85.63%) showed significant positive heterosis for grain yield.

Netravati et al. (2013) recorded that for grain yield per plant there is considerable positive better parent heterosis ranged from -4.48 per cent to 87.29 per cent and standard heterosis (-31.58% - 22.11%). For days to 50% maturity and 50% tasseling they also reported significant negative better parent heterosis and negative standard heterosis.

Kapoor et al. (2014) reported significant positive standard heterosis for cob placement height, grain yield, cob length, ear circumference and harvest index. For grain yield the standard heterosis ranged from (6.24% - 42.93%).

Ulaganathan et al. (2015) reported mid parent heterosis (14.77% - 98.73%) and better parent heterosis (2.17% - 64.83%) for grain yield.

Mesenbet et al. (2016) estimated heterosis in maize hybrids for grain yield and yield related traits. The standard heterosis for grain yields varied from -38.72 per cent to 33.65 per cent.

Kumar and Babu (2016) reported significant standard heterosis for days to 50% tasseling, days to 50% silking, days to maturity, cob length, plant height, kernel rows per cob, protein content and 100-seed weight.

Kumar et al. (2019) reported that traits *viz.,* ear circumference, ear length, number of kernel rows per ear, seed index, harvest index and grain yield per plant, across two environments and reported that hybrid $P_1 \times P_9$ had significant positive standard heterosis for harvest index across E1 (13.40%), E2 (10.96%) and pooled over environment (13.23%).

Patel et al. (2019) reported significant positive mid parent, better parent and standard heterosis for grain yield per plant, cob length, cob weight, cob circumference, number of kernel rows per cob, 100-grain weight and number of kernels per row when compared to best check GAYMH-1 and reported that mid parent heterosis (0.10%-16.85%), better parent (1.41%-16.57%) and standard heterosis (6.31%-21.80%) for grain yield per plant.

Tafa et al. (2020) estimated heterosis using forty-five F_1 single crosses and observed maximum mid parent (240.34%), better parent (220.85%) and standard heterosis (18.79%) for grain yield.

Chandel et al. (2020) reported that significant positive standard heterosis for grain yield and ranged from 11.74 per cent to 44.40 per cent.

Sharma et al. (2021) recorded significant positive standard heterosis for grain yield in two F_1s *viz.,* $P_1 \times P_4$ and $P_2 \times P_4$ in individual as well as pooled environments. $P_1 \times P_4$ showed significant positive heterosis in E1 (16.05%), in E2 (12.65%) and in pooled environments (16.15%), whereas, $P_2 \times P_4$ exhibited significant positive heterosis in E1 (13.40%), in E2 (13.14%) and in pooled environments (15.45%).

2.3 Disease reaction

Diseases are threat to global food security, although plants have developed a wide range of defense mechanisms to combat invading pathogens. Among the various maize diseases, banded leaf and sheath blight (BLSB) caused by *Rhizoctonia solani f. sp. sasaki*i, Turcicum leaf blight (TLB) caused by *Exserohilum turcicum*, and Maydis leaf blight caused by *Bipolaris maydis* are found in abundance across the maize growing regions. Turcicum leaf blight is a serious maize disease in the Himalayan region, owing to somewhat low temperatures and excessive humidity throughout the maize season (Mir et al. 2015). As a result identifying disease resistant sources is the first and most important step for crop management.

Meena (2004) identified nine inbred lines *viz.,* PRD-340, HKH-1140, PAC79001, NMH-9858, FH-3097, NECH-01, FH-3133, BIO-81009 and F-7001 resistant to banded leaf and sheath blight under artificial condition.

Huang et al. (2007) reported that during the maize growing season, high temperatures, high humidity and extended wet and cloudy weather give ideal conditions for banded leaf and sheath blight disease of maize.

Rai (2009) screened fifty-one genotypes for resistant against maydis leaf blight and recorded resistance in twenty-six genotypes under artificial inoculated conditions.

Bhavana and Gadag (2011) evaluated forty maize inbred lines against banded leaf and sheath blight disease under epiphytotic condition and none of the inbreds showed resistant to banded leaf and sheath blight either due to shortage of resistance in the inbreds or higher virulence of the pathogen.

Hooda et al. (2012) studied two-hundred elite maize lines for ten major diseases and revealed that out of two hundred lines, sixteen lines showed resistance against turcicum leaf blight and twenty-eight lines had resistance against maydis leaf blight under artificial epiphytotics condition.

Sood (2012) evaluated forty inbred lines for banded leaf and sheath blight and observed moderate resistance only in one inbred line CL02450.

Kumar et al. (2013) reported that out of seventeen QPM inbreds, two inbreds DQL 2015 and DQL 2071 showed resistance for maydis leaf blight under artificial epiphytotic condition.

Chen et al. (2013) evaluated that two hundred eighty-two maize inbred lines are disease resistant to banded leaf and sheath blight and four inbred *viz.,* 18-599, Qi-318, PA23 and Shen-3336 were moderately resistant under artificial conditions.

Izhar and Chakraborty (2013) studied the genetics of resistance to banded leaf and sheath blight in maize and found resistance in five testers and three lines while twelve lines were moderately resistance under artificial inoculation.

Thakur (2014) screened forty-eight genotypes for banded leaf and sheath blight resistance and reported that five lines were moderately resistant, eighteen were moderately susceptible and two were severely susceptible under natural epiphytotic conditions.

Omprakash et al. (2016) screened fifty-six inbreds of maize across four environments and identified twenty-five resistant and seventeen moderately resistant for maydis leaf blight.

Kachapur et al. (2016) screened fifty maize germplasm lines for turcicum leaf blight of maize and found that only 6 per cent germplasm lines showed resistance, 46 per cent were moderately resistant, 23.0 per cent were moderately susceptible and 10 per cent were completely susceptible under artificial epiphytotic conditions.

Yousuf et al. (2018) screened seventy landraces against turcicum leaf blight under artificial conditions and observed resistance in forty lines.

Thakur et al. (2018) screened twenty-seven inbred lines, two testers and fifty-four crosses for turcicum leaf blight under natural and artificial epiphytotic conditions and reported resistance in five inbred lines and thirty-one cross combinations under both natural and artificial epiphytotic conditions.

Razzaq et al. (2019) screened thirty lines of maize for turcicum leaf blight. He reported three genotypes *viz.,* Karamat bar-25, SZP13200 and NCEV-1530-11 exhibited resistance towards turcicum leaf blight.

Sharma et al. (2021) screened eight parents, twenty-one F_1s for turcicum and maydis leaf blight under both natural and artificial epiphytotic conditions. Three parents *viz.*, P_3, P_6, P_4 and four F_1s *viz.,* $P_3 \times P_4$, $P_3 \times P_5$, $P_3 \times P_6$ and $P_7 \times P_8$ showed resistance against both the diseases.

Yadav et al. (2022) screened one hundred two entries through artificial inoculations under field conditions. He reported thirty-four entries showed resistant and thirty-six entries were moderately resistant against banded leaf and sheath blight.

3. MATERIAL AND METHODS

The present investigation was carried out during *kharif*, 2021 at the Experimental Farm of Shivalik Agriculture Research and Extension Centre, Kangra. The details of present investigation are presented below:

3.1 Experiment site

The Experiment Farm is located at 32°09'N latitude and 76°22'E longitude at an elevation of 700m amsl at the foothills of North -Western Himalayas. It is situated in the mid-hills region (Zone –II) of the state. The soil is clay loam in texture having pH around 6.5.

3.2 Experimental material

The experimental material consisted of seven parental lines, their twenty-one crosses and three standard checks *viz.,* Palam Sankar Makka-2, Bio 9544 and Bio 605. The details of inbred lines and standard checks are presented in Table 3.1.

Table 3.1 Details of inbred lines along with check (s)

Symbol/Code	**Pedigree/Source**
P_1	EC611063(B)AAA[KGI-109]
P_2	LM-18
P_3	DMEL143
P_4	DMEL156
P_5	CM139
P_6	DMR139
P_7	HEY Pool-2011-15-3-7-3-4-1AAA KGI-110
Standard checks	Palam Sanker Makka-2, Bio 9544, Bio 605

3.3 Methodology

3.3.1 Crossing plan

These lines were crossed in 7 × 7 diallel mating system excluding reciprocals at Winter Nursery Centre, ICAR- Indian Institute of Maize Research, Hyderabad during *rabi*, 2020-21.

3.3.2 Experiment design and layout

The experimental material consisted of seven parents, twenty-one crosses and three checks *viz.,* Palam Sankar Makka-2, Bio 9544 and Bio 605 were evaluated in Randomized

Block Design (RBD) with two replications in a plot size of 3.0 × 1.2m (3.6 m^2) at a spacing of 60 × 20 cm during *kharif,* 2021 at Shivalik Agricultural research and Extension Centre, Kangra.

3.4 Observations recorded

3.4.1 Yield and its component traits

Observations were recorded on ten competitive plants and mid parent was worked out except for days to 50% pollen shed, days to 50% silking and days to 75% brown husk where observations were recorded on plot basis.

i. Grain yield (g/plant)

Fresh ear weight was recorded at the time of harvest and moisture of grains was determined using "Universal moisture meter". Ear weight was first converted into grain weight after calculating shelling (%) of each entry. Grain weight was adjusted at 15 per cent moisture content and the grain yield in gram per plant was calculated.

ii. 1000-kernel weight (g)

1000-kernels were selected randomly from a mixed sample of ten plants and their weight expressed in grams was recorded for each treatment.

iii. Shelling (%)

Shelling percentage for each treatment was recorded. The shelling percentage is calculated as

Shelling (%) = weight of total grains/weight of cob including grain × 100

iv. Number of kernels per row

Number of kernels in each row was recorded for all cobs of ten selected plants and average was worked out for each treatment.

v. Number of kernel rows per ear

Number of kernel rows in each cob of ten selected plants was counted and average was worked out for each treatment.

vi. Ear length (cm)

Ear length of each cob of ten selected plants was measured from the base to the filled grain point with a measuring tape. Average value was worked out for each treatment.

vii. Ear circumference (cm)

The cob circumference was measured in centimeters in the center of each cob from the ten ears and mean was worked out.

3.4.2 Maturity and Physiological characters

i. Days to 50% pollen shed

The number of days taken for 50% pollen shed in a treatment from the day of sowing was recorded on plot basis.

ii. Days to 50% silking

Days taken for the emergence of 50% silk in a treatment from the date of sowing was recorded on plot basis.

iii. Days to 75% brown husk

The number of days from sowing to the time when 75% of the plants in a treatment had attained brown husk was recorded on plot basis.

iv. Ear height (cm)

The ear height was measured at dry silk stage in centimeters from the base of the plant to the base of the uppermost cob from the same randomly selected ten plants whose plant height was recorded and average was worked out.

v. Plant height (cm)

From the ten plants selected at random the plant height was recorded in centimeters from the base of the plant to the tassel bearing node at maturity using a measuring rod and then averaged.

3.4.3 Reaction to diseases under natural conditions

The experimental material was screened against turcicum leaf blight (TLB), maydis leaf blight (MLB) and banded leaf and sheath blight (BLSB) under natural conditions. The disease rating of turcicum leaf blight was done at dough stage following 1-9 scale (Chung et al., 2010; Mitiku et al., 2014). The rating scale for recording maydis leaf blight reaction consists of 9 broad categories designated by numerals 1 to 9 (Balint-Kurti et al., 2006; Chung et al., 2010 and Mitiku et al., 2014). banded leaf and sheath blight was recorded after 75 days of sowing on basis of following modified 1-9 rating scale of AICMIP (1983) and Muisa and Quimiob (2006). Infection against these diseases was rated on a scale of 1 to 9, where 1 indicated no or very slight infection and nine represents very heavy infections.

Table 3.2 Disease rating scale for banded leaf and sheath blight, turcicum leaf blight and maydis leaf blight

Rating Scale	Degree of infection	Disease reaction
1.0	Nil to very slight infection (<10%).	Resistance (Score: ≤ 3.0)
2.0	Slight infection, a few lesions scattered on two lower leaves (10.1-20%).	
3.0	Light infection, moderate number of lesions scattered on four lower leaves (20.1-30%).	
4.0	Light infection, moderate number of lesions scattered on lower leaves, a few lesions scattered on lower leaves, a few lesions scattered on middle leaves below the cob (30.1-40%).	Moderately Resistance (MR) (Score: 3.1–5.0)
5.0	Moderate infection, abundant number of lesions scattered on lower leaves, moderate number of lesions scattered on middle leaves below the cob (40.1-50%).	
6.0	Heavy infection, abundant number of lesions scattered on lower leaves, moderate infections on middle leaves and a few lesions on two leaves above the cob (50.1-60%).	Moderately Susceptible (MS) (Score: 5.1-7.0)
7.0	Heavy infestation, abundant number of lesions scattered on lower and middle leaves and moderate number of lesions on two or four leaves above the cob (60.1-70%).	
8.0	Very heavy infection, lesions abundantly scattered on lower and middle leaves and middle leaves and spreading up to the flag leaf (70.1-80%)	Susceptible (Score: >7.0-9.0)
9.0	Very heavy infection, lesions abundantly scattered on almost all leaves, premature dead plants (>80%).	

3.5 Statistical analyses

Mean values of all characters under study were subjected to statistical analysis.

3.5.1 Analysis of variance for randomized block design

The data were subjected to randomized block design as described by Panse and Sukhatme (1984). The significance was tested by 'F' test at 5 % level of probability. The analysis of variance (ANOVA) was constructed based on the linear model given by Fisher (1954):

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

where,

Y_{ij} = phenotypic observation of i^{th} genotype grown in the j^{th} block

μ = general population mean

gi = effect of i^{th} genotype

rj = effect of j^{th} replication

eij = error associated with i^{th} genotype and j^{th} replication

ANOVA for Randomized Block design

Sources of Variation	Degree of freedom (df)	Sum of squares (SS)	Mean sum of squares (MS)	F value (calculated)	Expected MS
Replication	(r-1)	Sr	$M_r = Sr/(r-1)$	M_r/M_e	$\sigma^2_e + g\,\sigma^2_r$
Genotypes	(g-1)	Sg	Mg = Sg(g-1)	M_g/M_e	$\sigma^2_e + \sigma^2_g$
Error	(r-1)(g-1)	Se	Me = Se/ (r-1)(g-1)		σ^2_e
Total	(rg-1)	-	-	-	-

where,

r = number of replications

g = number of genotypes

σ^2_e = error variance = Me

σ^2_g = variance due to genotypes = $(M_g - M_e)/r$

σ^2_r = variance due to replications = $(M_r - M_e)/g$

σ^2_p = phenotypic variance = $\sigma^2_g + \sigma^2_e$

The standard error (SE) of mean SE(m)(±) and critical difference(CD at 5%) for comparing the mean of any two lines were computed as follows:

i. Standard error of mean

$$\text{SE (m)} = \pm \sqrt{\frac{\text{Me}}{\text{r}}}$$

ii. Standard error (SE) of difference

$$\text{SE (d)} = \pm \sqrt{\frac{\text{2Me}}{\text{r}}}$$

iii. Critical difference (CD)

CD = SE (d) ×‘t’

where,

SE (d) ± = Standard error of difference

‘t’ = tabulated value of ‘t’ at 5% level of significance at error degree of freedom.

The calculated F valued were compared with table F value at 5% level of significance. If the calculate value was higher than the tabulated value, it was considered to be significant. All the characters which showed significant differences among genotypes were further subjected to the analysis of different parameters.

3.5.2 Combining ability analysis of the parents and crosses

The data obtained from F_1 population was subjected to combining ability analysis Griffing's (1956^a) experimental method II model I was considered to be the most appropriate for the material under study. Method II (half diallel) was applicable to the present investigation as parents and one set of F_1s were included without reciprocals. Model I is the fixed model i.e. it assumes that the variety and block effects are constant but the environmental effect (error) is a random variable such that $e_{ij}kl$ are normally and independently distributed with mean zero and variance one.

When the F-test revealed significant differences among the genotypes, combining ability analysis was followed. A linear mathematical model for an observation made on ijth genotype could be expressed as:

$$Yij = \mu + gi + gj + sij + \frac{1}{rc}\sum_k \sum_1 e_{ij}kl$$

i, j = 1,2,………..n.

k = 1, 2,……….r.

l = 1,2,…….........c.

where,

Y_{ij} = phenotype of the hybrid between ith and jth parents in kth block

μ = general mean,

g_i= GCA effect of the ith parent,

g_j= GCA effect of the jth parent,

s_{ij}= SCA effect of the hybrid between ith and jth parents

such that, $s_{ij} = s_{ji}$,

r = number of replications,

c = total number of observations in per plot,

$e_{ij}kl$ = The effect of the environment on ijklth observation

$\frac{1}{bc}\sum_k \sum_1 e_{ij}kl =$ is the mean error effect

The following restrictions were placed on this model:

$\sum_i gi = 0$, and

$\sum_j s_{ij} + s_{ji} = 0\ (For\ each\ 1)$

ANOVA for combining ability Method 2 Model 1 (Griffing, 1956b)

Sources of Variation	Degree of freedom (df)	Sum of squares (SS)	Mean sum of squares (MS)	F value (calculated)	Expected MSS
GCA	(p-1)	S_g	M_g	M_g/M_e’	$\sigma^2 e + \frac{(p+2)}{(p-1)}\sum_i g^2 i$
SCA	$\frac{p(p-1)}{2}$	S_s	Ms	M_s/M_e’	$\sigma^2 e$ $+\frac{2}{p(p-1)}\sum_i \sum_j s^2 ij$
Error	(b-1) $\left[\frac{p(p-1)}{2} + (p-1)\right]$	S_e	Me’(= Me/r)		σ^2_e

where,

GCA = general combining ability

SCA = specific combining ability

$Sg = \frac{1}{p+2}\left[\sum_i (y_{i.} + y_{ii})^2 - \frac{4}{p} y^{2..}\right]$, and

$$Ss = \sum_{is}\sum_{j} y_i^2 - \frac{1}{p+2}\sum_{I}(y_i + y_{ji})2 + \frac{2}{(p+1)(p+2)} y^{2..}$$

p = number of parents

b = number of replications

$M_e’ = \frac{\text{Mean square of error in RBD}}{r}$

M_g = mean square GCA

M_s = mean square of SCA

$y_{i.}$ = total number of array of ith parent

y_{ij} = mean value of ith parent

$y_{..}$ = grand total of parental values and [p (p-1)/2] progenies

yij = ijth cross mean value

The effects and standard errors of GCA and SCA were estimated when the mean squares for both were squares for both were confirmed to be significant.

3.5.3 Combining ability estimates/effects and their standard errors

The following 'F' ratios were used to test for GCA and SCA effects.

(a) To test differences among GCA effect of a character, following ratio is used

$F_{[(p-1),m]} = M_g / M_e$'

(b) The following ratio is used to compare the SCA effects of a characters.

$F_{[p(p-1)/2,m]} = M_s/M_e$'

The GCA (g_i) effect of ith inbred line and SCA (S_{ij}) effect of ijth cross were estimated as follows:

$$\hat{\mu} = \frac{2}{p(p+1)} y \dots$$

General combining ability effects of ith parent:

$$\hat{}\hat{g}_i = \frac{1}{(p+2)}(y_{i.} + y_{ii}) - \frac{2}{p} y_{..}$$

Specific combining ability effect of ijth crosses:

$$\hat{s}_{ij} = y_{ij} - \frac{1}{(p+2)}(y_i + y_{ii} + y_{j.} + y_{jj}) + \frac{2}{(p+1)(p+2)} y_{..}$$

where,

p = number of parents

$y_{i.}$ = total number of array ith parent

$y_{j.}$ = total of array involving jth parent

y_{ii} = value of the ith parent

y_{jj} = value of jth parent

y. .= total of all the $\left[\frac{p(p-1)}{p}\right]$ items in diallel table

y_{ij} = the mean value of the cross involving ith and jth parent

Standard error to test the significance of general and specific combining ability and the standard error of difference between the two estimates were computed from the following formulae:

1. Standard error for testing GCA (gi) effects $= \pm\sqrt{\frac{Me'(p-1)}{p(p+2)}}$

2. Standard error for testing difference between two GCA (gi – gj)effect = $\pm\sqrt{\frac{2Me'}{(p+2)}}$

3. Standard error for testing SCA (sij) effects = $\pm\sqrt{\frac{Me'(p^2+p+2)}{(p+1)(p+2)}}$

4 (i) Standard error for testing difference between two specific combinig ability effects in the same array (S_{ij}-S_{ik})

$$= \pm\sqrt{\frac{2(p+1)Me'}{(p+2)}}$$

(ii) Standard error for testing difference between two Specific combinig ability effects in the different arrays (S_{ij} - S_{kl})

$$= \pm\sqrt{\frac{2p(Me')}{(p+2)}}$$

Test of significance for general combining ability and specific combining ability effects

(a) t_i (cal) for general combining ability of parents = (gi-0)/SE(g_i)

(b) t_{ij} (cal) for specific combining ability of crosses =(Sij-0)/SE(S_{ij})

where,

t_i(cal) and t_{ij} (cal) are the calculated 't' values,

g_i = general combining ability effect of i^{th} parent,

s_{ij} = specific combining ability effects of ij^{th} cross.

When the values of t_i (cal) and t_{ij} (cal) had ≥ 't' tabulated value at error degree of freedom of individual environment, the GCA effects of parents as well as SCA effects of crosses were marked significant(*).

Furthermore, the CD (critical difference) were calculated to make pair wise comparisons between different effects (Singh and Chaudhary, 1985). C.D. was calculated using the following formula.

CD = SE (g_i-g_i) ×'t' tab value at 5% level of significance.

The difference between GCA of any two parents and SCA of any two crosses were considered significant when the differences were > respective CD values.

3.5.4 Variance components of combining ability

To estimate the GCA and SCA variances, the analysis is carried out as follows:

(i) Components due to general combining ability

$$\hat{\sigma}^2\text{GCA} = \frac{1}{p+2}\left[M_g - M_e\right]$$

(ii) Components due to specific combining ability

$$\hat{\sigma}^2\text{SCA} = [M_s - M_e]$$

where,

$\hat{\sigma}^2$ GCA = variance component due to GCA

$\hat{\sigma}^2$ SCA = variance component due to SCA

p = number of parent involved

M_g = mean square of GCA

M_s = mean square of SCA

M_e= mean square of error

3.5.5. Estimation of additive (σ^2A) and dominance (σ^2D) components of variance:

For computing the additive and dominance components of variance, following formulae has been used (Singh and Chaudhary, 1985).

$\sigma^2 A = 2\sigma^2 gca$

$\sigma^2 D = \sigma^2 sca$

where,

σ^2A = additive variance, and

σ^2D =dominance variance.

3.5.6 Estimation of heterosis

Heterosis expressed as percent increase or decrease in the performance of F_1 hybrid over the mid-parent (relative or average) heterosis, better parent (heterobeltiosis) and check parent (standard heterosis) were computed for each character using the following formula:

Mid parent heterosis = $(\overline{F}_1-\overline{MP})/\overline{MP} \times 100$

Better parent heterosis = $(\overline{F}_1- \overline{BP})/ \overline{BP} \times 100$

Standard heterosis = $(\overline{F}_1- \overline{CV})/ \overline{CV} \times 100$

Where,

$\bar{F}_1$ =Mean performance of F_1 hybrid

$\bar{P}_1$= Mean performance of parent one

$\bar{P}_2$ = Mean performance of parent two

$\overline{BP}$ = Mean performance of better parent

$\overline{CV}$ =Mean performance of check variety

$\overline{MP}$ = Mean performance of mid parental value i.e. $(P_1\text{-}P_2)/2$

The significance of heterosis was tested with ‘t’ as shown below:

(a) For relative heterosis

$$t = \frac{\bar{F}_1 - \overline{MP}}{\sqrt{3\ Me/2r}}$$

(b) For better parent heterosis

$$t = \frac{\bar{F}_1 - \overline{BP}}{\sqrt{2Me/r}}$$

(c) For standard heterosis

$$t = \frac{\bar{F}_1 - \overline{CV}}{\sqrt{2Me/r}}$$

where,

$\bar{F}_1$= Mean of F_1 hybrid

$\overline{BP}$ = mean performance of better parent

$\overline{CV}$ = Mean performance of check variety

$\overline{MP}$ = Mean performance of mid parent

Me = Error mean square

r = Number of replication

4. RESULTS AND DISCUSSION

The results of the present study "Heterosis and combining ability analysis of sub-tropical maize (*Zea mays* L.) inbred lines" were obtained from twenty-one maize F_1s developed by crossing seven inbred lines with three check lines *viz.,* Palam Sankar Makka-2, Bio 9544 and Bio 605 using a half diallel mating scheme. The experimental data were evaluated with appropriate statistical biometrical models and the results are presented and explained under the following heading:

4.1 Analysis of variance for RBD
4.2 Mean performance of parents and crosses
4.3 ANOVA for combining ability
4.4 Estimation of heterosis
4.5 Disease reaction
4.6. Promising hybrid combinations

4.1 Analysis of variance for randomized block design

Genetic variability is the most essential requirement of any breeding programme. Hence, it becomes very essential to confirm that whether there is presence of sufficient genetic variability or not, before initiation of any crop improvement programme for various traits. Significant differences among parents and their F_1's represented that there are inherent genetic differences among genotypes for all the characters studied. This proved suitability of the experimental material chosen for the present investigation.

The analysis of variance for RBD for different traits is presented in Table 4.1. Analysis of variance for RBD revealed that mean sum of squares due to genotypes was significant for all the traits except number of kernel rows per ear revealed that the material under investigation had sufficient amount of variability. Similar results were also observed earlier for analysis of variance for RBD by Krupakar et al. (2013); Kumar et al. (2013); Dar et al. (2015); Amadabade (2017); Kumar et al. (2017) and Hosamani et al. (2018) for different traits *viz.,* days to 50% pollen shed, days to 50% silking, plant height, ear height, ear length, ear circumference, grain yield, 1000-grain weight, number of kernels per row, ear circumference; days to maturity. El Hosary et al. (2018) and kumar et al. (2022) also reported non-significant differences for shelling (%).

Table .4.1: Analysis of variance for randomized block design

S.No.	Characters	Source		
		Replication	Genotype	Error
		[1]	[30]	[30]
1	Days to 50% pollen shed	4.13	8.31*	0.96
2	Days to 50% silking	4.67	11.14*	1.53
3	Days to 75% brown husk	0.15	21.03*	1.71
4	Plant height (cm)	64.02	1261.25*	55.20
5	Ear height (cm)	11.76	389.47*	34.56
6	Number of kernel rows per ear	1.613	3.19	0.95
7	Number of kernels per row	0.02	81.39*	3.25
8	Ear length (cm)	0.02	25.34*	2.25
9	Ear circumference (cm)	0.51	2.56*	0.54
10	1000-kernel weight (g)	108.45	3662.19*	79.65
11	Shelling (%)	0.54	10.32 *	2.20
12	Grain yield (g/plant)	56.07	1606.59 *	30.39

* Significant at 5%

4.2 Mean performance of parents and crosses for different traits

For each trait under study general mean and range along with mean performance of parents and crosses was compared to the mean performance of the corresponding best check, the results are in Appendix I.

4.2.1 Days to 50% pollen shed

The general mean for days to 50% pollen shed was 54.82 days ranged from 51.50 days (P_1 × P_4) to 58.0 days (P_4 × P_6). Five parents *viz.,* P_1 (52.50 days), P_7 (52.50 days), P_6 (53.00 days), P_3 (53.50 days) and P_4 (55.00 days) showed desired mean values when compared with the best check PSM-2 (56.50 days). Among twenty one crosses, ten crosses *viz.,* P_2 × P_5 (51.50 days), P_1 × P_4 (51.50 days), P_2 × P_3 (52.50 days), P_1 × P_6 (52.50 days), P_2 × P_6 (53.00 days), P_3

× P_7 (53.50 days), P_3 × P_5 (53.50 days), P_3 × P_4 (53.50 days), P_1 × P_7 (54.00 days) and P_2 × P_4 (54.00 days) were superior to the best check PSM-2 (56.50 days)[Appendix I]

4.2.2 Days to 50% silking

The general mean for days to 50 % silking was 58.05 days ranged from 54.00 days (P_2 × P_5) to 61.50 days (P_4 × P_6). For days to 50% silking the best check was PSM-2 (60.50 days). Four parents P_1 (55.50 days), P_7 (55.50 days), P_6 (56.50 days), P_3 (57.00 days) and ten crosses *viz.,* P_2 × P_5 (54.00 days), P_1 × P_4 (54.50 days), P_2 × P_3 (55.00 days), P_1 × P_6 (55.50 days), P_2 × P_6 (56.00 days), P_3 × P_4 (56.00 days), P_3 × P_5 (56.50 days), P_3 × P_7 (56.50 days), P_2 × P_4 (57.00 days) and P_6 × P_7 (57.00 days) showed mean values less than best check Palam Sankar Makka-2 (60.50 days). However, three inbreds and ten crosses were statistically at par with the best check PSM-2 (60.50 days) [Appendix I].

4.2.3 Days to 75% brown husk

Six inbreds *viz.,* P_3 (88.50 days), P_1 (89.00 days), P_5 (89.00 days), P_7 (89.00 days), P_6 (90.00days), P_2 (91.00 days) and eleven crosses *viz.,* P_1 × P_6 (88.50 days), P_2 × P_3 (89.00 days), P_3 × P_7 (89.00 days), P_2 × P_5 (89.00 days), P_1 × P_7 (89.50 days), P_2 × P_6 (89.50 days), P_3 × P_6 (90.00days), P_2 × P_4 (90.50 days), P_1 × P_5 (91.50 days), P_3 × P_5 (91.00 days) and P_3 × P_4 (91.50 days) were superior to the best check Bio 605 (95.00 days), However, one inbred and nine crosses were statistically at par with the best check. The general mean for days to 75% brown husk was 92.27 days and ranged from 88.50 days (P_3, P_1 × P_6) to 98.50 (P_1 × P_3) [Appendix I.].

4.2.4. Plant height (cm)

General mean for plant height was 175.02 cm and ranged from 102.50 cm (P_7) to 228.25 cm (P_2 × P_5). Inbred P_7 (102.50 cm), P_3 (136.00 cm), P_2 (149.00 cm), P_4 (150.00 cm), P_5 (153.50 cm), P_1 (161.25 cm) and cross P_4 × P_7 (146.50 cm), P_4 × P_6 (149.75 cm), P_3 × P_6 (159.50 cm), P_4 × P_5 (160.00 cm), P_6 × P_7 (161.25 cm), P_1 × P_3 (169.50 cm), P_3 × P_4 (171.25 cm), P_1 × P_2 (173.00 cm) and P_2 × P_4 (174.25 cm) were exhibited less plant height as compared to the best check PSM-2 (192.50 cm). One parent and eleven crosses were statistically at par with the best check PSM-2 (192.50 cm) [Appendix I].

4.2.5. Ear height (cm)

For ear height the best check was PSM-2 (91.00 cm). The all parents *viz.,* P_7 (52.00 cm), P_2 (60.25 cm), P_3 (61.75 cm), P_5 (66.75 cm), P_1 (71.75 cm), P_4 (71.75 cm), P_6 (76.25) and three crosses P_1 × P_7 (75.25 cm), P_1 × P_4 (79.50 cm) and P_6 × P_7 (79.00 cm) exhibited lower mean value for ear height as compared to best check PSM-2 (91.00 cm). However, sixteen F$_1$s were statistically at par with the best check PSM-2 (91.00 cm) [Appendix I].

4.2.6 Number of kernel rows per cob

Bio 9544 (13.00) was the best check for number of kernel rows per cob. General mean for this trait was 13.06 and varied from 10 (P_5) to 15 ($P_1 \times P_4$). Five crosses *viz.,* $P_1 \times P_3$ (15), $P_1 \times P_4$ (15), $P_2 \times P_4$ (15), $P_3 \times P_7$ (15) and $P_4 \times P_5$ (15) were superior to the best check. All inbreds and sixteen crosses were statistically at par with Bio 9544 (13.00) [Appendix I].

4.2.7 Number of kernels per row

General mean for number of kernels per row was 30.65 and ranged from 15.00 (P_7) to 43.00 ($P_6 \times P_7$). The two crosses $P_6 \times P_7$ (42.00) and $P_1 \times P_4$ (41.00) were superior than the best check Bio 9544 (35.00). However, twelve crosses were statistically at par with best check Bio 9544 (35.00) [Appendix I].

4.2.8 Ear length (cm)

For ear length the best check was Bio 605 (19.85 cm). Seven crosses were statistically at par with best check. Among twenty-one F$_1$s, two crosses *viz.,* $P_1 \times P_4$ (23.10 cm) and $P_6 \times P_7$ (22.90 cm) were superior as compared to best check. General mean for ear length was 16.23 cm and ranged from 9.05 cm (P_2) to 23.10 cm ($P_1 \times P_4$) [Appendix I].

4.2.9 Ear circumference (cm)

General mean for ear circumference was 12.95 cm and varied from 10.40 cm (P_7) to 15.55 cm ($P_3 \times P_7$). Palam Sankar Makka-2 (14.25 cm) was best check for ear circumference. Only one cross $P_3 \times P_7$ (15.55 cm) were superior than best check PSM-2 (14.25 cm). Nine crosses were statistically at par with best check PSM-2 (14.25) [Appendix I].

4.2.10 1000-kernel weight (g)

For 1000-kernel weight the best check was PSM-2 (279 g). Seven crosses *viz.,* $P_1 \times P_5$ (315 g), $P_2 \times P_3$ (315 g), $P_3 \times P_5$ (315 g), $P_2 \times P_5$ (310 g), $P_1 \times P_4$ (309 g), $P_6 \times P_7$ (304 g) and $P_3 \times P_7$ (301 g) outperformed the best check Palam Sankar Makka-2 (279 g). General mean for 1000-kernel weight was 255.19 g ranged from 135 g (P_7) to 315 g ($P_2 \times P_3$). Three crosses were statistically at par with best check PSM-2 (279 g) [Appendix I].

4.2.11 Shelling (%)

The general mean for shelling (%) was 83.03 per cent and ranged from 76.04 per cent to 86.99 per cent. Two parents P_4 (86.08%), P_6 (85.37%) and eight crosses *viz.,* $P_1 \times P_3$ (86.99%), $P_1 \times P_7$ (86.26%), $P_2 \times P_7$ (86.12%), $P_3 \times P_6$ (85.13%), $P_3 \times P_7$ (84.71%), $P_1 \times P_2$ (84.48%), $P_2 \times P_6$ (84.30%) and $P_6 \times P_7$ (84.13%) were superior to best check Bio 9544

(80.93%). However, four inbreds and thirteen F_1s were statistically at par with Bio 9544 (80.93%) [Appendix I].

4.2.12 Grain yield (g/plant)

The general mean yield for grain yield was 73.89 g/plant and varied from 26.40 g/plant (P_7) to 117.9 g/plant ($P_1 \times P_4$). Among the crosses, thirteen crosses *viz.*, $P_1 \times P_4$ (117.90 g/plant), $P_1 \times P_3$ (114.79 g/plant), $P_2 \times P_3$ (113.03 g/plant), $P_6 \times P_7$ (108.82 g/plant), $P_3 \times P_7$(105.51 g/plant), $P_2 \times P_5$ (104.46 g/plant), $P_1 \times P_6$ (103.26 g/plant), $P_1 \times P_5$ (100.12 g/plant), $P_3 \times P_5$ (93.23 g/plant), $P_3 \times P_6$ (91.26 g/plant), $P_4 \times P_5$ (90.98 g/plant), $P_4 \times P_7$ (90.38 g/plant) and $P_1 \times P_2$ (83.52 g/plant) were superior than best check PSM-2 (72.61 g/plant). Four crosses were statistically at par with PSM-2 (72.61 g/plant) [Appendix I].

On the basis of mean performance, parent P_1 showed earliness for days to 50% pollen shed, days to 50% silking and days to 75% brown husk and also showed maximum 1000-kernel weight. For plant and ear height P_7 exhibited shorter height and maximum kernel rows per ear, P_4 exhibited maximum number of kernels per row and shelling (%), P_3 showed maximum ear length and ear circumference, whereas, P_6 exhibited maximum grain yield per plant, whereas, among the crosses, $P_2 \times P_5$ showed earliness for days to 50% pollen shed and days to 50% silking, $P_1 \times P_6$ exhibited earliness for days to 75% brown husk, $P_3 \times P_6$ exhibited shorter plant height and $P_1 \times P_7$ showed shorter ear height. $P_1 \times P_4$ exhibited maximum number of kernel rows per ear and ear length, $P_6 \times P_7$ showed maximum number of kernels per row, $P_3 \times P_7$ exhibited highest ear circumference, $P_2 \times P_3$ exhibited highest 1000-kernel weight, $P_1 \times P_3$ showed maximum shelling (%) and $P_1 \times P_4$ exhibited highest grain yield per plant. Superior crosses were reported for all characters as compared to three standard check viz., PSM-2, Bio 9544 and Bio 605. Similar results were reported earlier by Amiruzzaman et al. (2010); Kumar and Babu (2016); Tafa et al. (2020).

4.3 ANOVA for combining ability

In every hybridization programme, combining ability is a useful tool for finding superior parents and best specific hybrid combinations for yield and yield components. The concept of combining ability was first given by Sprague and Tatum (1942). Specific combining ability (SCA) is the relative performance of a cross that is associated with non-additive gene action, whereas, general combining ability (GCA) is directly related to the breeding value of a parent and associated with additive genetic effects. The combining ability of twenty-one crosses and their seven parents was investigated using the diallel mating system (Method II, Model I) without reciprocals (Griffing,1956b). The results of analysis of variance of the combining ability presented in Table 4.2.

Table 4.2 ANOVA for combining ability for various traits

Source of variation	d.f.	Days to 50% pollen shed	Days to 50% silking	Days to 75% brown husk	Plant height (cm)	Ear height (cm)	Number of kernel rows per ear
		Mean Squares					
GCA	6	1.45*	0.99	4.06*	781.02*	182.64*	1.61*
SCA	21	4.87*	5.88*	9.95*	588.86*	203.27*	1.76*
ERROR	27	0.49	0.76	0.84	19.24	12.17	0.42

* -Significant at 5%

Table 4.2 Contd…

Source of variation	d.f.	Number of kernels per row	Ear length (cm)	Ear circumference (cm)	1000-kernel weight (g)	Shelling (%)	Grain yield (g/plant)
		Mean Squares					
GCA	6	10.86*	2.87*	0.80*	1898.34*	2.36	263.76*
SCA	21	52.71*	16.69*	1.37*	2031.73*	5.81*	1035.29*
ERROR	27	1.50	0.74	0.20	36.70	1.10	10.12

* -Significant at 5%

Analysis of variance for combining ability showed significant mean sum of squares due to GCA and SCA for all traits except significant mean squares due to GCA for days to 50% silking and shelling (%). These findings revealed that there were both additive and non-additive gene effects in the material under investigation for various traits. Similar results were also observed earlier by Kara (2001); Krupakar et al. (2013); Dar et al. (2015); Amadabade (2017); Chandel et al. (2019) and Kumar et al. (2019) for various traits *viz.,* grain yield, 1000-kernel weight, number of kernels per row, ear circumference; days to 50% anthesis, days to 50% silking, plant height, ear height, ear length, ear diameter, number of kernel rows per ear, number of kernels per row, days to maturity. El Hosary et al. (2018) also reported non-significant differences for shelling (%).

4.3.1 Estimates of combining ability effects

The estimates of combining ability for the experimental material are presented in Table 4.3 to Table 4.5. For days to 50% pollen shed, days to 50% silking, days to 75% brown husk, ear height and plant height negative general and specific combining ability effects are desirable and for remaining traits *viz.,* ear circumference, ear length, kernels per row, kernel rows per cob, 1000-kernel weight, shelling (%) and grain yield per plant positive general and specific combining ability effects are desirable. The results obtained for all traits are presented below:

4.3.1.1 Days to 50% pollen shed

General combining ability effect for days to 50% pollen shed ranged from -0.62 (P_1) to 0.49 (P_3). Only one parent P_1 (-0.62) showed significant negative general combining ability effect (Table 4.3).

Specific combining ability effect for days to 50% pollen shed varied from -3.18 ($P_2 \times P_5$) to 3.76 ($P_1 \times P_2$). Among the crosses, $P_2 \times P_5$ (-3.18) showed maximum significant negative specific combining ability effects followed by $P_1 \times P_4$ (-2.90), $P_2 \times P_3$ (-2.35), $P_3 \times P_4$ (-2.01), $P_3 \times P_5$ (-2.01), $P_3 \times P_7$ (-1.63), $P_2 \times P_6$ (-1.24), $P_2 \times P_4$ (-0.68) and $P_1 \times P_6$ (-1.46) (Table 4.4).

4.3.1.2 Days to 50% silking

General combining ability effects for days to 50% silking ranged from -0.37 (P_3) to 0.52 (P_4). None of the parents showed significant negative GCA effects for days to 50% silking (Table 4.3).

Estimates of specific combining ability effects for days to 50 % silking ranged from -3.87 ($P_2 \times P_5$) to 4.29 ($P_1 \times P_2$). Eight crosses exhibited significant negative SCA effects for this trait. $P_2 \times P_5$ (-3.87) showed maximum significant negative specific combining ability effects followed by $P_1 \times P_4$ (-3.37), $P_2 \times P_3$ (-2.15), $P_1 \times P_6$ (-1.87), $P_3 \times P_4$ (-1.82), $P_2 \times P_6$ (-1.54), $P_3 \times P_5$ (-1.15) and $P_2 \times P_4$ (-1.04) (Table 4.4).

4.3.1.3 Days to 75% brown husk

General combining ability effects for days to 75% brown husk varied from -0.90 (P_3) to 1.21 (P_4). General combining ability effects was observed significantly negative for P_3 (-0.90) (Table 4.3).

Estimates of specific combining ability effects ranged from -3.07 ($P_1 \times P_6$) to 7.49 ($P_1 \times P_3$) for days to 75% brown husk. $P_1 \times P_6$ (-3.07) exhibited highest significant negative specific combining ability effects followed by $P_2 \times P_5$ (-2.57), $P_1 \times P_7$ (-2.51), $P_2 \times P_4$ (-2.01), $P_3 \times P_7$ (-1.96), $P_2 \times P_6$ (-1.46) and $P_2 \times P_3$ (-1.40) (Table 4.4).

Table 4.3 Estimates of General combining ability effects of inbred lines for different traits

Genotype	Days to 50% pollen shed	Days to 50% silking	Days to 75% brown husk	Plant height (cm)	Ear height (cm)	Number of kernel rows per ear	Number of kernels per row	Ear length (cm)	Ear circum-ference (cm)	1000-kernel weight (g)	Shelling (%)	Grain yield (g/plant)
P_1	-0.62 *	-0.31	0.15	5.00 *	-2.50 *	0.02	1.21 *	0.59 *	0.20	14.32 *	0.74 *	5.74 *
P_2	- 0.34	-0.14	-0.46	5.47 *	3.25 *	0.35	-0.29	0.05	0.18	-4.90 *	0.03	-0.13
P_3	0.49 *	-0.37	-0.90 *	-4.86 *	-2.44 *	0.02	0.93 *	0.39	0.49 *	6.32 *	-0.03	6.29 *
P_4	0.33	0.52	1.21 *	-10.56 *	1.53	0.24	-0.07	-0.86 *	-0.30 *	-14.46 *	-0.17	-7.07 *
P_5	0.33	0.36	0.26	11.14 *	-1.53	-0.76 *	-1.57 *	-0.57 *	-0.05	19.21 *	-0.09	1.24
P_6	-0.12	0.02	-0.35	6.58 *	2.58 *	-0.32	0.98 *	0.56 *	-0.24	-0.02	0.41	-1.05
P_7	-0.06	-0.09	0.10	-12.78*	-7.81 *	0.46 *	-1.18 *	-0.17	-0.28	-20.46 *	-0.89 *	-7.12 *
S.E.(gij)	0.21	0.27	0.28	1.35	1.08	0.20	0.38	0.26	0.14	1.87	0.32	0.98
S.E.(gi-gj)	0.33	0.41	1.30	2.07	1.65	0.30	0.58	0.40	0.21	2.86	0.49	1.50

*-Significant at 5%

Table 4.4 Estimates of specific combining ability effects of crosses for days to 50%pollen shed, days to 50% silking, days to 75% brown husk, plant height (cm), ear height (cm) and number of kernel rows per ear

Crosses	Days to 50% pollen shed	Days to 50% silking	Days to 75% brown husk	Plant height (cm)	Ear height(cm)	Number of kernel rows per ear
$P_1 \times P_2$	3.76 *	4.29 *	5.04 *	-10.10 *	2.06	-1.47 *
$P_1 \times P_3$	1.93 *	3.01 *	7.49 *	-3.26	7.01 *	1.86 *
$P_1 \times P_4$	-2.90 *	-3.37 *	-0.13	17.18 *	-3.72 *	1.64 *
$P_1 \times P_5$	0.60*	0.29	-0.68	3.24	3.17 *	-0.36
$P_1 \times P_6$	-1.46 *	-1.87 *	-3.07 *	15.79 *	4.98 *	0.19
$P_1 \times P_7$	-0.01	0.74 *	-2.51 *	19.90 *	6.68*	0.42
$P_2 \times P_3$	-2.35 *	-2.15 *	-1.40 *	9.26 *	7.51 *	0.53
$P_2 \times P_4$	-0.68 *	-1.04 *	-2.01 *	6.71 *	7.53 *	1.31 *
$P_2 \times P_5$	-3.18 *	-3.87 *	-2.57 *	39.01 *	19.92 *	1.31 *
$P_2 \times P_6$	-1.24 *	-1.54 *	-1.46 *	-1.93	6.48 *	-0.14
$P_2 \times P_7$	1.71 *	2.07 *	2.10 *	26.18 *	16.87 *	0.08
$P_3 \times P_4$	-2.01 *	-1.82 *	-0.57	14.04 *	-0.77	-0.36
$P_3 \times P_5$	-2.01 *	-1.15 *	-0.13	19.85 *	7.87 *	-0.36
$P_3 \times P_6$	1.43 *	2.68 *	-0.51	-14.85 *	5.67 *	-0.81 *
$P_3 \times P_7$	-1.63 *	-0.71	-1.96 *	28.76 *	7.81 *	1.42 *
$P_4 \times P_5$	2.15 *	1.96 *	1.76 *	-13.21 *	18.65 *	2.42 *
$P_4 \times P_6$	3.10 *	3.29 *	2.88 *	-18.90 *	5.45 *	-2.03 *
$P_4 \times P_7$	1.04 *	1.40 *	1.43 *	-2.79	3.84 *	-1.81 *
$P_5 \times P_6$	1.10 *	0.46	2.82 *	11.65 *	3.59 *	0.97 *
$P_5 \times P_7$	3.04 *	3.07 *	5.38 *	22.26 *	3.23 *	-0.81 *
$P_6 \times P_7$	-0.01	-0.60	1.49 *	-5.18 *	0.03	1.81 *
S.E.(sij)	0.29	0.36	0.37	1.79	1.42	0.26
S.E.(sij-sik)	0.93	1.16	1.22	5.85	4.65	0.86
S.E.(sij-skl)	0.87	1.09	1.14	5.47	4.35	0.81

***-Significant at 5 %**

Table 4.5 Estimates of specific combining ability effects of crosses for number of kernels per row, ear length (cm), ear circumference (cm), 1000-kernel weight (g), shelling (%) and grain yield (g/plant)

Crosses	Number of kernels per row	Ear length (cm)	Ear circumference (cm)	1000-kernel weight (g)	Shelling (%)	Grain yield (g/plant)
$P_1 \times P_2$	4.69 *	3.06 *	-0.66 *	-3.06	0.42	3.17 *
$P_1 \times P_3$	3.47 *	1.37 *	0.44 *	-19.28 *	2.99 *	28.02 *
$P_1 \times P_4$	9.47 *	7.42 *	-0.13	55.50 *	-0.48	44.50 *
$P_1 \times P_5$	1.97 *	-0.72 *	0.42 *	27.83 *	-0.42	18.40 *
$P_1 \times P_6$	3.42 *	1.24 *	1.07 *	22.06 *	-1.88 *	21.73 *
$P_1 \times P_7$	0.58	-2.37 *	1.15 *	-2.50	3.14 *	-11.16 *
$P_2 \times P_3$	5.97 *	5.41 *	0.46 *	59.94 *	0.24	32.12 *
$P_2 \times P_4$	2.97 *	3.11 *	0.94 *	20.72 *	-1.09 *	2.22
$P_2 \times P_5$	6.47 *	2.97 *	2.14 *	42.06 *	-0.02	28.61 *
$P_2 \times P_6$	0.92	-0.91 *	0.03	-23.72 *	0.58	2.90 *
$P_2 \times P_7$	4.58 *	0.37	0.17	11.72 *	3.70 *	13.93 *
$P_3 \times P_4$	-3.75*	-6.58 *	0.38 *	-30.50 *	-0.79	-10.45 *
$P_3 \times P_5$	1.25 *	0.89 *	-0.82 *	35.83 *	0.71	10.96 *
$P_3 \times P_6$	0.69	-0.35	-0.97 *	-14.94 *	1.46 *	9.18 *
$P_3 \times P_7$	6.86 *	3.69 *	2.52 *	61.50 *	2.36 *	31.60 *
$P_4 \times P_5$	0.25	-0.82 *	0.67 *	26.61 *	-0.01	22.07 *
$P_4 \times P_6$	-4.31 *	0.95 *	0.21	-29.17 *	-3.21 *	-8.30 *
$P_4 \times P_7$	1.86 *	-0.21	0.10	6.28 *	-0.69	0.04
$P_5 \times P_6$	2.19 *	0.76 *	0.36	2.17	-0.79	13.35 *
$P_5 \times P_7$	0.36	0.95 *	-0.20	7.61 *	1.08 *	-6.34 *
$P_6 \times P_7$	11.81 *	6.56 *	-0.01	70.83 *	1.33 *	40.15 *
S.E.(sij)	0.50	0.35	0.18	2.47	0.43	1.30
S.E.(sij-sik)	1.63	1.14	0.59	5.94	1.40	4.24
S.E.(sij-skl)	1.53	1.07	0.55	7.56	1.30	3.97

*- Significant at 5%

4.3.1.4 Plant height (cm)

General combining ability effects for plant height ranged from -12.78 (P_7) to 11.14 (P_5). Parent P_7 (-12.78) showed highest significant negative GCA effects followed by P_4 (-10.56) and P_3 (-4.86) (Table 4.3).

Estimates of specific combining ability effects varied from -18.90 ($P_4 \times P_6$) to 39.01 ($P_2 \times P_5$) for plant height. Among the crosses, $P_4 \times P_6$ (-18.90) exhibited maximum significant negative specific combining ability effects followed by $P_3 \times P_6$ (-14.85), $P_4 \times P_5$ (-13.21), $P_1 \times P_2$ (-10.10) and $P_6 \times P_7$ (-5.18) (Table 4.4).

4.3.1.5 Ear height (cm)

General combining ability effects ranged from -7.81 (P_7) to 3.25 (P_2). Parent P_7 (-7.81) showed highest significant negative general combining ability followed by P_1 (-2.50) and P_3 (-2.44) (Table 4.3).

Estimates of specific combining ability effects ranged from -3.72 ($P_1 \times P_4$) to 19.92 ($P_2 \times P_5$). Among all the crosses, $P_1 \times P_4$ (-3.72) had significant negative specific combining ability effects for ear height (Table 4.4).

4.3.1.6 Number of kernel rows per ear

Estimates of general combining ability effects for number of kernel rows per ear varied from -0.76 (P_5) to 0.46 (P_7). Only one parent P_7 (0.46) had significant positive general combining ability effect for kernel rows per ear (Table 4.3).

For number of kernels rows per ear SCA effects varied from -2.03 ($P_4 \times P_6$) to 2.42 ($P_4 \times P_5$). Highest specific combining ability effect showed by $P_4 \times P_5$ (2.42) followed by $P_1 \times P_3$ (1.86), $P_6 \times P_7$ (1.81), $P_1 \times P_4$ (1.64), $P_3 \times P_7$ (1.42), $P_2 \times P_4$ (1.31), $P_2 \times P_5$ (1.31) and $P_5 \times P_6$ (0.97) (Table 4.4).

4.3.1.7 Number of kernels per row

Estimates of GCA effects ranged from -1.57 (P_5) to 1.21 (P_1) for number of kernels per row. P_1 (1.21) showed highest significant positive general combining ability effect followed by P_6 (0.98) and P_3 (0.93) for this trait (Table 4.3).

Estimates of specific combining ability effects for the number of kernels per row varied from -4.31 ($P_4 \times P_6$) to 11.81 ($P_6 \times P_7$). Among the F1s, $P_6 \times P_7$ (11.81) had maximum significant positive specific combining ability effect for number of kernels per row followed by $P_1 \times P_4$ (9.47), $P_3 \times P_7$ (6.86), $P_2 \times P_5$ (6.47), $P_2 \times P_3$ (5.97), $P_1 \times P_2$ (4.69), $P_2 \times P_7$ (4.58), $P_1 \times P_3$ (3.47), $P_1 \times P_6$ (3.42), $P_2 \times P_4$ (2.97), $P_5 \times P_6$ (2.19), $P_1 \times P_5$ (1.97), $P_4 \times P_7$ (1.86) and $P_3 \times P_5$ (1.25) (Table 4.5).

4.3.1.8 Ear length (cm)

General combining ability effects ranged from -0.86 (P_4) to 0.59 (P_1) for ear length. Two parent P_1 (0.59) and P_6 (0.56) had significant positive GCA effects for this trait (Table 4.3).

Estimates of specific combining ability effects for ear length varied between -6.58 ($P_3 \times P_4$) to 7.42 ($P_1 \times P_4$). The hybrid $P_1 \times P_4$ (7.42) had significant positive specific combining ability effect for ear length followed by $P_6 \times P_7$ (6.56), $P_2 \times P_3$ (5.41), $P_3 \times P_7$ (3.69), $P_2 \times P_4$ (3.11), $P_1 \times P_2$ (3.06), $P_2 \times P_5$ (2.97), $P_1 \times P_3$ (1.37), $P_1 \times P_6$ (1.24), $P_5 \times P_7$ (0.95), $P_4 \times P_6$ (0.95), $P_3 \times P_5$ (0.89) and $P_5 \times P_6$ (0.76) (Table 4.5).

4.3.1.9 Ear circumference (cm):

Estimates of general combining ability effects for ear circumference ranged from -0.30 (P_4) to 0.49 (P_3). Only one parent P_3 (0.49) had significant positive GCA effect (Table 4.3).

SCA effects ranged from -0.97 ($P_3 \times P_6$) to 2.52 ($P_3 \times P_7$). Highest significant positive SCA effect exhibited by $P_3 \times P_7$ (2.52) and followed by $P_2 \times P_5$ (2.14), $P_1 \times P_7$ (1.15), $P_1 \times P_6$ (1.07), $P_2 \times P_4$ (0.94), $P_4 \times P_5$ (0.67), $P_2 \times P_3$ (0.46), $P_1 \times P_3$ (0.44), $P_1 \times P_5$ (0.42) and $P_3 \times P_4$ (0.38) (Table 4.5).

4.3.1.10 1000-kernel weight (g)

Estimates of general combining ability effects for 1000-kernel weight varied from -20.46 (P_7) to 19.21 (P_5). Parent P_5 (19.21) showed maximum significant positive GCA effects followed by P_1 (14.32) and P_3 (6.32) (Table 4.3).

Estimates of specific combining ability effects for 1000-kernel weight ranged from -30.50 ($P_3 \times P_4$) to 70.83 ($P_6 \times P_7$). Highest significant positive SCA effect showed by $P_6 \times P_7$ (70.83) and followed by $P_3 \times P_7$ (61.50), $P_2 \times P_3$ (59.94), $P_1 \times P_4$ (55.50), $P_2 \times P_5$ (42.06), $P_3 \times P_5$ (35.83), $P_1 \times P_5$ (27.83), $P_4 \times P_5$ (26.61), $P_1 \times P_6$ (22.06), $P_2 \times P_4$ (20.72), $P_2 \times P_7$ (11.75), $P_5 \times P_7$ (7.61) and $P_4 \times P_7$ (6.28) (Table 4.5).

4.3.1.11 Shelling (%)

General combining ability effects for shelling (%) varied from -0.89 (P_7) to 0.74 (P_1). Only one parent P_1 (0.74) had significant positive general combining ability effect for shelling (%) (Table 4.3)

Estimates of SCA effects ranged from -3.21 ($P_4 \times P_6$) to 3.70 ($P_2 \times P_7$) of shelling (%). $P_2 \times P_7$ (3.70) exhibited maximum significant positive specific combining ability effect for this trait followed by $P_1 \times P_7$ (3.14), $P_1 \times P_3$ (2.99), $P_3 \times P_7$ (2.36), $P_3 \times P_6$ (1.46), $P_6 \times P_7$ (1.33) and $P_5 \times P_7$ (1.08) (Table 4.5).

4.3.1.12 Grain yield (g/plant)

Estimates of GCA effects ranged from -7.12 (P_7) to 6.29 (P_3) for grain yield. P_3 (6.29) and 5.74 (P_1) had significant positive GCA effects for grain yield (Table 4.4)

Specific combining ability effects for grain yield varied from -11.16 ($P_1 \times P_7$) to 44.50 ($P_1 \times P_4$). Highest significant positive SCA effects exhibited by $P_1 \times P_4$ (44.50) followed by $P_6 \times P_7$ (40.15), $P_2 \times P_3$ (32.12), $P_3 \times P_7$ (31.60), $P_2 \times P_5$ (28.61), $P_1 \times P_3$ (28.02), $P_4 \times P_5$ (22.07), $P_1 \times P_6$ (21.73), $P_1 \times P_5$ (18.40), $P_2 \times P_7$ (13.93), $P_5 \times P_6$ (13.35), $P_3 \times P_5$ (10.96), $P_3 \times P_6$ (9.18), $P_1 \times P_2$ (3.17) and $P_2 \times P_6$ (2.90) (Table 4.5).

4.3.2 Estimates of genetic components and other parameters

Estimates of genetic components such as σ^2GCA, σ^2SCA, σ^2GCA/σ^2SCA, σ^2A and σ^2D for various traits are given in Table 4.6. For all attributes, it was revealed that the estimates of σ^2SCA were greater than the estimates of σ^2GCA. This demonstrated that non-additive genetic effects contributed more to the expression of various traits in hybrids than additive genetic effects. The ratio of variance of σ^2GCA to σ^2SCA was less than one therefore, result indicated that non-additive gene action played important role in the inheritance of all the studied traits. Average degree of dominance was more than one for all traits due to preponderance of non-additive gene action. These results were similar to previous studies of Kanagarasu et al. (2010; Amadabade et al. (2018), Negi et al. (2018); and Chandel et al. (2019) they reported the preponderance of non-additive gene action for different traits *viz.,* days to 50% silking, days to 50% tasseling , days to 75% maturity, plant height, ear height, plant hieght, ear height ,ear circumference, kernel rows per cob, kernels per row, 1000-grain weight, shelling (%) and grain yield.

Table 4.6 Estimates of genetic components for different traits

S.No.	Characters	ơ ^{2}gca	o^{2}sca	o^{2}gca/ o^{2}sca	ơ ^{2}A	o^{2}D	[o^{2}D/o^{2}A]$^{1/2}$
1	Days to 50% pollen shed	0.11	4.39	0.025	0.22	4.39	4.47
2	Days to 50% silking	0.025	5.12	0.01	0.05	5.12	10.12
3	Days to 75% brown husk	0.36	9.11	0.04	0.72	9.11	3.57
4	Plant height (cm)	84.64	569.63	0.15	169.28	569.63	1.83
5	Ear height (cm)	18.94	191.11	0.10	37.88	191.11	5.05
6	Number of kernel rows per ear	0.13	1.35	0.098	0.26	1.35	2.28
7	Number of kernels per row	1.04	51.20	0.02	2.08	51.21	4.96
8	Ear length (cm)	0.24	15.96	0.015	0.48	15.96	5.77
9	Ear circumference (cm)	0.07	1.18	0.06	0.14	1.18	8.49
10	1000-kernel weight (g)	206.85	1995.03	0.10	413.70	1995.03	2.20
11	Shelling (%)	0.14	4.72	0.03	0.28	4.72	4.11
12	Grain yield (g/plant)	28.12	1025.18	0.03	56.24	1025.18	4.27

Table 4.7 Summary of GCA effects of parents for different traits

S.No.	**Characters**	**Parent**						
		P1	**P2**	**P3**	**P4**	**P5**	**P6**	**P7**
1	**Days to 50%pollen shed**	G	A	P	A	A	A	A
2	**Days to 50% silking**	A	A	A	A	A	A	A
3	**Days to 75% brown husk**	A	A	G	P	A	A	A
4	**Plant height (cm)**	G	G	P	P	G	G	P
5	**Ear height (cm)**	P	G	P	A	A	G	P
6	**Number of kernel rows per ear**	A	A	A	A	P	A	G
7	**Number of kernels per row**	G	A	G	A	P	G	P
8	**Ear length (cm)**	G	A	A	P	P	G	A
9	**Ear circumference(cm)**	A	A	G	P	A	A	A
10	**1000-kernel weight (g)**	G	P	G	P	G	A	P
11	**Shelling (%)**	G	A	A	A	A	A	P
12	**Grain yield (g/plant)**	G	A	G	P	A	A	P

G = Good general combiner having significant GCA effects in desired direction
A = Mid parent general combiner having either positive or negative but non-significant GCA effects
P = Poor general combiner having significant GCA effects in opposite direction

Table 4.8 Promising parents and crosses with respect to combining ability and *per se performance* for different traits.

S. No.	Characters	Parents		Crosses		GCA of parents in high SCA crosses
		Per se performance	GCA	*Per se performance*	SCA	
1	**Days to 50% pollen shed**	P_1	P_1	$P_1 \times P_4$	$P_2 \times P_5$	A/A
		P_7	P_6	$P_2 \times P_5$	$P_1 \times P_4$	G/A
		P_6	P_7	$P_1 \times P_6$	$P_3 \times P_5$	P/A
2	**Days to 50% silking**	P_1	P_3	$P_2 \times P_5$	$P_2 \times P_5$	A/A
		P_7	P_1	$P_1 \times P_4$	$P_1 \times P_5$	A/A
		P_6	P_2	$P_2 \times P_3$	$P_1 \times P_6$	A/A
3	**Days to 75% brown husk**	P_3	P_3	$P_1 \times P_6$	$P_1 \times P_6$	A/A
		P_1	P_2	$P_2 \times P_3$	$P_2 \times P_5$	A/A
		P_7	P_6	$P_2 \times P_5$	$P_1 \times P_7$	A/A
4	**Plant height (cm)**	P_6	P_5	$P_2 \times P_5$	$P_2 \times P_5$	G/G
		P_1	P_6	$P_3 \times P_5$	$P_3 \times P_7$	P/P
		P_5	P_2	$P_5 \times P_7$	$P_2 \times P_7$	G/P
5	**Ear height (cm)**	P_6	P_2	$P_2 \times P_5$	$P_2 \times P_5$	G/A
		P_1	P_6	$P_4 \times P_5$	$P_4 \times P_5$	A/A
		P_4	P_4	$P_2 \times P_7$	$P_2 \times P_7$	G/P
6	**Number of kernel rows per ear**	P_7	P_7	$P_4 \times P_5$	$P_4 \times P_5$	A/P
		P_2	P_2	$P_1 \times P_3$	$P_1 \times P_3$	A/A
		P_4	P_4	$P_1 \times P_4$	$P_1 \times P_4$	A/A

Table 4.8 Contd…

7	**Number of kernels per row**	P_4	P_1	$P_6 \times P_7$	$P_6 \times P_7$	G/P
		P_3	P_6	$P_1 \times P_4$	$P_3 \times P_7$	G/P
		P_6	P_3	$P_2 \times P_3$	$P_2 \times P_5$	A/P
8	**Ear length (cm)**	P_3	P_1	$P_1 \times P_5$	$P_1 \times P_4$	G/P
		P_6	P_6	$P_1 \times P_4$	$P_6 \times P_7$	G/A
		P_5	P_3	$P_2 \times P_3$	$P_2 \times P_3$	A/A
9	**Ear circumference (cm)**	P_3	P_3	$P_3 \times P_7$	$P_3 \times P_7$	G/A
		P_1	P_1	$P_1 \times P_6$	$P_2 \times P_5$	A/A
		P_2	P_2	$P_2 \times P_3$	$P_1 \times P_7$	A/A
10	**1000-kernel weight (g)**	P_1	P_5	$P_1 \times P_5$	$P_6 \times P_7$	A/P
		P_6	P_1	$P_2 \times P_3$	$P_3 \times P_7$	G/P
		P_5	P_3	$P_2 \times P_5$	$P_2 \times P_3$	P/G
11	**Shelling (%)**	P_4	P_1	$P_1 \times P_3$	$P_2 \times P_7$	A/P
		P_6	P_6	$P_1 \times P_7$	$P_1 \times P_7$	G/P
		P_1	P_2	$P_2 \times P_7$	$P_1 \times P_3$	G/A
12	**Grain yield (g/plant)**	P_6	P_3	$P_1 \times P_4$	$P_1 \times P_4$	G/P
		P_3	P_1	$P_1 \times P_3$	$P_6 \times P_7$	A/P
		P_4	P_5	$P_2 \times P_3$	$P_2 \times P_3$	A/G

G = Good general combiner having significant GCA effects in desired direction
A = Mid parent general combiner having either positive or negative but non-significant GCA effects
P = Poor general combiner having significant GCA effects in opposite direction

Top ranking parents

The data presented in the Table 4.7 showed that none of the parents was promising for all the traits. It suggested that importance of multiple crosses realize substantial improvement in grain yield. However, some of the parents revealed good GCA for at least combination of four traits. Analyzing general combining ability effects, it was noticed that parental lines P_1, P_3 and P_6 had good GCA for combination of seven traits.P_1 showed significant general combining effects for days to 50% pollen shed, plant height, number of kernels per row, ear length, test weight, shelling (%) and grain yield; P_3 for days to 75% brown husk, number of kernels per row, ear diameter, 1000-kernel weight and grain yield per plant and P_6 for plant height, ear height number of kernels per row and ear length. Fan et al. (2008); Amadabade (2017); Kumar et al. (2019); Chaurasia et al. (2020) and Aly et al. (2022) also identified good general combiners for these traits in maize.

Parental performance has been suggested as relevant criterion in maize for choosing parents for hybridization. When the observations for the three top parents were taken into account, the results showed (Table 4.8) that *per se performance* of the parents could give a good indication of their general combining ability effects for plant height, ear height, number of kernels per row, ear length, ear circumference, test weight and grain yield, 50% pollen shed, days to 75% brown husk, 1000-kernel weight and grain yield per plant, whereas, parents with maximum GCA effects did not had the highest mean values. This indicated that parental line selection based solely on *per se performance* will be ineffective unless it is supplemented with evaluation of parental lines for their general combining ability effects. The lack of correlation between *per se performance* and general combining ability might be due to predominance of non-additive gene effects. Therefore, the parents high mean performance may not be transferrable to the progenies in such cases.

Top ranking crosses

SCA effects represent especially dominance, dominance × dominance and additive × dominance effects. F_1s showing specific combining ability effects involving parents with good general combining ability could be used. However, if a F_1 has a high specific combining ability and has one parent as poor or mid parent combiner, such F_1 are likely produce some good segregants only if an additive genetic system is present in a good general combiner and epistatic effects in F_1 behave in the same direction to maximize the useful expression of the characters in question (Whitehouse et al., 1958)

Presence of significant specific combining ability is pre-requisite for hybrid development. Studies on SCA showed none of the F_1s had significant SCA effects for all traits. Possible combinations of parental general combining ability effects such as “good/good”, “good/poor”, “good/average”, “average/average”, “average/poor”, “average/good”, “poor/good”, “poor/average” and “poor/poor” were involved in crosses with high SCA. This indicated presence of non-additive gene effect, mainly in “good × poor”, “average × poor” and “poor × poor” cross combinations. Studies on specific combining ability showed that $P_2 \times P_5$ exhibited highest combining ability for days to 50% pollen shed, days to 50% silking (average /average), plant height (good/good) and ear height (good/ average); $P_1 \times P_6$ exhibited highest combining ability for days to 75% brown husk (average). Similarly, $P_4 \times P_5$ (average/poor) number of kernel rows per ear. $P_6 \times P_7$ for number of kernels per row (good/average) and 1000-kernel weight (average/poor); $P_3 \times P_7$ for ear circumference (good/average); $P_2 \times P_7$ (average/poor) for shelling (%), whereas, for ear length and grain yield with good × poor parental combination. Similar results were also reported earlier by Petrovic et al. (1998); Uddin et al. (2008) and Niyonzima et al. (2015).

Furthermore, promising crosses with high *per se performance* as well as significant SCA effects were $P_2 \times P_5$ for days to 50% silking; $P_1 \times P_6$ for days to 75% brown husk; $P_2 \times P_5$ for plant height; $P_2 \times P_5$, $P_4 \times P_5$ and $P_2 \times P_7$ for ear height; $P_4 \times P_5$, $P_1 \times P_4$ and $P_1 \times P_3$ for number of kernel rows per ear; $P_6 \times P_7$ for number of kernels per row; $P_1 \times P_4$ and $P_2 \times P_3$ for grain yield per plant. Crosses with high specific combining ability effects sometimes had high *per se performance* but not always. Therefore, both *per se performance* and specific combining ability need to be considered for development of high yielding single cross hybrids, SCA effects were negative for crosses involving parents with the same genetic background, whereas, it was positive for crosses involving parents with different genetic backgrounds (Hallauer and Miranda, 1988).

4.4 Estimation of Heterosis

The degree of heterosis can be explained in terms of relative performance of F_1 cross as compared to the mid parent, better parent and standard heterosis. For traits like days to 75% brown husk, days to 50% silking, days to 50% pollen shed, plant height, ear height negative heterosis is desirable, whereas, positive heterosis is desirable for other traits. Standard heterosis (SH%) is calculated against best check based on the mean values. Presence of significant standard heterosis (SH%) is pre-requisite for any breeding programme. The comparison of mid parent, better parent heterosis and standard heterosis for all the crosses is presented in Table 4.9 to Table 4.11.

4.4.1 Days to 50% pollen shed

Mid parent heterosis (MPH %) ranged from -7.08 ($P_2 \times P_3$) to 8.41 ($P_5 \times P_7$). For days to 50% pollen shed five crosses showed significant negative mid parent heterosis (%). $P_2 \times P_3$ (-7.08%) showed maximum significant negative mid parent heterosis (%) followed by $P_2 \times P_5$ (-5.94%), $P_3 \times P_4$ (-5.31 %), $P_3 \times P_5$ (-4.89 %) and $P_1 \times P_4$ (-4.19 %) (Table 4.9).

Better parent heterosis (BPH %) varied from -9.48 ($P_2 \times P_3$) to 6.42 ($P_5 \times P_7$) for days to 50% pollen shed. $P_2 \times P_3$ (-9.81%) exhibited highest negative better parent heterosis followed by $P_3 \times P_4$ (-7.76 %), $P_3 \times P_5$ (-7.76 %), $P_3 \times P_7$ (-7.76 %), $P_1 \times P_4$ (-6.36%) and $P_2 \times P_5$ (-6.36%) (Table 4.9).

Standard heterosis (SH %) for days to 50% pollen shed ranged from -8.85 ($P_1 \times P_4$, $P_2 \times P_5$) to 2.65 ($P_4 \times P_6$, $P_5 \times P_7$). Maximum significant negative standard heterosis showed by hybrid $P_1 \times P_4$ (-8.85%) followed by $P_2 \times P_5$ (-8.85%), $P_1 \times P_6$ (-7.08%), $P_2 \times P_3$ (-7.08%), $P_2 \times P_6$ (-6.19%), $P_3 \times P_4$ (-5.31%), $P_3 \times P_5$ (-5.31%), $P_3 \times P_7$ (-5.31%), $P_1 \times P_7$ (-4.42%), $P_2 \times P_4$ (-4.42%) and $P_6 \times P_7$ (-3.54%) (Table 4.9).

4.4.2 Days to 50% silking

MPH (%) varied from –7.30 ($P_2 \times P_5$) to 8.44 ($P_5 \times P_7$) for days to 50% silking. Three crosses displayed significant negative mid parent heterosis. $P_2 \times P_5$ (-7.30%) showed maximum significant negative mid parent heterosis followed by $P_2 \times P_3$ (-4.76%) and $P_1 \times P_4$ (-4.39%). (Table 4.9)

BPH (%) ranged from -7.69 ($P_2 \times P_5$) to 5.26 ($P_1 \times P_3$, $P_3 \times P_6$). Highest significant negative better parent heterosis exhibited by $P_2 \times P_5$ (-7.69%) and followed by $P_1 \times P_4$ (-6.84%) and $P_2 \times P_3$ (-5.98%) (Table 4.9).

For days to 50% silking, the SH (%) ranged from -10.74 ($P_2 \times P_5$) to 1.65 ($P_1 \times P_2$). For this trait, twelve crosses revealed significant negative standard heterosis (SH%). $P_2 \times P_5$ (-10.74%) showed maximum significant standard heterosis followed by $P_1 \times P_4$ (-9.92%), $P_2 \times P_3$ (9.09%), $P_1 \times P_6$ (-8.26%), $P_2 \times P_6$ (-7.44%), $P_3 \times P_4$ (-7.44%), $P_3 \times P_5$ (-6.61%), $P_3 \times P_7$ (-6.61%), $P_6 \times P_7$ (-5.79%), $P_2 \times P_4$ (-5.79%), $P_1 \times P_5$ (-4.13%) and $P_1 \times P_7$ (-4.13%) (Table 4.9).

4.4.3 Days to 75% brown husk

MPH (%) varied from -1.36 ($P_2 \times P_4$) to 10.99 ($P_1 \times P_3$). None of the crosses had significant negative mid parent heterosis for days to 75% brown husk (Table 4.9).

BPH (%) ranged from -2.20 ($P_2 \times P_3$, $P_2 \times P_5$) to 10.67 ($P_1 \times P_3$). None of the crosses had significant negative better parent heterosis for days to 75 % brown husk (Table 4.9).

The SH (%) varied between -6.84 ($P_1 \times P_6$) to 3.68 ($P_1 \times P_3$). For days to 75% brown husk, eleven crosses showed significant negative standard heterosis. Highest significant negative standard heterosis was observed in $P_1 \times P_6$ (-6.84%) and followed by $P_2 \times P_3$ (-6.32%), $P_2 \times P_5$ (-6.32%), $P_3 \times P_7$ (-6.32%), $P_1 \times P_7$ (-5.79%), $P_2 \times P_6$ (-5.79%), $P_3 \times P_6$ (-5.26%), $P_2 \times P_4$ (4.74%), $P_3 \times P_5$ (-4.21%), $P_1 \times P_5$ (-3.68%) and $P_3 \times P_4$ (-3.68%) (Table 4.9).

4.4.4 Plant height (cm)

The MPH (%) for ear height ranged from -12.55 ($P_4 \times P_6$) to 54.09 ($P_3 \times P_7$). For this trait $P_4 \times P_6$ (-12.55%) showed significant negative mid parent heterosis for this trait (Table 4.9).

BPH (%) varied from -22.21 ($P_4 \times P_6$) to 48.70 ($P_2 \times P_5$) for plant height. $P_4 \times P_6$ (-12.55%) and $P_3 \times P_6$ (-17.14%) exhibited significant negative better parent heterosis (Table 4.9).

SH (%) ranged from -28.36 ($P_4 \times P_7$) to 11.61 ($P_2 \times P_5$) for plant height. Fifteen crosses showed significant negative standard heterosis for plant height. $P_4 \times P_7$ (-28.36) exhibited highest significant negative standard heterosis followed by $P_4 \times P_6$ (-26.77%), $P_3 \times P_6$ (-22.00%), $P_4 \times P_5$ (-21.76%), $P_6 \times P_7$ (-21.15%), $P_1 \times P_3$ (-17.11%), $P_3 \times P_4$ (-16.26%), $P_1 \times P_2$ (-15.40%), $P_2 \times P_4$ (-14.79%), $P_2 \times P_3$ (-10.76%) $P_2 \times P_6$ (-10.64%), $P_3 \times P_7$ (-10.15%), $P_1 \times P_4$ (-9.90%), $P_1 \times P_7$ (-9.66%) and $P_2 \times P_7$ (-6.36%) (Table 4.9).

4.4.5 Ear height (cm)

MPH (%) varied between 10.80 ($P_1 \times P_4$) to 77.21 ($P_2 \times P_5$). For ear height none of the crosses showed significant negative mid parent heterosis (Table 4.10).

BPH (%) ranged from 3.61 ($P_6 \times P_7$) to 68.91 ($P_2 \times P_5$). None of the crosses exhibited significant negative better parent heterosis (Table 4.10).

SH (%) varied from -25.94 ($P_1 \times P_7$) to 10.97 ($P_2 \times P_5$). Twelve crosses showed significant negative standard heterosis for this trait. $P_1 \times P_7$ (-25.94%) exhibited maximum significant negative standard heterosis followed by $P_6 \times P_7$ (-22.24%), $P_1 \times P_4$ (-21.75%), $P_3 \times P_7$ (-19.54%), $P_4 \times P_7$ (-19.54%), $P_3 \times P_4$ (-18.80%), $P_5 \times P_7$ (-16.34%), $P_1 \times P_3$ (-15.11%), $P_1 \times P_2$ (-14.37%), $P_1 \times P_6$ (-12.16%), $P_3 \times P_6$ (-11.42%) and $P_1 \times P_5$ (-11.17%) (Table 4.10).

4.4.6 Number of kernel rows per ear

MPH (%) ranged from -15.38 ($P_4 \times P_6$) to 30.43 ($P_4 \times P_5$) showed in Table 4.11. Six crosses exhibited significant positive relative heterosis for number of kernel rows per ear. $P_4 \times P_5$ (30.43%) showed maximum significant positive mid parent heterosis followed by $P_1 \times P_3$ (25.00%), $P_2 \times P_5$ (21.74%) $P_1 \times P_3$ (20.00%), $P_1 \times P_4$ (15.38%), $P_3 \times P_7$ (15.38%) (Table 4.10).

BPH (%) varied from -15.38 ($P_4 \times P_6$) to 25.00($P_1 \times P_3$) for number of kernel rows per ear. $P_1 \times P_3$ (25.00%) exhibited highest significant positive better parent heterosis $P_1 \times P_4$ (15.38%), $P_2 \times P_4$ (15.38%) and $P_4 \times P_5$ (15.38%) (Table 4.10).

SH (%) ranged from -15.38 (P_4 × P_6) to 15.38 (P_1 × P_4). Five crosses exhibited significant positive standard heterosis for number of kernel rows per ear. P_1 × P_3 (15.38%) showed maximum significant positive standard heterosis followed by P_1 × P_4 (15.38%), P_2 × P_4 (15.38%), P_3 × P_7 (15.38%) and P_4 × P_5 (15.38%) (Table 4.10).

4.4.7 Number of kernels per row

The MPH (%) varied from 3.85 (P_4 × P_6) to 110.00 (P_6 × P_7) (Table 4.11). Nineteen crosses exhibited significant positive mid parent heterosis for number of kernels per row. Highest significant positive mid parent heterosis showed by P_6 × P_7 (110.00%) and followed by P_2 × P_7 (109.38%), P_1 × P_2 (89.47%), P_3 × P_7 (85.00%), P_2 × P_5 (84.21%), P_2 × P_3 (76.19%), P_1 × P_7 (72.22%), P_1 × P_4 (70.83%), P_1 × P_3 (56.52%), P_1 × P_6 (56.52%), P_5 × P_7 (55.56%), P_1× P_5 (52.38%), P_2 × P_6 (52.38%), P_2 × P_4 (50.00%), P_4 × P_7 (47.62%), P_5 × P_6 (39.13%), P_3 × P_5 (34.78%), P_3 × P_6 (32.00%) and P_4 × P_5 (20.83%) (Table 4.10).

The BPH (%) ranged from 1.85 (P_3 × P_4) to 97.06 (P_2 × P_7). Eighteen crosses showed significant positive better parent heterosis for number of kernels per row. P_2 × P_7 (97.06%) exhibited maximum significant positive better parent heterosis followed by P_1 × P_2 (71.43%), P_6× P_7 (68.00%), P_2 × P_5 (66.67%), P_1 × P_5 (52.38%), P_1 × P_4 (51.85%), P_3× P_7 (48.00%), P_2 × P_3 (48.00%), P_1 × P_7 (47.62%), P_1 × P_3 (44.00%) , P_1 × P_6 (44.00%), P_5 × P_7 (33.33%), P_3 × P_6 (32.00%), P_2 × P_6 (28.00%), P_5 × P_6 (28.00%), P_2 × P_4 (22.22%) and P_4 × P_7 (14.81%) (Table 4.10).

The SH (%) varied from -22.86 (P_4 × P_6) to 20.00 (P_6 × P_7). P_6 × P_7 (20.00) exhibited highest positive standard heterosis for number of kernels per row followed by P_1 × P_4 (17.14%) (Table 4.10).

4.4.8 Ear length (cm)

MPH (%) ranged from -33.58 (P_3 × P_4) to 90.44 (P_6 × P_7). Nineteen crosses exhibited significant positive mid parent heterosis for ear length. P_6 × P_7 (90.44%) showed maximum significant positive mid parent heterosis followed by P_1 × P_4 (89.07%), P_1 × P_2 (85.14%), P_2 × P_3 (85.14%), P_2 × P_4 (70.96%), P_2× P_5 (68.42%), P_2 × P_7 (60.79%), P_3 × P_7 (55.08%), P_1 × P_6 (46.30%), P_2 × P_6 (42.27%), P_1 × P_3 (37.41%), P_5× P_7 (35.15%) , P_4 × P_6 (31.49%), P_5 × P_6 (29.71%), P_4× P_7 (25.64%), P_1 × P_5 (22.32%), P_3 × P_5 (21.98%), P_3 × P_6 (51.58%) and P_1 × P_7 (20.51%) (Table 4.10).

BPH (%) varied from -38.62 (P_3 × P_4) to 87.80 (P_1 × P_4) for ear length. Highest significant positive better parent heterosis showed by P_1 × P_4 (87.80%) and followed by P_6 × P_7 (76.83%), P_1 × P_2 (61.93%), P_2× P_3 (50.34%), P_2 × P_4 (48.37%), P_2 × P_7 (45.95%), P_2 × P_5 (43.75%), P_1

× P_6 (41.70%) P_3 × P_7 (36.90%), P_5 × P_6 (28.96%), P_4 × P_6 (28.19%), P_1 × P_3 (26.21%), P_5 × P_7 (26.17%) and P_2 × P_6 (20.85%) (Table 4.10).

SH (%) ranged from -51.89 (P_3 × P_4) to 24.86 (P_1 × P_4) for ear height. P_1 × P_4 (24.86%) exhibited maximum significant positive standard heterosis followed by P_6 × P_7 (23.78%) and P_2 × P_3 (17.84%) (Table 4.10).

4.4.9 Ear circumference (cm)

MPH (%) ranged from -2.42 (P_3 × P_6) to 34.05 (P_3 × P_7). Fourteen hybrids had significant positive mid parent heterosis for ear circumference. Highest significant positive mid parent heterosis observed by P_3 × P_7 (34.05%) followed by P_2 × P_5 (30.74%), P_1 × P_7 (23.67%), P_2 × P_4 (19.74%), P_2 × P_7 (17.01%), P_4 × P_5 (16.37%), P_1 × P_6 (15.03%), P_4 × P_7 (14.62%), P_2 × P_3 (14.11%), P_1 × P_5 (13.90%), P_5 × P_7 (12.59%) , P_1 × P_3 (12.14%), P_3 × P_4 (11.90%) and P_5 × P_6 (10.02%) (Table.4.11).

BPH (%) varied from –5.47 (P_3 × P_6) to 29.6 (P_2 × P_5). Seven crosses exhibited significant positive better parent heterosis for ear circumference. P_2 × P_5 (29.61%) showed maximum significant positive better parent heterosis followed by P_3 × P_7 (21.48%), P_2 × P_4 (17.17%), P_1 × P_7 (15.07%), P_1 × P_6 (14.65%), P_4 × P_5 (14.85%) and P_1 × P_5 (10.93%) (Table 4.11).

The SH (%) ranged from -13.26 (P_3 × P_6) to 11.47 (P_3 × P_7). Only one cross P_3 ×P_7 (11.47%) had significant positive standard heterosis for ear circumference (Table 4.11).

4.4.10 1000-kernel weight (g)

MPH (%) ranged from -4.55 (P_4 × P_6) to 69.58 (P_3 × P_7). Seventeen crosses had significant positive mid parent heterosis for 1000-kernel weight. Highest significant positive mid parent heterosis showed by P_3 × P_7 (69.58%) followed by P_6 × P_7 (62.13%), P_2 × P_3 (53.66%), P_2 × P_5 (50.85%), P_2 × P_7 (47.69%), P_5 × P_7 (46.07%), P_3 × P_5 (42.86%), P_1 × P_4 (39.82%), P_1 × P_5 (36.07%), P_4 × P_5 (35.39%), P_4 × P_7 (34.33%), P_2 × P_4 (30.77%), P_1 × P_7 (29.97%), P_1 × P_2 (20.37%), P_1 × P_6 (20.33%), P_5 × P_6 (19.31%) and P_1 × P_3 (10.39%) (Table 4.11).

BPH (%) varied from -12.50 (P_4 × P_6) to 43.18 (P_2 × P_3). Fifteen crosses revealed significant positive better parent heterosis for 1000-kernel weight. P_2 × P_3 (43.18%) showed maximum significant positive better parent heterosis followed by P_3 × P_5 (42.53%), P_2 × P_5 (40.27%), P_3 × P_7 (36.82%), P_1 × P_5 (30.17%), P_4 × P_5 (28.96%), P_1 × P_4 (27.69%), P_2 × P_4 (27.50%), P_6 × P_7 (26.67%), P_2 × P_7 (26.32%), P_1 × P_6 (19.83%), P_5 × P_7 (17.65%), P_5 × P_6 (14.58%) and P_4 × P_7 (12.50%) (Table 4.11).

SH (%) for 1000-kernel weight ranged from -24.73 (P_4 × P_6) to 12.90 (P_1 × P_5). Seven crosses exhibited significant positive standard heterosis. Highest significant positive economic heterosis showed by P_1 × P_5 (12.90%) followed by P_2 × P_3 (12.90%), P_3 × P_5 (12.90%), P_2 × P_5 (11.11%), P_1 × P_4 (10.75%), P_6 × P_7 (8.96%) and P_3 × P_7 (7.89%) (Table 4.11).

4.4.11 Shelling (%)

MPH (%) ranged from -6.31 (P_4 × P_6) to 9.39 (P_2 × P_7). Seven crosses showed significant positive mid parent heterosis for shelling (%). P_2 × P_7 (9.39%) exhibited maximum significant positive mid parent heterosis followed by P_3 × P_7 (8.77%), P_1 × P_7 (8.56%), P_1 × P_3 (6.98%), P_5 × P_7 (4.97%), P_6 × P_7 (4.25%) and P_2 × P_3 (3.64%) (Table 4.11).

BPH (%) varied between -4.40 (P_3 × P_4) to 6.24 (P_3 × P_7). Four crosses had significant positive better parent heterosis for shelling (%). Highest significant positive better parent heterosis showed by P_3 × P_7 (6.24%) followed by P_2 × P_7 (5.77%), P_1 × P_3 (4.95%) and P_1 × P_7 (4.08%) (Table 4.11).

SH (%) ranged from -0.75 (P_4 × P_6) to 7.49 (P_1 × P_3). Eight crosses showed significant positive standard heterosis for shelling (%). P_1 × P_3 (7.49%) exhibited maximum significant positive standard heterosis followed by P_1 × P_7 (6.60%), P_2 × P_7 (6.42%), P_3 × P_6 (5.19%), P_3 × P_7 (4.68%) P_1 × P_2 (4.39%) and P_2 × P_6 (4.17) (Table 4.11).

4.4.12 Grain yield (g/plant)

MPH (%) varied from 65.77 (P_4 × P_6) to 241.49 (P_6 × P_7). All the F_1s had significant positive mid parent heterosis for grain yield per plant (g). P_6 × P_7 (241.49), P_1 × P_4 (239.54), P_3 × P_7 (234.86), P_2 × P_3 (224.64), P_1 × P_3 (213.46), P_2 × P_5 (213.20), P_1 × P_5 (196.26), P_1 × P_6 (189.97), P_2 × P_7 (174.13), P_3 × P_5 (165.18), P_4 × P_5 (162.74), P_5 × P_6 (154.48), P_1 × P_2 (146.46), P_3 × P_6 (146.81), P_2 × P_6 (123.36), P_5 × P_7 (108.07), P_1 × P_7 (106.37), P_2 × P_4 (103.47), P_4 × P_7 (95.59), P_3 × P_4 (75.98) and P_4 × P_6 (65.77) (Table 4.11).

BPH (%) ranged from 61.83 (P_4 × P_6) to 231.57 (P_1 × P_4). Twenty-one crosses revealed significant positive heterosis for grain yield per plant (g). Mid parent heterosis was observed by crosses P_1 × P_4 (231.57%), P_1 × P_3 (213.46%), P_2 × P_5 (210.02%), P_2 × P_3 (208.64%), P_1 × P_5 (195.41%), P_6 × P_7 (191.48%), P_3 × P_7 (188.13%), P_1 × P_6 (176.59%), P_4 × P_5 (155.85%), P_3 × P_5 (154.59%), P_2 × P_7 (146.68%), P_1 × P_2 (146.46%), P_3 × P_6 (144.45%), P_5 × P_6 (142.08%), P_2 × P_6 (110.42%), P_2 × P_4 (96.18%), P_5 × P_7 (86.55%), P_1 × P_7 (83.56%), P_3 × P_4 (73.43%), P_4 × P_7 (70.40%) and P_4 × P_6 (61.83%) (Table 4.11).

SH (%) for grain yield varied from -21.89 (P_4 × P_6) to 52.42 (P_1 × P_4). Twelve crosses had significant positive standard heterosis for grain yield per plant (g). P_1 × P_4 (52.42%) showed maximum standard heterosis followed by P_1 × P_3 (48.39%), P_2 × P_3 (46.11%), P_6 × P_7 (40.68%),

P_3 × P_7 (36.40%), P_2 × P_5 (35.04%), P_1 × P_6 (34.49%), P_1 × P_5 (29.42%), P_3 × P_5 (20.52%), P_3 × P_6 (17.98%), P_4 × P_5 (17.61%) and P_5 × P_6 (16.84%) for grain yield per plant (g) (Table 4.11).

Table 4.9 Estimates of mid parent, better parent and standard heterosis for days to 50% pollen shed, Days to 50% Silking, days to 75% brown husk and plant height

Crosses	Days to 50% pollen shed			Days to 50% silking			Days to 75% brown husk			Plant heigh (cm)		
	MPH(%)	BPH(%)	SH(%)	MPH(%)	BPH(%)	SH(%)	MPH(%)	BPH(%)	SH(%)	MPH(%)	BPH(%)	SH(%)
$P_1 \times P_2$	6.98 *	4.55 *	1.77	7.89 *	5.13 *	1.65	7.22 *	6.04 *	1.58	11.52 *	7.29	-15.40 *
$P_1 \times P_3$	2.26	-2.59	0.00	6.67 *	5.26 *	-0.83	10.99 *	10.67*	3.68 *	14.05 *	5.12	-17.11 *
$P_1 \times P_4$	-4.19 *	-6.36 *	-8.85 *	-4.39 *	-6.84 *	-9.92 *	2.48	0.54	-2.11	18.39 *	14.26 *	-9.90 *
$P_1 \times P_5$	2.80	0.92	-2.65	2.20	0.00	-4.13 *	2.81 *	2.81	-3.68 *	22.00 *	19.07 *	-6.11
$P_1 \times P_6$	-0.47	-0.94	-7.08 *	-0.89	-1.77	-8.26 *	-1.12	-1.67	-6.84 *	13.07 *	3.90	-2.20
$P_1 \times P_7$	2.86	2.86	-4.42 *	5.45 *	4.50	-4.13 *	0.56	0.56	-5.79 *	40.09 *	14.57 *	-9.66 *
$P_2 \times P_3$	-7.08 *	-9.48 *	-7.08 *	-4.76 *	-5.98 *	-9.09 *	-0.84	-2.20	-6.32 *	28.07 *	22.48 *	-10.76 *
$P_2 \times P_4$	-1.82	-1.82	-4.42 *	-2.56	-2.56	-5.79 *	-1.36	-2.16	-4.74 *	16.56 *	16.17 *	-14.79 *
$P_2 \times P_5$	-5.94 *	-6.36 *	-8.85 *	-7.30 *	-7.69 *	-10.74*	-1.11	-2.20	-6.32 *	50.91 *	48.70 *	11.61 *
$P_2 \times P_6$	-1.85	-3.64	-6.19 *	-2.61	-4.27	-7.44 *	-1.10	-1.65	-5.79 *	7.03 *	-5.06	-10.64 *
$P_2 \times P_7$	4.19 *	1.82	-0.88	5.31 *	1.71	-1.65	3.89 *	2.75	-1.58	52.29 *	28.52 *	-6.36 *
$P_3 \times P_4$	-5.31 *	-7.76 *	-5.31 *	-3.03	-4.27	-7.44 *	1.10	-1.08	-3.68 *	19.76 *	14.17 *	-16.26 *
$P_3 \times P_5$	-4.89 *	-7.76 *	-5.31 *	-1.74	-2.59	-6.61 *	2.54	2.25	-4.21 *	37.31 *	29.48 *	-2.81
$P_3 \times P_6$	1.80	-2.59	0.00	5.73 *	5.26 *	-0.83	0.84	0.00	-5.26 *	-2.89	-17.14*	-22.00 *
$P_3 \times P_7$	-3.17	-7.76 *	-5.31 *	1.35	-0.88	-6.61 *	0.28	0.00	-6.32 *	54.09 *	35.11 *	-10.15 *
$P_4 \times P_5$	5.02 *	4.55 *	1.77	3.86 *	3.42	0.00	4.68 *	2.70	0.00	5.44	4.23	-21.76 *
$P_4 \times P_6$	7.41 *	5.45 *	2.65	6.96 *	5.13 *	1.65	4.66 *	3.24 *	0.53	-12.55 *	-22.21 *	-26.77 *
$P_4 \times P_7$	4.19 *	1.82	-0.88	5.31 *	1.71	-1.65	4.13 *	2.16	-0.53	16.04 *	-2.33	-28.36 *
$P_5 \times P_6$	4.19 *	2.75	-0.88	2.18	0.86	-3.31	5.59 *	5.00 *	-0.53	16.76 *	4.94	-1.22
$P_5 \times P_7$	8.41 *	6.42 *	2.65	8.44 *	5.17 *	0.83	9.55 *	9.55 *	2.63	50.98 *	25.90 *	-5.50
$P_6 \times P_7$	3.32	2.83	-3.54 *	2.70	0.88	-5.79 *	3.91 *	3.33 *	-2.11	9.32 *	-16.23*	-21.15 *

Table 4.10 Estimates of mid parent, better parent and standard heterosis for ear height (cm), number of kernel rows per ear, number of kernels per row and ear length (cm)

Crosses	Ear height (cm)			Number of kernel rows per ear			Number of kernels per row			Ear length (cm)		
	MPH(%)	BPH(%)	SH(%)	MPH(%)	BPH(%)	SH(%)	MPH(%)	BPH(%)	SH(%)	MPH(%)	BPH(%)	SH(%)
$P_1 \times P_2$	31.57 *	21.25 *	-14.37 *	-4.00	-7.69	-7.69	89.47 *	71.43 *	2.86	85.51 *	61.93 *	6.22
$P_1 \times P_3$	29.21 *	20.21 *	-15.11 *	25.00 *	25.00 *	15.38 *	56.52 *	44.00 *	2.86	37.41 *	26.21 *	-1.08
$P_1 \times P_4$	10.80	10.80	-21.75 *	20.00 *	15.38 *	15.38 *	70.83 *	51.85 *	17.14 *	89.07 *	87.80 *	24.86 *
$P_1 \times P_5$	30.32 *	25.78 *	-11.17 *	9.09	0.00	-7.69	52.38 *	52.38 *	-8.57	22.32 *	19.14	-17.57 *
$P_1 \times P_6$	20.61 *	17.05 *	-12.16 *	4.00	0.00	0.00	56.52 *	44.00 *	2.86	46.30 *	41.70 *	-0.81
$P_1 \times P_7$	21.62 *	4.88	-25.94 *	7.69	0.00	7.69	72.22 *	47.62 *	-11.43 *	20.51 *	15.37	-24.32 *
$P_2 \times P_3$	51.33 *	49.80 *	-8.96	12.00	7.69	7.69	76.19 *	48.00 *	5.71	85.14 *	50.34 *	17.84 *
$P_2 \times P_4$	45.94 *	34.49 *	-5.02	15.38 *	15.38 *	15.38 *	50.00 *	22.22 *	-5.71	70.96 *	48.37 *	-1.35
$P_2 \times P_5$	77.21 *	68.91 *	10.97 *	21.74 *	7.69	7.69	84.21 *	66.67 *	0.00	68.42 *	43.75 *	-0.54
$P_2 \times P_6$	41.13 *	26.56 *	-5.02	0.00	0.00	0.00	52.38 *	28.00 *	-8.57	42.27 *	20.85 *	-15.41 *
$P_2 \times P_7$	71.56 *	59.50 *	-5.02	3.70	0.00	7.69	109.38 *	97.06 *	-4.29	60.79 *	45.95 *	-12.43
$P_3 \times P_4$	23.60 *	14.98 *	-18.80 *	4.00	0.00	0.00	5.77	1.85	-21.43 *	-33.58 *	-38.62 *	-51.89 *
$P_3 \times P_5$	47.86 *	42.32 *	-6.50	9.09	0.00	-7.69	34.78 *	24.00 *	-11.43 *	21.98 *	14.83	-10.00
$P_3 \times P_6$	30.43 *	18.03 *	-11.42 *	-4.00	-7.69	-7.69	32.00 *	32.00 *	-5.71	20.58 *	14.14	-10.54
$P_3 \times P_7$	43.74 *	32.39 *	-19.54 *	15.38 *	7.14	15.38 *	85.00 *	48.00 *	5.71	55.08 *	36.90 *	7.30
$P_4 \times P_5$	58.48 *	52.96 *	8.02	30.43 *	15.38 *	15.38 *	20.83 *	7.41	-17.14 *	9.16	7.03	-25.95 *
$P_4 \times P_6$	26.69 *	22.95 *	-7.73	-15.38 *	-15.38 *	-15.38 *	3.85	0.00	-22.86 *	31.49 *	28.19 *	-10.27
$P_4 \times P_7$	32.12 *	13.94	-19.54 *	-11.11	-14.29 *	-7.69	47.62 *	14.81 *	-11.43 *	25.64 *	19.51	-20.54 *
$P_5 \times P_6$	33.92 *	25.57 *	-5.76	13.04	0.00	0.00	39.13 *	28.00 *	-8.57	29.71 *	28.96 *	-9.73
$P_5 \times P_7$	43.16 *	27.34 *	-16.34 *	0.00	-14.29 *	-7.69	55.56 *	33.33 *	-20.00 *	35.15 *	26.17 *	-12.70
$P_6 \times P_7$	23.20 *	3.61	-22.24 *	3.70	0.00	7.69	110.00 *	68.00 *	20.00 *	90.44 *	76.83 *	23.78 *

Table 4.11 Estimates of mid parent, better parent and standard heterosis for ear circumference (cm), 1000-kernel weight (g), shelling (%) and grain yield per plant (g)

Crosses	Ear circumference (cm)			1000-kernel weight (g)			Shelling (%)			Grain yield per plant (g)		
	MPH(%)	BPH(%)	SH(%)	MPH(%)	BPH(%)	SH(%)	MPH(%)	BPH(%)	SH(%)	MPH(%)	BPH(%)	SH(%)
$P_1 \times P_2$	5.77	3.89	-10.04	20.37 *	7.44 *	-6.81 *	2.82	1.92	4.39 *	149.70 *	146.46 *	7.98
$P_1 \times P_3$	12.14 *	8.98	0.00	10.39 *	5.37	-8.60 *	6.98 *	4.95 *	7.49 *	225.60 *	213.46 *	48.39 *
$P_1 \times P_4$	8.48	4.30	-9.68	39.82 *	27.69 *	10.75 *	-1.32	-3.15	3.02	239.54 *	231.57 *	52.42 *
$P_1 \times P_5$	13.90 *	10.93 *	-3.94	36.07 *	30.17 *	12.90 *	0.78	0.75	3.19	196.26 *	195.41 *	29.42 *
$P_1 \times P_6$	15.03 *	14.65 *	-0.72	20.33 *	19.83 *	3.94	-1.87	-3.30	2.01	189.97 *	176.59 *	33.49 *
$P_1 \times P_7$	23.67 *	15.07 *	-0.36	29.97 *	1.24	-12.19 *	8.56 *	4.08 *	6.60 *	106.37 *	83.56 *	-19.58 *
$P_2 \times P_3$	14.11 *	8.98	0.00	53.66 *	43.18 *	12.90 *	3.64 *	2.57	3.20	224.64 *	208.64 *	46.11 *
$P_2 \times P_4$	19.74 *	17.17 *	-2.15	30.77 *	27.50 *	-8.60 *	-2.03	-4.68 *	1.40	103.47 *	96.18 *	-9.82
$P_2 \times P_5$	30.74 *	29.61 *	8.24	50.85 *	40.27 *	11.11 *	1.30	0.44	2.81	213.20 *	210.02 *	35.04 *
$P_2 \times P_6$	8.25	6.67	-8.24	4.65	-6.25	-19.35 *	1.08	-1.25	4.17 *	123.36 *	110.42 *	1.56
$P_2 \times P_7$	17.01 *	10.73	-7.53	47.69 *	26.32 *	-13.98 *	9.39 *	5.77 *	6.42 *	174.13 *	146.68 *	5.27
$P_3 \times P_4$	11.90 *	4.69	-3.94	2.38	-2.27	-22.94 *	-0.75	-4.40 *	1.69	75.98 *	73.43 *	-17.90 *
$P_3 \times P_5$	2.68	-2.73	-10.75	42.86 *	42.53 *	12.90 *	3.18	1.25	3.64	165.18 *	154.59 *	20.52 *
$P_3 \times P_6$	-2.42	-5.47	-13.26 *	6.52	2.08	-12.19 *	3.11	-0.29	5.19 *	146.81 *	144.45 *	17.98 *
$P_3 \times P_7$	34.05 *	21.48 *	11.47 *	69.58 *	36.82 *	7.89 *	8.77 *	6.24 *	4.68 *	234.86 *	188.13 *	36.40 *
$P_4 \times P_5$	16.37 *	14.85 *	-5.73	35.39 *	28.96 *	2.15	-1.71	-3.57 *	2.58	162.74 *	155.85 *	17.61 *
$P_4 \times P_6$	7.99	4.17	-10.39	-4.55	-12.50 *	-24.73 *	-6.31 *	-6.70 *	-0.75	65.77 *	61.83 *	-21.89 *
$P_4 \times P_7$	14.62 *	10.76	-11.47 *	34.33 *	12.50 *	-19.35 *	0.58	-5.29 *	0.75	95.59 *	70.40 *	-21.67 *
$P_5 \times P_6$	10.02 *	7.50	-7.53	19.31 *	14.58 *	-1.43	-1.52	-2.99	2.34	154.48 *	142.08 *	16.84 *
$P_5 \times P_7$	12.59 *	7.42	-11.83 *	46.07 *	17.65 *	-6.81 *	4.97 *	0.66	3.03	108.07 *	85.55 *	-19.18 *
$P_6 \times P_7$	9.82	2.50	-11.83 *	62.13 *	26.67 *	8.96 *	4.25 *	-1.45	3.96 *	241.49 *	191.48 *	40.68 *

Presence of significant amount of heterosis for grain yields and yield component traits is pre-requisite for hybrids and synthetics development and even in isolation of transgressive segregants for development of superior homozygous inbred lines. The results presented above have been discussed under following paragraphs.

Most promising F_1s with respect to MPH (%) was observed in $P_2 \times P_3$ for days to 50% pollen shed, $P_2 \times P_5$ for days to 50% silking, $P_4 \times P_6$ for plant height, $P_4 \times P_5$ for number of kernel rows per ear, $P_2 \times P_7$ for shelling (%), $P_3 \times P_7$ for ear circumference and 1000-kernel weight, $P_6 \times P_7$ for number of kernels per row, ear length and grain yield per plant. None of crosses showed significant MPH (%) for all traits.

The most promising F_1s with respect to BPH (%) was observed in $P_2 \times P_3$ for days to 50% pollen and 1000-kernel weight, $P_2 \times P_5$ for days to 50% silking and ear circumference, $P_4 \times P_6$ for plant height (cm), $P_1 \times P_3$ for number of kernels rows per ear, $P_2 \times P_7$ for number of kernels per row, $P_3 \times P_7$ for shelling (%) and $P_1 \times P_4$ for ear length and grain yield per plant (g) while, none of the crosses showed significant better parent heterosis for days to 75% brown husk and ear height. None of the crosses showed significant heterosis for all traits.

Among three types of heterosis, standard heterosis (%) is considered desirable from breeding point of view. Detailed study of standard heterosis revealed by crosses might be considered necessary. The crosses showed significant standard heterosis (SH %) for grain yield per plant (g) over best check Palam Sankar Makka-2 were $P_1 \times P_4$, $P_1 \times P_3$, $P_2 \times P_3$, $P_6 \times P_7$ and $P_3 \times P_7$. These F_1s were found superior for most of the characters and identified as promising cross combinations.

Netaji et al. (2000) and Geetha (2001) also observed significant standard heterosis and better parent heterosis for grain yield. Malik et al. (2004) earlier also observed MPH (%) and BPH (%) for grain yield**.** Muraya et al. (2006) also reported significant positive mid parent heterosis for cob length, cob diameter, number of kernel rows per ear, number of kernels per row, whereas, negative significant mid parent heterosis for days to 50 % tasseling. Elmyhum (2013) and Ulaganathan et al. (2015) observed better parent heterosis for grain yield. Patel et al. (2019) reported significant positive mid parent, better parent and standard heterosis for grain yield per plant, cob length, cob weight, cob circumference, number of kernel rows per ear, 100-kernel weight and number of kernels per row. Chandel et al. (2020) and Sharma et al. (2021) also observed significant positive standard heterosis for grain yield.

4.5 Disease reaction

Experimental material including seven parents, twenty-one crosses along with three checks were screened against banded leaf and sheath blight (BLSB), turcicum leaf blight (TLB) and maydis leaf blight (MLB) under natural epiphytotic conditions. All genotypes were screened and classified into different groups using 1-9 disease rating scale. They were then divided into four categories: resistant (R) genotypes with a score of (≤ 3.0), moderately resistant (3.1-5.0), moderately susceptible (5.1-7.0), and susceptible (> 7.0-9.0). Appendix II revealed the mean of disease ratings of parents, crosses and checks for banded leaf and sheath blight, turcicum leaf blight and maydis leaf blight.

4.5.1 Disease reaction to Banded Leaf and Sheath Blight (BLSB)

Under natural epiphytotic conditions, genotypes were screened for their resistance against banded leaf and sheath blight. Five parents P_1, P_2, P_3,P_6, P_7, seventeen crosses *viz.,* $P_1 \times P_2$, $P_1 \times P_3$, $P_1 \times P_4$, $P_1 \times P_5$, $P_1 \times P_6$, $P_1 \times P_7$, $P_2 \times P_3$, $P_2 \times P_5$, $P_2 \times P_6$, $P_2 \times P_7$, $P_3 \times P_4$, $P_3 \times P_5$, $P_3 \times P_7$, $P_4 \times P_7$, $P_5 \times P_6$, $P_5 \times P_7$, $P_6 \times P_7$ and three checks *viz.,* Palam Sankar Makka-2, Bio 9544, Bio 605 were found moderately resistant (3.1-5.0) and two parents and four crosses were observed moderately susceptible (5.1-7.0). None of the genotypes were resistance and susceptible against banded leaf and sheath blight (Table 4.12). Similar result were also reported earlier for banded leaf and sheath blight by Sood (2012); Chen et al. (2013); Thakur (2014); Thakur et al. (2018) and Meena et al. (2020).

4.5.2 Disease reaction to Turcicum leaf blight (TLB)

Under natural condition, genotypes were screened for their resistance against turcicum leaf blight. Six crosses *viz.*, $P_1 \times P_4$, $P_2 \times P_3$, $P_3 \times P_7$, $P_6 \times P_7$, $P_1 \times P_3$ and $P_2 \times P_5$ showed resistance (≤ 3.0) against turcicum leaf blight. All parents, fifteen crosses *viz.,* $P_1 \times P_2$, $P_1 \times P_5$, $P_1 \times P_6$, $P_1 \times P_7$, $P_2 \times P_4$, $P_2 \times P_6$, $P_2 \times P_7$, $P_3 \times P_4$, $P_3 \times P_5$, $P_3 \times P_6$, $P_4 \times P_5$, $P_4 \times P_6$, $P_4 \times P_7$, $P_5 \times P_6$, $P_5 \times P_7$ and three checks *viz.,* Palam Sankar Makka-2, Bio 9544, Bio 605 were moderately resistance (3.1-5.0) against turcicum leaf blight. None of genotypes were susceptible against turcicum leaf blight (Table 4.13). Similar results were also reported earlier by Kachapur et al. (2016); Yousuf et al. (2018); Razzaq et al. (2019) and Sharma et al. (2021).

4.5.3 Disease reaction to Maydis leaf blight (MLB)

Under natural epiphytotic conditions, only one parent (P_6) and six crosses *viz.,* $P_1 \times P_4$, $P_2 \times P_3$, $P_3 \times P_7$, $P_6 \times P_7$, $P_1 \times P_3$ and $P_2 \times P_5$ were found moderately resistant (3.1-5.0) against maydis leaf blight. Seventeen genotypes *viz.*, P_1,P_2, P_3, P_5, $P_1 \times P_2$, $P_1 \times P_5$, $P_1 \times P_6$, $P_1 \times P_7$, $P_2 \times P_6$, $P_2 \times P_7$, $P_3 \times P_4$, $P_3 \times P_5$, $P_3 \times P_6$, $P_4 \times P_5$, $P_4 \times P_7$, $P_5 \times P_6$, $P_5 \times P_7$ and checks *viz.,* Palam

Sankar Makka-2, Bio 9544, Bio 605 were moderately susceptible (5.1-7.0) and four genotypes (P_4, P_7, $P_2 \times P_4$ and $P_4 \times P_6$) were susceptible (Table 4.14). Similar disease reaction against maydis leaf blight also reported by Hooda et al. (2012); Rai et al. (2009); Kumar et al. (2013); Omprakash et al.(2016) and Sharma et al. (2021).

Table 4.12 Disease reaction to Banded leaf and sheath blight

Disease Reaction type	**Parent (s)**	**Crosses**	**Checks**
Resistant ≤ 3.0		-	-
Moderately Resistant 3.1-5.0	P_1, P_2, P_3,P_6, P_7	$P_1 \times P_2$, $P_1 \times P_3$, $P_1 \times P_4$, $P_1 \times P_5$, $P_1 \times P_6$, $P_1 \times P_7$, $P_2 \times P_3$, $P_2 \times P_5$, $P_2 \times P_6$, $P_2 \times P_7$, $P_3 \times P_4$, $P_3 \times P_5$, $P_3 \times P_7$, $P_4 \times P_7$, $P_5 \times P_6$, $P_5 \times P_7$, $P_6 \times P_7$	Palam Sankar Makka-2, Bio 9544 , Bio 605
Moderately Susceptible 5.1-7.0	P_4, P_5	$P_2 \times P_4$, $P_3 \times P_6$, $P_4 \times P_6$, $P_4 \times P_5$	-
Susceptible >7.0-9.0		-	-

Table 4.13 Disease reaction to Turcicum leaf blight

Disease Reaction Type	**Parent (s)**	**Crosses**	**Checks**
Resistant ≤ 3.0	-	$P_1 \times P_4$, $P_2 \times P_3$, $P_3 \times P_7$, $P_6 \times P_7$, $P_1 \times P_3$, $P_2 \times P_5$	-
Moderately Resistant 3.1-5.0	P_1, P_2, P_3, P_4, P_5, P_6, P_7	$P_1 \times P_2$, $P_1 \times P_5$, $P_1 \times P_6$, $P_1 \times P_7$, $P_2 \times P_4$, $P_2 \times P_6$, $P_2 \times P_7$, $P_3 \times P_4$, $P_3 \times P_5$, $P_3 \times P_6$, $P_4 \times P_5$, $P_4 \times P_6$, $P_4 \times P_7$, $P_5 \times P_6$, $P_5 \times P_7$	Palam Sankar Makka-2, Bio 9544 , Bio 605
Moderately Susceptible 5.1-7.0	-	-	-
Susceptible >7.0-9.0	-	-	-

Table 4.14 Disease reaction to Maydis leaf blight

Disease Reaction Type	Parent (s)	Crosses	Check
Resistant ≤ 3.0	-	-	-
Moderately Resistant 3.1-5.0	P_6	$P_1 \times P_4$, $P_2 \times P_3$, $P_3 \times P_7$, $P_6 \times P_7$, $P_1 \times P_3$, $P_2 \times P_5$	-
Moderately Susceptible 5.1-7.0	P_1,P_2, P_3, P_5	$P_1 \times P_2$, $P_1 \times P_5$, $P_1 \times P_6$, $P_1 \times P_7$, $P_2 \times P_6$, $P_2 \times P_7$, $P_3 \times P_4$, $P_3 \times P_5$, $P_3 \times P_6$, $P_4 \times P_5$, $P_4 \times P_7$, $P_5 \times P_6$,$P_5 \times P_7$	Palam Sankar Makka-2, Bio 9544, Bio 605
Susceptible >7.0-9.0	P_4, P_7	$P_2 \times P_4$, $P_4 \times P_6$	-

4.6. Promising hybrid combinations

In the present study six crosses *viz.,* $P_1 \times P_4$, $P_1 \times P_3$, $P_2 \times P_3$, $P_6 \times P_7$, $P_3 \times P_7$ and $P_2 \times P_5$ exhibited more grain yield per plant (g) than the best check Palam Sankar Makka-2 based upon mean performance and SCA effects (Table 4.15).

SCA effects of these crosses involved all possible combination between parents of good, poor and average combining ability. This indicted that GCA had not any bearing on SCA effects of these crosses. High SCA effects manifested by crosses where both the parents were good general combiners is attributed due to additive × additive gene action, whereas, the high SCA effects of crosses involving good × poor general combiner parent is due to favorable additive effects of good general combiner parent and epistatic effects of poor general combiner.

Table 4.15 List of best hybrid combinations on the basis grain yield (g /plant) and SCA effects

Hybrid combination	Mean grain yield (g/plant)	SCA effects (yield)	GCA of parents in SCA crosses
P_1 × P_4	117.9	44.50	G/P
P_1 × P_3	114.79	28.02	G/G
P_6 × P_7	108.82	40.15	A/P
P_2 × P_3	113.03	32.12	A/G
P_3 × P_7	105.51	31.60	G/P
P_2 × P_5	104.46	28.61	A/A

Promising cross combinations

5. SUMMARY AND CONCLUSIONS

The present study "Heterosis and combining ability analysis of sub-tropical maize (*Zea mays* L.*)* inbred lines" was conducted on experimental materials obtained by crossing seven maize inbred lines in half diallel mating scheme. The experimental material of seven inbreds, 21 crosses and three checks *viz.,* Palam Sankar Makka-2, Bio 9544 and Bio 605 were evaluated in Randomized Block Design with two replications in a plot size of 3.6 m^2 (3.0 × 1.2) with spacing of 60 × 20 cm at the Experimental Farm of Shivalik Agricultural Research and Extension Centre, Kangra (latitude-32°09'N, longitude-76°22'E and altitude-700 m amsl) during *kharif*, 2021. The data were recorded for twelve traits *viz.,* days to 50% pollen shed, days to 50% silking, days to 75% brown husk, cob placement (cm) plant height (cm), number of kernel rows per ear, number of kernels per row, ear length (cm), ear circumference (cm), 1000-kernel weight (g), shelling (%) and grain yield per plant (g) were subjected to statistical analysis to derive the information on the nature and magnitude of gene action, estimation of heterosis and combining ability effects for grain yield and its component traits.

These characters were analyzed using appropriate statistical and biometrical models and the salient findings are summarized as below:

Analysis of variance revealed the significant mean squares due to genotypes for all of the studied traits except number of kernel rows per ear. This indicated presence of sufficient amount of genetic variability in experimental material.

On the basis of mean performance, parent P_6 had maximum 1000-kernel weight (g) and grain yield per plant (g). Among the crosses, $P_1 \times P_4$ recorded maximum grain yield per plant (g), ear length (cm), number of kernel rows per ear and also showed earliness for days to 50% pollen shed and days to 50% silking. $P_1 \times P_6$ exhibited earliness for days to 75% brown husk, $P_1 \times P_3$ exhibited maximum shelling (%), $P_2 \times P_3$ showed maximum 1000-kernel weight (g) and $P_6 \times P_7$ recorded maximum ear circumference (cm) and number of kernels per row.

Analysis of variance for combining ability showed significant mean sum of squares due to general combining ability and specific combining ability for all the characters except mean squares due to GCA for days to 50% siliking and shelling (%). This indicated preponderance of both additive and non-additive gene actions for the inheritance of these traits.

Based on general combining ability effects of parents, none of the parent was good combiner for all the characters. However, the parent P_1 exhibited significant general combining ability effects for days to 50% pollen shed, ear height (cm), number of kernels per row, ear length (cm), 1000-kernel weight (g), shelling (%) and for grain yield per plant (g); P_3 for days to 75% brown husk, plant height (cm), ear height (cm), number of kernels per row, ear circumference (cm), 1000-kernel weight (g) and grain yield per plant (g); P_4 for plant height (cm); P_5 for 1000-kernel weight (g); P_6 for number of kernels per row and ear length (cm), whereas, P_7 for plant and ear height (cm) and also for number of kernel rows per ear. The parent with maximum *per se performance* did not always had maximum general combining ability effects. Therefore, *per se performance* and GCA effects both were considered for identification of promising parents. On the basis of mean performance and general combining ability effect parent P_3 and P_1 were identified as promising parents.

Based on specific combining ability effects cross $P_1 \times P_4$ exhibited maximum combining ability for grain yield per plant (g) followed by $P_6 \times P_7$, $P_2 \times P_3$, $P_3 \times P_7$, $P_2 \times P_5$, whereas, $P_2 \times P_5$ showed significant SCA effects for days to 50% pollen shed and days to 50% silking. Similarly, $P_1 \times P_6$ for days to 75% brown husk, $P_4 \times P_6$ for plant height (cm), $P_1 \times P_4$ for ear height (cm), $P_4 \times P_5$ for number of kernel rows per ear, $P_6 \times P_7$ for number of kernels per row and 1000-kernel weight (g), $P_2 \times P_7$ for shelling (%), $P_3 \times P_7$ for ear circumference (cm) and $P_1 \times P_4$ for ear length (cm) exhibited significant SCA effects. Crosses with maximum mean performance did not always had maximum specific combining ability effects. Therefore, both mean performance and specific combining ability effects should be considered for development of single cross hybrids.

While assessing the performance of parents on the basis of GCA, it was observed that a majority of specific cross combinations were the product of crosses between good × poor or poor × good or poor × poor general combiners. In general, there was no generalized pattern among the parents to produce desirable combinations. Any combination of parents might result in hybrid vigour, which could be due to favorable dominant genes, overdominance or epistatic action of genes.

The magnitude of dominance variance (σ^2D) was higher than additive variance ($\sigma^2 A$) for all the studied traits which indicated the preponderance of non additive gene action thereby suggesting the exploitation of hybrid vigour in maize.

MPH(%), BPH (%) and SH (%) were estimated for different traits and crosses. P_6 × P_7 recorded maximum significant positive MPH (%) for grain yield per plant, whereas, P_1 × P_4 exhibited maximum significant positive BPH (%) and SH (%) followed by P_1 × P_3, P_2 × P_3, P_3 × P_7 and P_2 × P_5.

The crosses *viz.,* P_1 × P_4, P_1 × P_3, P_2 × P_3, P_6 × P_7, P_3 × P_7 and P_2 × P_5 were identified as promising combinations based upon mean performance, specific combining ability effects and standard heterosis. In addition, these crosses also showed resistance against turcicum leaf blight and moderately resistance against maydis leaf bilght and banded leaf and sheath blight

Conclusion

- Analysis of variance revealed significant differences among genotypes for all the studied traits except number of kernel rows per ear suggesting presence of sufficient amount of genetic variability in the experimental material.
- Analysis of variance for combining ability showed significant mean sum of squares due to general combining ability and specific combining ability for all the traits except GCA for days to 50% silking and shelling (%) indicated the preponderance of both additive and non-additive gene actions for the inheritance of the studied traits.
- The GCA to SCA variance ratio was less than unity for all traits under study indicated preponderance of non-additive gene action governing the inheritance of these traits.
- On the basis of GCA effects of inbred lines P_1 (KGI-109) and P_3 (DMEL-143) were good general combiner for grain yield per plant (g) and for most of the traits except days to 50% silking and number of kernel rows per ear.
- The best cross combinations *viz.,* P_1 × P_4 (KGI-109 × DMEL-156), P_1 × P_3 (KGI-109 × DMEL-143), P_2 × P_3 (LM-18 × DMEL-143), P_6 × P_7 (DMR139 × KGI-110), P_3 × P_7 (DMEL-143 × KGI-110) and P_2 × P_5 (LM-18 × CML139) were identified for grain yield per plant on the basis of mean performance, SCA effect and significant standard heterosis. In addition, these crosses also showed resistance to Turcicum leaf blight and moderately resistant to Banded leaf and sheath blight and Maydis leaf blight.
- These promising cross combinations need to be further evaluated in multi-location trials over the years to assess their suitability in different agro climatic zones of the State.

LITERATURE CITED

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Mean performance of parents, crosses and checks for different traits

Appendix-I

Parents	Days to 50% pollen shed	Days to 50 % Silking	Days to 75% brown husk	Plant height (cm)	Ear height (cm)	Number of kernel rows per ear	Number of kernels per row	Ear length (cm)	Ear circum-ference (cm)	1000-kernel weight (g)	Shelling (%)	Grain yield (g/plant)
P1	52.50	55.50	89.00	161.25	71.75	12.00	21.00	12.14	12.08	242.00	82.88	33.89
P2	55.00	58.50	91.00	149.00	60.50	13.00	17.00	9.05	11.65	190.00	81.43	33.01
P3	53.50	57.00	88.50	136.00	61.75	12.00	25.00	14.50	12.80	220.00	79.74	36.62
P4	55.00	58.50	92.50	150.00	71.75	13.00	27.00	12.30	11.15	200.00	86.08	35.56
P5	54.50	58.00	89.00	153.50	66.75	10.00	21.00	12.80	11.45	221.00	82.83	33.70
P6	53.00	56.50	90.00	192.50	76.25	13.00	25.00	12.95	12.00	240.00	85.37	37.34
P7	52.50	55.50	89.00	102.50	52.00	14.00	15.00	11.10	10.40	135.00	76.04	26.40
$P_1 \times P_2$	57.50	61.50	96.50	173.00	87.00	12.00	36.00	19.65	12.55	260	84.48	83.52
$P_1 \times P_3$	56.50	60.00	98.50	169.50	86.25	15.00	36.00	18.30	13.95	255	86.99	114.79
$P_1 \times P_4$	51.50	54.50	93.00	184.25	79.50	15.00	41.00	23.10	12.60	309	83.37	117.90
$P_1 \times P_5$	55.00	58.00	91.50	192.00	90.25	12.00	32.00	15.25	13.40	315	83.51	100.12
$P_1 \times P_6$	52.50	55.50	88.50	200.00	89.25	13.00	36.00	18.35	13.85	290	82.56	103.26
$P_1 \times P_7$	54.00	58.00	89.50	184.75	75.25	14.00	31.00	14.00	13.90	245	86.26	62.21
$P_2 \times P_3$	52.50	55.00	89.00	182.50	92.50	14.00	37.00	21.80	13.95	315	83.51	113.03
$P_2 \times P_4$	54.00	57.00	90.50	174.25	96.50	15.00	33.00	18.25	13.65	255	82.06	69.76
$P_2 \times P_5$	51.50	54.00	89.00	228.25	112.75	14.00	35.00	18.40	15.10	310	83.20	104.46
$P_2 \times P_6$	53.00	56.00	89.50	182.75	96.50	13.00	32.00	15.65	12.80	225	84.30	78.56

$P_2 \times P_7$	56.00	59.50	93.50	191.50	96.50	14.00	33.50	16.20	12.90	240	86.12	81.43
$P_3 \times P_4$	53.50	56.00	91.50	171.25	82.50	13.00	27.50	8.90	13.40	215	82.29	63.51
$P_3 \times P_5$	53.50	56.50	91.00	198.75	95.00	12.00	31.00	16.65	12.45	315	83.87	93.23
$P_3 \times P_6$	56.50	60.00	90.00	159.50	90.00	12.00	33.00	16.55	12.10	245	85.13	91.26
$P_3 \times P_7$	53.50	56.50	89.00	183.75	81.75	15.00	37.00	19.85	15.55	301	84.71	105.51
$P_4 \times P_5$	57.50	60.50	95.00	160.00	109.75	15.00	29.00	13.7	13.15	285	83.01	90.98
$P_4 \times P_6$	58.00	61.50	95.50	149.75	93.75	11.00	27.00	16.6	12.50	210	80.32	60.42
$P_4 \times P_7$	56.00	59.50	94.50	146.50	81.75	12.00	31.00	14.7	12.35	225	81.53	60.60
$P_5 \times P_6$	56.00	58.50	94.50	202.00	95.75	13.00	32.00	16.70	12.90	275	82.82	90.38
$P_5 \times P_7$	58.00	61.00	97.50	193.25	85.00	12.00	28.00	16.15	12.30	260	83.38	62.52
$P_6 \times P_7$	54.50	57.00	93.00	161.25	79.00	14.00	42.00	22.90	12.30	304	84.13	108.82
PSM-2	56.50	60.50	99.00	192.50	91.00	12.00	31.00	18.35	14.25	279	80.34	72.61
Bio 9544	58.00	61.50	97.00	204.50	101.75	13.00	35.00	18.50	13.95	260	80.93	64.46
Bio 605	58.00	62.00	95.00	195.00	97.50	13.00	33.00	19.85	14.20	270	80.80	60.78
Mean	54.82	58.05	92.27	175.02	85.40	13.06	30.65	16.23	12.95	255.19	83.03	73.89
Range	51.00-58.00	53.50 – 62.50	88.00-99.50	102.50-228.25	52.00-112.75	10.00 – 15.00	14.50 – 42.00	9.05 - 23.10	10.40 – 15.50	135.00 – 315.00	0.76 – 0.88	26.40-117.91
CD(5%)	2.03	2.52	2.65	12.71	10.12	1.87	3.55	2.49	1.29	17.56	3.03	9.22
SE±(m)	0.70	0.87	0.92	4.39	3.49	0.65	1.23	0.86	0.44	6.06	1.04	3.18
CV (%)	1.81	2.14	1.41	3.59	5.86	6.89	5.71	7.61	4.90	3.38	1.77	6.02

Mean value of disease score of parents, crosses and checks for MLB, TLB and BLSB

Appendix-II

Diseases			
Parents	**MLB**	**TLB**	**BLSB**
P_1	6.5	3.5	4.0
P_2	6.5	4	3.5
P_3	5.5	3.5	5.0
P_4	7.5	4	5.5
P_5	4.0	5	6.5
P_6	4.5	4	4.5
P_7	7.5	4.5	3.5
Crosses			
$P_1 \times P_2$	5.5	3.5	3.5
$P_1 \times P_3$	4.5	2	4.0
$P_1 \times P_4$	3.5	1.5	3.5
$P_1 \times P_5$	5.5	3.5	3.5
$P_1 \times P_6$	6.0	4	4.0
$P_1 \times P_7$	7.0	3.5	3.5
$P_2 \times P_3$	3.5	2	4.5
$P_2 \times P_4$	7.5	4	3.5
$P_2 \times P_5$	6.5	2.5	4.5
$P_2 \times P_6$	6.5	4.5	5.0
$P_2 \times P_7$	6.0	3.5	3.5
$P_3 \times P_4$	6.5	4	4.5
$P_3 \times P_5$	5.5	5	3.5
$P_3 \times P_6$	5.5	4.5	4.0
$P_3 \times P_7$	3.5	1.5	3.5
$P_4 \times P_5$	5.5	3.5	4.5
$P_4 \times P_6$	7.5	5	5.0
$P_4 \times P_7$	5.5	3.5	4.5
$P_5 \times P_6$	6.0	5	3.5
$P_5 \times P_7$	5.5	4.5	4.5
$P_6 \times P_7$	4.0	1.5	3.5
Check (s)			
PSM-2	5.5	3.5	3.5
Bio 9455	6.5	4	3.5
Bio 605	5.5	3.5	3.5

BRIEF BIODATA OF STUDENT

Name : Ambika

Mother's Name : Smt. Jaram Dei

Father's Name : Sh. Lal Pat

Date of Birth : 31th December,1997

Permanent Address: Village Madgram, P.O. Udaipur, Teh. Keylong, Distt. Lahaul & Spiti (H.P.)-175142

Academic Qualification

Examination passed	Year	School/Board/ University	Marks (%)	Division	Major Subjects
10th	2013	HP Board	78.00	First	English, Mathematics, Hindi, Social Science, Science, Arts, Sanskrit
12th	2015	HP Board	72.00	First	English, Biology, Physics, Chemistry, Computer Science
B.Sc. (Agriculture)	2020	CSK HPKV Palampur	69.20	First	All Agriculture and Allied subjects
M.Sc. Agri. (Genetics and Plant Breeding)	2022	CSK HPKV Palampur	76.90	First	Major Discipline: Genetics and Plant Breeding Minor Discipline: Plant Pathology