

**GENETIC ANALYSIS FOR YIELD AND
EVALUATION OF HYBRIDS FOR
CHARCOAL ROT RESISTANCE IN
MAIZE (*Zea mays* L.)**

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B.Sc. (Hons.) Ag.

**MASTER OF SCIENCE IN AGRICULTURE
(GENETICS AND PLANT BREEDING)**



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EVALUATION OF HYBRIDS FOR
CHARCOAL ROT RESISTANCE IN MAIZE
(*Zea mays* L.)**

BY

NIKADI TEJASWINI

B.Sc. (Hons.) Ag.

**THESIS SUBMITTED TO THE PROFESSOR JAYASHANKAR
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THE DEGREE OF**

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CHAIRPERSON: Dr. K. SUKUMAR



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2022

DECLARATION

I, Ms. **NIKADI TEJASWINI**, hereby declare that the thesis entitled “**GENETIC ANALYSIS FOR YIELD AND EVALUATION OF HYBRIDS FOR CHARCOAL ROT RESISTANCE IN MAIZE (*Zea mays* L.)**” submitted to the **Professor Jayashankar Telangana State Agricultural University** for the degree of **Master of Science in Agriculture** is the result of original research work done by me. I also declare that no material contained in the thesis has been published earlier in any manner.

Place: Jagtial

Date:

(NIKADI TEJASWINI)

I.D.No. JAM/2020-08

CERTIFICATE

Ms. **NIKADI TEJASWINI** has satisfactorily prosecuted the course of research and that the thesis entitled “**GENETIC ANALYSIS FOR YIELD AND EVALUATION OF HYBRIDS FOR CHARCOAL ROT RESISTANCE IN MAIZE (*Zea mays L.*)**” submitted is the result of original research work done and is of sufficiently high standard to warrant its presentation to the examination. I also certify that neither the thesis nor its part thereof has been previously submitted by her for a degree of any University.

Date:

(Dr. K. SUKUMAR)
Chairperson

CERTIFICATE

This is to certify that the thesis entitled “**GENETIC ANALYSIS FOR YIELD AND EVALUATION OF HYBRIDS FOR CHARCOAL ROT RESISTANCE IN MAIZE (*Zea mays* L.)**” submitted in partial fulfillment of the requirements for the degree of ‘Master of Science in Agriculture’ of the Professor Jayashankar Telangana State Agricultural University, Hyderabad, is a record of the bonafide original research work carried out by **Ms. NIKADI TEJASWINI** under our guidance and supervision.

No part of the thesis has been submitted by the student for any other degree or diploma. The published part and all assistance and help received during the course of the investigation have been duly acknowledged by the author of the thesis.

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LIST OF CONTENTS

Chapter No.	Title	Page No.
I	INTRODUCTION	
II	REVIEW OF LITERATURE	
III	MATERIAL AND METHODS	
IV	RESULTS AND DISCUSSION	
V	SUMMARY AND CONCLUSIONS	
	LITERATURE CITED	

LIST OF TABLES

Table No.	Title	Page No.
3.1	List of maize inbred lines used in present investigation	
3.2	Scoring for stay green trait (Belicuas <i>et al.</i> 2014)	
3.3	Disease rating scale for maize charcoal rot (Payak and Sharma, 1983)	
4.1	Analysis of variance for yield and its attributing traits among selected maize genotypes	
4.2	Mean performance of parents, crosses and standard check for yield and its attributing traits of maize genotypes	
4.3	Estimates of heterosis over mid parent, better parent and standard check for yield and yield attributing traits in maize hybrids	
4.4	Standard heterosis, heterobeltiosis and relative heterosis for top crosses for each trait in maize hybrids	
4.5	Analysis of variance for combining ability for yield and its attributing traits in maize genotypes	
4.6	Estimates of general combining ability (<i>gca</i>) effects of the parents for yield and yield attributing traits	
4.7	Estimates of specific combining ability (<i>sca</i>) effects of the hybrids for yield and yield attributing traits	
4.8	Estimates of general and specific combining ability variances and proportionate gene action in maize genotypes	
4.9	Top five hybrids with high <i>sca</i> effects, <i>per se</i> performance and <i>gca</i> effects of parents for yield and its attributing traits in maize hybrids	
4.10	Promising general combiners for earliness, yield and its attributing traits	
4.11	Promising specific combiners for earliness, yield and its attributing traits	
4.12	Phenotypic and genotypic correlation coefficients for yield and its attributing traits in maize genotypes	
4.13	Path coefficient analysis for yield and its attributing traits in maize genotypes	
4.14	Scoring of maize genotypes for stay green trait	
4.15	Screening of maize genotypes for charcoal rot resistance using 0-9 scale (Payak and Sharma, 1983)	
4.16	Overall performance of the superior hybrids (top five high yielders) identified in the study	

LIST OF ILLUSTRATIONS

S. No	Title	Page No.
4.1	Top five hybrids identified based on standard heterosis (over check, DHM-117) for grain yield per plant	
4.2	Top hybrids identified based on high <i>sca</i> effects with <i>per se</i> performance and <i>gca</i> effects of parents for grain yield per plant	
4.3	Phenotypic path diagram for grain yield per plant	
4.4	Genotypic path diagram for grain yield per plant	

LIST OF PLATES

S. No	Title	Page No.
3.1	Crossing block	
3.2	Bagging of tassel and silk	
3.3	Crossed ear	
3.4	Glimpse of the experimental field during evaluation programme	
3.5	Data collection on ear height (cm)	
3.6	General view of cobs at physiological maturity stage	
3.7	Pure culture of <i>Macrophomina phaseolina</i>	
3.8	Mass culture of <i>Macrophomina phaseolina</i> on tooth picks	
3.9	Tooth pick inoculation technique	
3.10	Data collection on charcoal rot resistance (scoring)	
4.1	Typical symptoms of charcoal rot of maize caused by <i>Macrophomina phaseolina</i>	
4.2	Most promising general combiners for yield and its attributing traits	
4.3	Most promising specific combiners for yield and its attributing traits	
4.4	Most promising experimental hybrid identified (PFSR-127×ML-14)	
4.5	Second most promising experimental hybrid identified (PFSR-127×MGC-49)	

LIST OF SYMBOLS AND ABBREVIATIONS

%	:	Per cent
Σ	:	Summation
ANOVA	:	Analysis of variance
ARI	:	Agricultural Research Institute
BP	:	Better parent
$^{\circ}\text{C}$:	Degree centigrade
C.D.	:	Critical difference
Cm	:	Centimeter
C.V.	:	Coefficient of variation
d.f.	:	Degrees of freedom
<i>et al.</i>	:	and others
FAO	:	Food and Agriculture organization
F ₁	:	First filial generation
G	:	gram
<i>Gca</i>	:	General combining ability
Ha	:	hectare
<i>i.e.,</i>	:	that is
Kg	:	kilogram
M	:	Million
MSS	:	Mean sum of squares
MRC	:	Maize Research Centre
MP	:	Mid parent
No.	:	Number
RBD	:	Randomized Complete Block Design
<i>Sca</i>	:	Specific combining ability
<i>viz.</i>	:	Namely
Vs	:	versus

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Plate 3.1 Crossing block



Plate 3.2 Bagging of tassel and silk

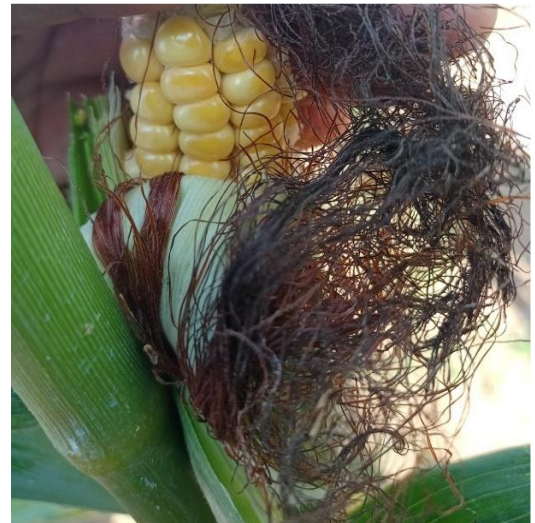


Plate 3.3 Crossed ear



Plate 3.4 Glimpse of the experimental field during evaluation programme



Plate 3.5 Data collection on ear height (cm)



Plate 3.6 General view of cobs at physiological maturity stage



Plate 3.7 Pure culture of *Macrophomina phaseolina*



Plate 3.8 Mass culture of *Macrophomina phaseolina* on tooth picks



Plate 3.9 Tooth pick inoculation technique



Plate 3.10 Data collection on charcoal rot resistance (scoring)



Plate 4.1 Typical symptoms of charcoal rot of maize caused by *Macrophomina phaseolina*



PFSR-127



PFSR-151



BML-10

Plate 4.2 Most promising general combiners for yield and its attributing traits



PFSR-151 x BPDT-5009



PFSR-73 x ML-14



PFSR-127 x BPDT-5009



PFSR-151 x MGC-49



BML-10×PFSR-92



PFSR-73×MGC-49

Plate 4.3 Most promising specific combiners for yield and its attributing traits

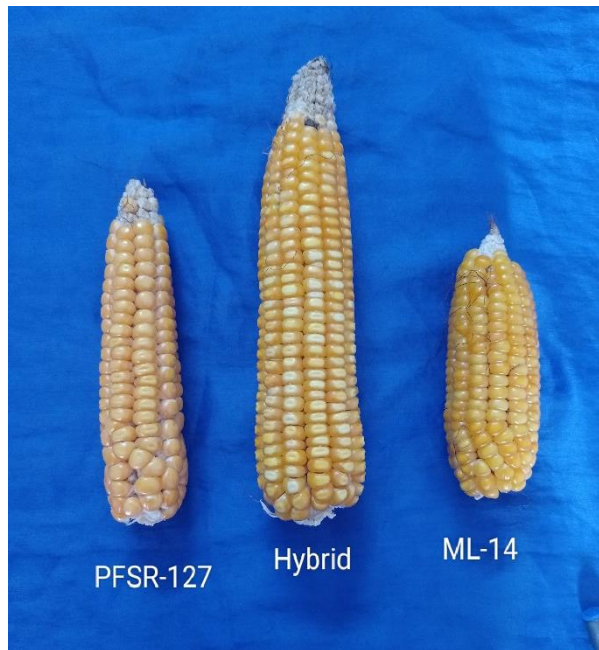


Plate 4.4 Most promising experimental hybrid identified (PFSR-127×ML-14)



**Plate 4.5 Second most promising experimental hybrid identified
(PFSR-127×MGC-49)**

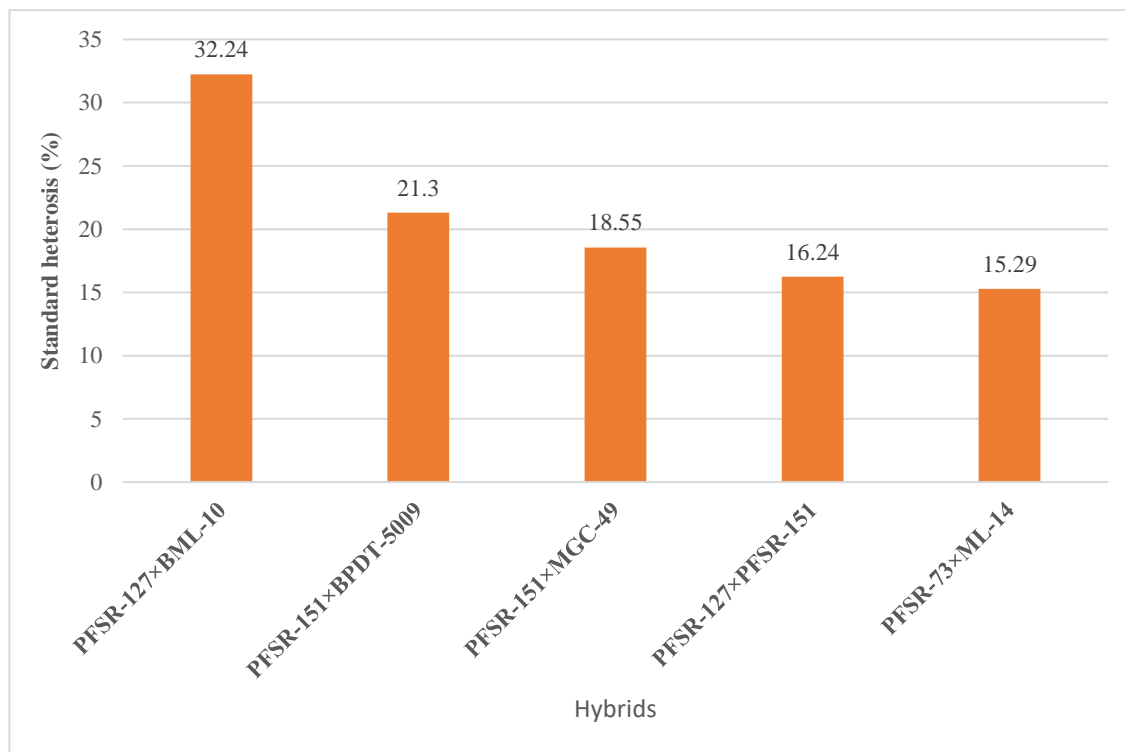


Figure 4.1. Top five hybrids identified based on standard heterosis (over the check, DHM-117) for grain yield per plant.

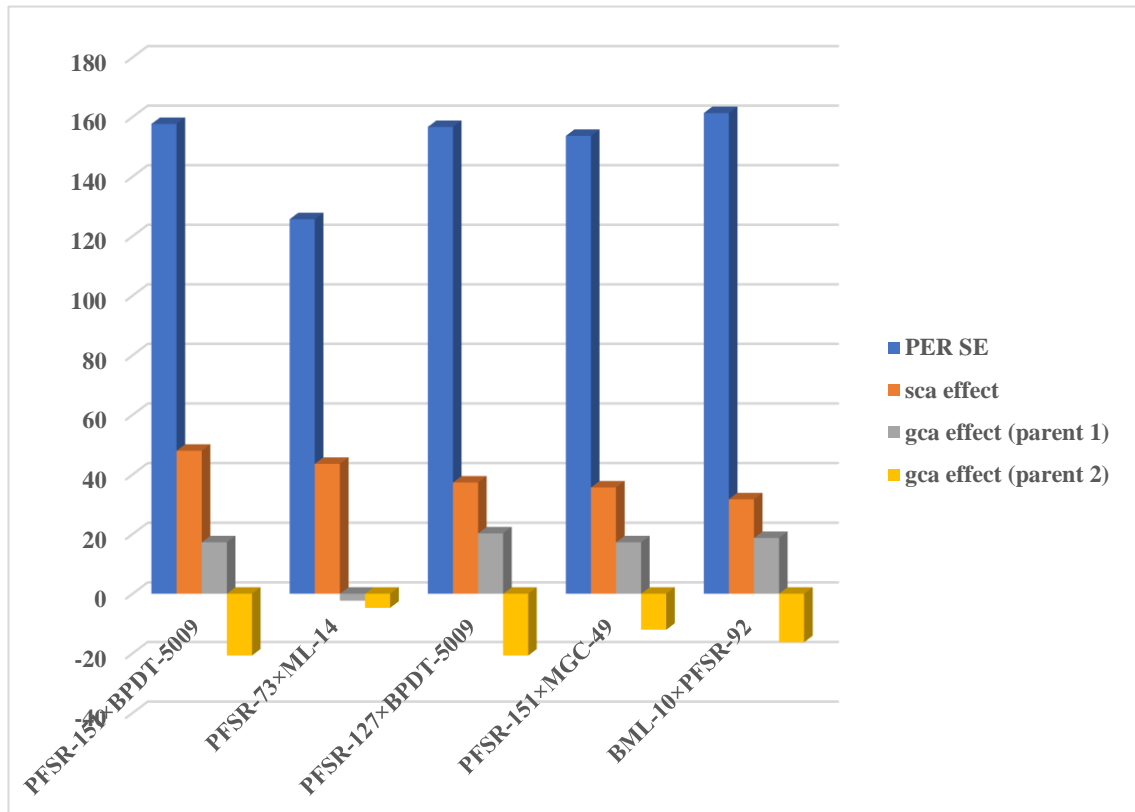


Figure 4.2. Top five hybrids identified based on high *sca* effects with *per se* performance and *gca* effects of parents for grain yield per plant.

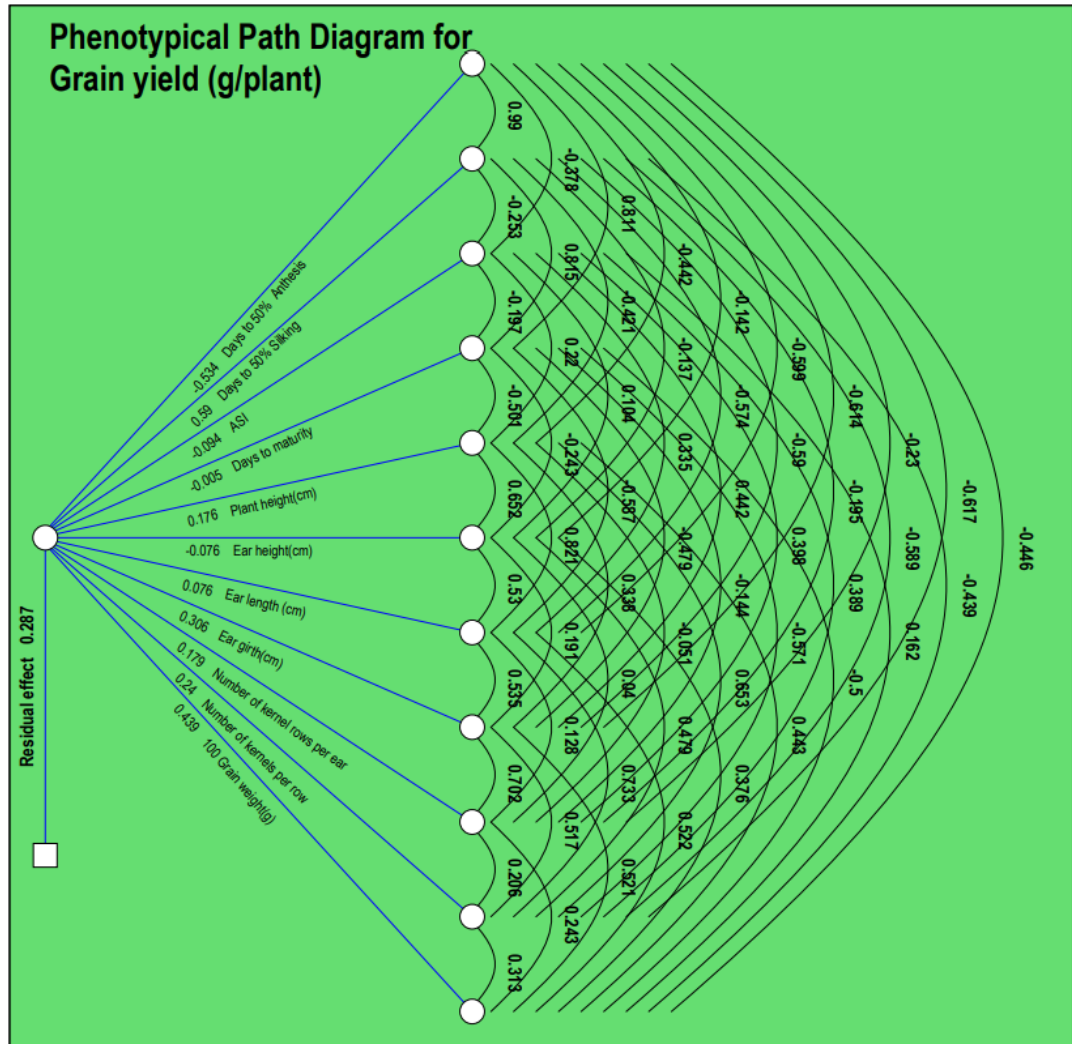


Figure 4.3. Phenotypic path diagram for grain yield per plant.

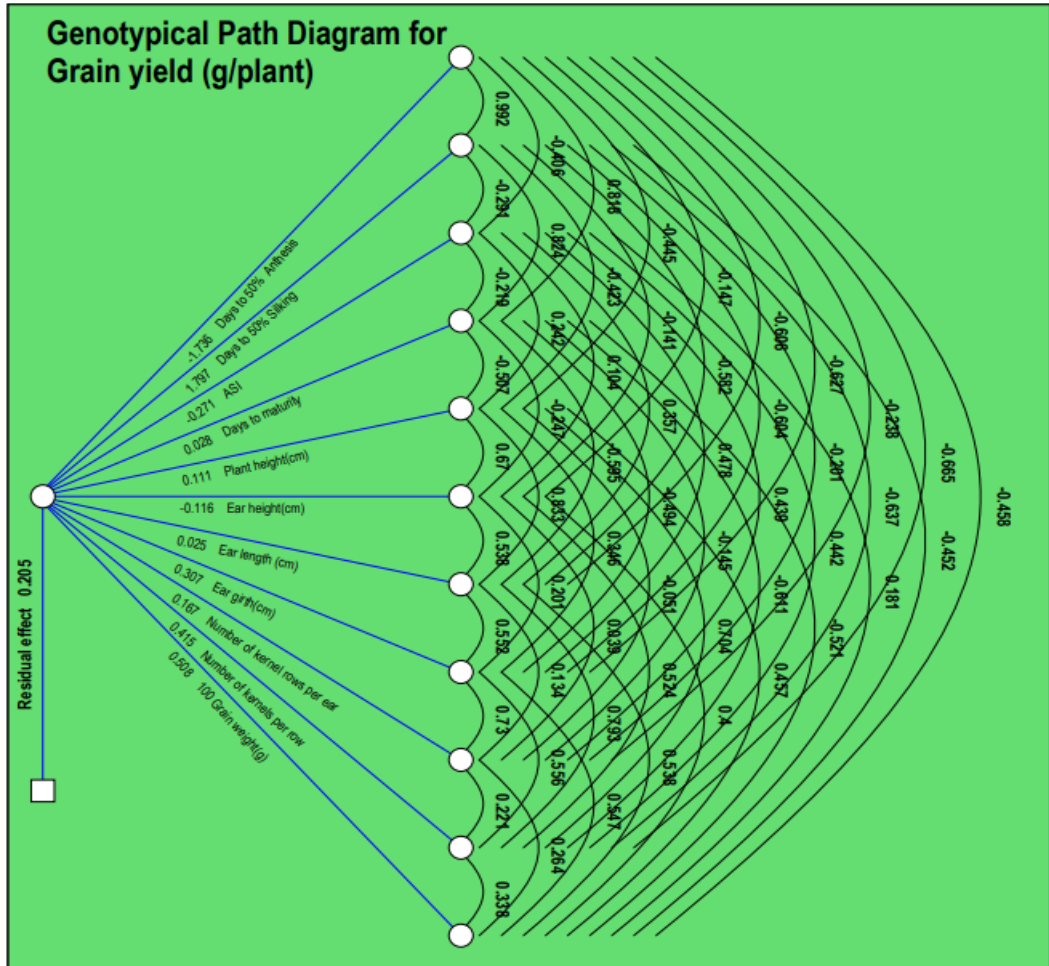


Figure 4.4. Genotypic path diagram for grain yield per plant.

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ABSTRACT

The present investigation “Genetic analysis for yield and evaluation of hybrids for charcoal rot resistance in Maize (*Zea mays* L.) was under taken with eight inbred lines.

The analysis of variance of treatments (genotypes) for yield and its component traits revealed that the mean sum of squares due to treatments were significant for all the characters. Indicating the presence of sufficient amount variation in the breeding material.

The inbred lines, BML-10 and PFSR-151 were found to be the earliest while the hybrids, BML-10×BPDT-5009, PFSR-73×ML-14, ML-14×PFSR-92 and MGC-49×PFSR-92 were the earliest. The hybrid, PFSR-73×PFSR-92 recorded the highest 100-kernel weight (35.53 g). The hybrid, PFSR-127×ML-14 recorded highest grain yield per plant. Nine out of 28 experimental hybrids recorded significantly superior grain yield per plant over the check, DHM-117.

Twenty-four (24) out of 28 hybrids were showed significantly negative standard heterosis for days to 50% anthesis which is desirable for the development of early maturing hybrids. Two hybrids recorded significantly positive standard heterosis for 100-kernel weight. Thirteen among the 28 hybrids recorded significantly positive standard heterosis for grain yield per plant.

The analysis of variance for combining ability revealed that the parents showed significant differences for all the characters under study. The crosses also exhibited significant differences implying the varied performance of cross-combinations. The parent vs hybrids also showed significance for all the characters except number of kernel rows per ear. These results revealed that there exists sufficient amount of variability in breeding material under study.

The estimates of combining ability revealed that mean SCA variance was greater in magnitude than GCA variance for all the characters indicating the predominant role of non-additive gene action.

Combining ability analysis revealed that the parents, PFSR-127, BML-10 and PFSR-151 were found to be good general combiners for grain yield per plant, days to 50% anthesis, days to 50% silking, days to maturity, ear length, ear girth, number of kernel rows per ear, number of kernels per row and 100-kernel weight. The hybrids, PFSR-151×BPDT-5009, PFSR-73×ML-14 and PFSR-127×BPDT-5009 were identified as specific combiners for earliness, yield and its attributing traits.

Based on *per se* performance, *sca* effects and standard heterosis, PFSR-127×ML-14, BML-10×PFSR-92 and PFSR-151×MGC-49 were identified as the best hybrids for yield and its attributing traits.

Correlation and path analysis revealed that days to 50% silking, 100-kernel weight, ear girth, number of kernels per row and number of kernel rows per ear were identified as important traits for the development of high yielding hybrids.

Among parents, MGC-49 and PFSR-92 were found stay green while, among the hybrids, PFSR-127×MGC-49, PFSR-151×MGC-49, PFSR-151×PFSR-92, BML-10×PFSR-92, MGC-49×ML-14 and MGC-49×PFSR-92 were identified exhibiting stay green character.

Screening for charcoal rot resistance indicated that 15 hybrids were resistant, five hybrids were moderately resistant, five hybrids were moderately susceptible and three hybrids recorded the highly susceptible reaction to charcoal rot.

However, three out of five superior hybrids (PFSR-127 × ML-14, PFSR-127 × MGC-49 and PFSR-151 × BPDT-5009) based on mean performance for grain yield per plant were found to be resistant to charcoal rot, one hybrid (PFSR-127× BPDT-5009) was found to be moderately resistant and the other hybrid (BML-10 × PFSR-92) showed moderately susceptible reaction to charcoal rot.

Among the superior hybrids that recorded high grain yield per plant and *sca* effects, it was found that two hybrids were resistant to charcoal rot one is non-stay green (PFSR-127 × ML-14) and the other is stay green type (PFSR-127 × MGC-49).

Chapter II

REVIEW OF LITERATURE

The present investigation was carried out to analyse the combining ability, heterosis, correlation, path analysis and screening for charcoal rot resistance in maize (*Zea mays* L.) hybrids. The information related to present research has been reviewed here under the following sections:

2.1 Combining ability and gene action

2.2 Heterosis

2.3 Correlation analysis

2.4 Path analysis

2.5 Screening for charcoal rot

2.1 Combining ability and gene action

The concept of combining ability as a determinant of gene action was put forth by Sprague and Tatum in 1942 in maize. Combining ability refers to capacity or ability of a genotype to transmit superior performance to its crosses. The value of an inbred line depends on its ability to produce superior hybrids in combination with other inbreds. In general, there are two types of combining ability *viz.*, General combining ability (GCA) and Specific combining ability (SCA).

General combining ability is “the average performance of a strain or genotype in series of hybrid combinations”. It is estimated from half-sib families. The GCA variance is primarily a function of the additive genetic variance, but if epistasis is present GCA will also include additive \times additive type of non-allelic interaction. The GCA has positive correlation with narrow sense heritability. It aids in the selection of suitable parents from hybridization.

Specific combining ability is “the performance of a parent in a specific cross”. The SCA variance is mainly a function of dominance variance, but if epistasis is present, it includes additive \times additive, additive \times dominance and dominance \times dominance types of non-allelic interactions. The *sca* is estimated from full sib families. It has positive correlation with heterosis or hybrid vigour. It helps in the identification of superior cross combinations for commercial exploitation of heterosis.

Griffing (1956a, 1956b) proposed a generalized concept and methodology for combining ability analysis of diallel crosses with two models and four methods.

(i) Combining ability studies based on Diallel mating design:

Diallel cross refers to mating of selected parents in all possible combinations and analysis of set of diallel crosses is called diallel analysis. Diallel cross is of two types, *viz.*, full diallel and half diallel.

Begum *et al.* (2018) evaluated 21 hybrids which were produced by crossing seven parents in half diallel mating design and concluded that the parent, CML-509 was identified as the good general combiner for days to 50% anthesis and days to 50% silking; CML-395 for ear length and grain yield and CML-498 for ear height, plant height and grain yield. The hybrids, CML376×CML-247, CML-498×CML-395 and CML-498×CML-376 recorded significantly positive *sca* effects for grain yield.

Issa *et al.* (2018) evaluated 20 hybrids which were developed by crossing five inbred lines in diallel mating design and revealed that the lines, TZEI-25 and TZEI-23 showed significantly positive *gca* effects for grain yield. The hybrid, TZEI-25×TZEI-13 exhibited the highest significant and positive *sca* effects for grain yield.

Karim *et al.* (2018) evaluated 21 hybrids which were generated by crossing seven inbred lines in half diallel mating design and revealed that the parents, CML285, CML431 and CML223 were the good general combiners for grain yield. The inbred line, CML223 was found good combiner for earliness. The crosses, CML429×CLG1837, CML429×CML431, CML285×CML451, CML285×CML223, CML285×CML551 and CML451×CML431 recorded significant and positive *sca* effects for grain yield.

Murtadha *et al.* (2018) conducted an experiment with 15 hybrids which were produced by crossing six inbred lines in half diallel mating design and revealed that the inbred line, KSU 6–47 showed significant *gca* effect for grain yield. The least significant negative *gca* effects for days to 50% tasselling showed by KSU 3–69. The hybrid, KSU 6–47 × KSU 3–69 exhibited the highest *sca* effect for 1000 kernel weight and grain yield.

Hussain *et al.* (2019) conducted an experiment by crossing six purelines in half diallel mating design and revealed that mean square of genotypes, general combining ability and specific combining ability were significant for all characters indicating that the traits were governed by both additive and non-additive action. The parents, ZP- 197 and Ik 58 were identified as good general combiners for days to 75% tasselling and silking, plant and ear height, number of rows per ear, leaf area, number of grains per row and 300 kernel weight.

Yu *et al.* (2020) evaluated 724 hybrids which were divided into 136 tropical diallel hybrids and 325 temperate diallel hybrids developed in Griffing IV and 263 temperate by tropical hybrids developed in NCD II. The 13 temperate inbred lines showed negative

gca effects for plant height and ear height whereas, HZ1 and Qi319 inbred lines exhibited positive effects for grain number per ear, hundred grain weight and grain yield per plant.

AL-Aaty (2021) revealed that the two maize inbred lines, G54 and OH40 were good combiners for plant height, ear height, number of ears per plant, ear length, ear girth, number of rows per ear, number of grains per row, number of grains per ear, 300 grain weight and grain yield per plant. The hybrids, ZP-607 × G549, DK × G105 and OH40 × ZM51 were found as good specific combiners for grain yield per plant.

Eisele *et al.* (2021) revealed that both *gca* and *sca* effects were significant for all traits. *gca* effect was more for days to anthesis, days to silking, plant height and ear height indicating that these traits were influenced by additive effects while the crosses, CD 303 × DKB 747 and AG 9090 × SG 6015 proved best for grain yield based on the *sca* effects.

El-Shahed *et al.* (2021) conducted combining ability studies in 28 hybrids which were produced by crossing eight yellow maize inbred lines in half diallel mating design. They reported that the inbred lines, Gm.6013 and Gm.636 were good general combiners for yield while, Gm.2032 for earliness. The hybrids, Gm.42 × Gm.6013, Gm.36 × Gm.40 and Gm.636 × Gm.6013 exhibited desirable SCA effects for earliness. The crosses, Gz.666 × Gm.40, Gm.42 × Gm.636, Gm.2032 × Gm.36 and Gm.36 × Gm.6013 had shown high *sca* effects for grain yield.

Mesekal *et al.* (2021) evaluated 15 hybrids by crossing six landraces of maize in half diallel mating design. The results indicated that mean squares due to *gca* and *sca* effect were significant for most of the traits. The landrace, Ring-8 was identified as the best combiner for most of the traits under study. The landrace, Sennar was identified as good general combiner for days to 50% anthesis and silking, number of ears per plant and grain yield. Whereas, Hegeri showed high *gca* effects for 50% silking, ear length, plant height and ear height. Among the crosses, Hegeri × Ahmar Mahali, Hegeri × Ring-8 and Sennar × Ahmar Balady showed high *sca* effects for grain yield.

Mousa *et al.* (2021) conducted an experiment with 21 hybrids and indicated that the inbred lines, Gz-8092, Gz-7253 and Gz-8093 were good general combiners for earliness, Tep 6240 for grain yield and SC 131 for days to 50% silking, ear length, ear girth, number of ears per plant and grain yield. The hybrid, Gz-8093 × SC131 showed the desired *sca* effects for all characters. Additive gene effects were found more important than non-additive gene effects in the inheritance of days to 50% silking, ear length, number of ears per plants and ear diameter whereas, non-additive gene effects were more important than additive for number of rows per ear, grain yield and number of kernels per row.

Yadav *et al.* (2021) concluded that the inbred lines, D2-2, TSK11-1 and CML-150 were identified as good general combiners for most of the traits. The hybrids, P5 × P3, P7 × P5, P4 × P3 and P3 × P1 exhibited positive significant *sca* effects for plant height, number of kernel rows per ear, number of kernels per row and cob length. The traits, days to 50% silking and days to maturity showed significantly negative *gca* effects whereas, number of kernel rows per ear, 100 grain weight and grain yield showed significantly positive *gca* effects.

Belay (2022) inferred that both additive and non-additive gene effects are important for the expression of all traits. The lines, L3, L5, L1, L7, L8 and L13 showed significantly positive *gca* effects for grain yield, implying that these inbreds have a higher frequency of grain yield-improving genes while inbred lines, L6, L7, L11, L15 L4 and L5 were identified as good combiners for early maturity.

Italia *et al.* (2022) evaluated 20 hybrids and reported the significant differences in all traits except for days to tasseling and number of kernels per row, days to silking and number of kernels per row. They also reported that both additive and non-additive gene actions are important in controlling grain yield and other agronomic traits. The parents, TZEI-68, SAMMAZ-15, TZEI-112, TZEI-29, SAMMAZ-45, SAMMAZ-33 and SAMMAZ-51 were identified as good general combiners for grain yield.

Patel (2022) studied 36 hybrids that were developed by crossing nine parents in half diallel mating design and reported *gca* effects were significant for all the traits except cob length and cob girth whereas, *sca* effects were significant for all the traits except anthesis-silking interval, cob length and cob girth. The parents, WNC 31702 (5.47) and WNC 40228 (6.17) were identified as good general combiners with significantly positive *gca* effects for kernel yield per plant. The hybrids, Z 485-50 × Z 485-11 (22.77), WNC 40228 × BLD - 105 (20.13) and WNC 40228 × Z 485-11 (17.47) were identified as good specific combiners for kernel yield per plant.

Peric *et al.* (2022) developed 21 hybrids by crossing seven maize inbred lines in half diallel mating design. Specific combining abilities (*sca*) effects for days to 50% flowering range from -0.78 (ZPL1 × ZPL2) to 2.06 (ZPL2 × ZPL4). Two hybrid combinations had negative values *sca* effects, while ten hybrid combinations showed significantly positive *sca* effects.

Sayed *et al.* (2022) studied 36 hybrids for combining ability that were produced through half diallel mating design. The parent, Sd-14 was identified as good general combiner for lower ear height, earliness and for the development of semi dwarf types, Sk-12 and Sk-9 were reported as good general combiners for grain yield and ear length.

Thirteen out of 36 hybrids showed significantly positive *sca* effects.

(ii) Combining ability studies based on Line×Tester mating design:

Line×Tester mating design is a modified form of a top cross used for measuring general and specific combining ability variances and effects in large number of germplasm lines at a time.

Gazala *et al.* (2017) conducted combining ability studies in 27 hybrids that were developed by crossing nine females with three males in NCD II mating design and concluded that four lines *viz.*, VL1018816, ZL134937, VL110232 and VL107578 exhibited negative and significant *gca* effects for days to anthesis and days to silking; whereas the lines, VL1110175 and ZL126643 showed positive and significant *gca* effects for grain yield and number of kernels per ear. The hybrid, VL107578 × VL1010877 exhibited desirable positive significant *sca* effects for plant height and grain yield.

Gami *et al.* (2018) estimated combining ability for yield and yield components in 40 hybrids which were generated by crossing 8 lines with 5 testers in line x tester mating design and concluded that the tester, BLD 47 and the line, Z 488-4 were identified as good general combiners for kernel yield. The hybrids, BLD 254 × BLD 47 and HYN-10-RN 235-270 × IC 328963 were identified as good specific combiners for grain yield.

Nandhitha *et al.* (2018) carried out an experiment to study combining ability in 50 hybrids which were developed by crossing ten lines with five testers in line × tester mating design and reported that the lines, N10-153-1-2, N10-65-3, N67 and the tester, UMI1210 were found to good general combiners for yield. The cross, N10-65-3 × E.No.8 was identified good specific combiner for grain yield.

Ola *et al.* (2018) carried out an experiment with 36 hybrids which were developed by crossing twelve inbred lines with three testers in line x tester mating design. From their studies they concluded that the inbred line, L10 had good general combining ability for ear girth, number of grain rows per ear, grain yield per plant while the tester, T3 was identified as the good general combiner for grain yield. The crosses, L12 × T3, L11 × T2, L7 × T1, L1 × T2 and L4 × T2 showed positive and significant *sca* effects for grain yield.

Rajesh *et al.* (2018) evaluated 45 hybrids that were generated by crossing 15 lines with 3 testers in line × tester design. They inferred that the lines, BM 1234, BM 3511-2, BM 5050 and BM 3521 A-2 were found to be good general combiners for grain yield and yield traits. The testers, BML7 and BML10 were found to be good general combiners for grain yield and yield attributing traits. The hybrids, BM 3511-2 × BML 7, BM 5050 × BML 10, BM 1234 × BML 10, BM 1234 × BML 13 and BM 5050 × BML 7 were found to be good specific combiners.

Sandesh *et al.* (2018) conducted combining ability studies in 22 hybrids which were developed by Line \times Tester mating design and reported that the inbred lines N 14, N 107, UMI 1200-7-26-1-6-1 and N 285 were the best general combiners for grain yield. The hybrid, N 117 \times UMI 1200-7-26-1-6-1 exhibited negative significant *sca* effects for days to 50% anthesis and days to 50% silking among the 22 experimental hybrids.

Sun *et al.* (2018) evaluated 64 hybrids which were developed by crossing sixteen USA inbred lines with four Chinese maize inbred lines in NCII design and revealed that the inbred lines, BLA, 6F629, NL001, Lp215D, RS710, PHP76, FBLA and PHJ89 were found as good general combiners for days to silking and days to maturity. The inbred lines, LH191, LH192, and NL001 had significant positive *gca* effects for number of rows per ear. sixteen out of 64 hybrids showed positive and significant *sca* effects for yield while, 18 hybrids had negative *sca* effects for yield.

Tulu *et al.* (2018) studied combining ability of QPM inbred lines for grain yield and yield attributing traits and revealed that the inbred lines, L3 and L1 showed significantly positive *gca* effects and they were found as the best combiners for grain yield while, L1 and L9 inbred lines were good combiners for earliness. They also reported that hybrids, L16 \times T2, L9 \times T2, L20 \times T2, L22 \times T2 and L23 \times T1 recorded the highest positive but non-significant *sca* effects for grain yield.

Aboyousef (2019) conducted an experiment to evaluate 34 hybrids which were produced by seventeen yellow inbred lines with two testers in Line \times Tester mating design and reported that the inbred lines, Gm45, Gm23, Gm46 and Gm53 were found to be good general combiners for grain yield while, the hybrids, Gm46 \times Gm1021 found to be good specific combiners for grain yield.

Ambikabathy *et al.* (2019) developed 22 hybrids by crossing two lines with eleven testers in Line \times Tester mating design. The parents, VIM 58, VIM 61 and UMI 1200-7-25-1-6-1 were identified as the best general combiners for grain yield and yield related characters. The crosses, UMI 1200-7-25-1-6-1 \times UMI 61, UMI 1200-7-25-1-6-1 \times VIM 58 and UMI 1200-4-26-9-5-1 \times UMI 285 were found to be good specific combiners for cob weight.

Annor *et al.* (2019) conducted an experiment with 205 test crosses to study the combining ability under stressed and optimal conditions and concluded that inheritance of grain yield under optimal conditions was regulated by additive gene effects while, grain yield under stress conditions regulated by non-additive gene effects. The inbred lines TZEI 465, TZEI 462, TZEI 175 and TZEI 486 showed positive and significant *gca* effects for grain yield under low nitrogen.

Darshan and Marker (2019) evaluated 12 hybrids which were developed by crossing six quality protein maize inbred lines with two quality protein maize testers and estimated that SCA variances were more than GCA variances for most of the characters under study. The inbred lines, DMR-N21 and LM-13 were identified as good combiners for yield and yield attributing traits. The crosses, LM-13 × IC32809, DMR-N21 × IC-32809 and LM-13 × IC-31899 recorded high specific combining ability effects for grain yield and its related traits.

Diribu *et al.* (2019) carried out an experiment to evaluate 48 hybrids which were generated in Line x tester mating design. The lines, L5 and L6 showed positive and significant *gca* effects for grain yield. The inbred line, L6 showed positive *gca* effects for other yield attributing traits that included number of rows per ear, number of ears per plant, number of kernels per row and ear girth. The crosses, L8×T4, L7×T2 and L9×T1 recorded significant and positive *sca* effects for grain yield.

Kumar *et al.* (2019) evaluated sixty crosses that were developed by Line × Tester design. The inbred line, TNAU/CBE-83 was recorded as good general combiner for grain yield, biological yield, protein content and cob length. The tester, BAJIM-08-26 was identified as good general combiner for 1000 grain weight while, the tester, BAJIM-08-27 recorded the best general combining ability for grain yield, harvest index, cob girth, plant height and cob placement. Based on the *sca* effects they reported that the hybrids, TNAU/CBE-83×BAJIM 08-27, CML-292× BAJIM 08-27 and HKI-1040-7× BAJIM 08-27 were good specific combiners for yield and earliness.

Shehzad *et al.* (2019) conducted an experiment to evaluate eight hybrids which were generated by crossing four elite inbred lines and two testers and revealed that the lines, DRF-25, P-222 and PLP-23 were found to be good general combiners while hybrids, P-222 × Y-27, DRF-25 × Y-27 and DRF-25 × Y-36 were identified as good specific combiners.

Tesfaye *et al.* (2019) conducted combining ability studies for yield and yield attributing traits in 48 hybrids that were generated by crossing 24 lines with two testers in line × tester mating design. The results revealed that the parents, L2, L1, L20 and L9 were the best general combiners for grain yield. The crosses, L3 × T1 and L7 × T2 exhibited significantly positive *sca* effects.

Abd-Elaziz *et al.* (2021) evaluated 24 hybrids which were developed by Line × Tester mating design. It was found that the inbred lines, L-6, L-5, L-12, L-8 and the tester, Gz-666 were found to be the good combiners for earliness due to their negative *gca* effect. Based on the specific combining ability, the hybrids, L-11×Gz-658 and L-5×Gz-666 were

found best for grain yield. They also revealed that both additive and non-additive gene effects played an important role in inheritance of plant height, ear height and days to 50% silking.

El-Gazzar (2021) evaluated 50 crosses were developed by Line \times Tester mating design and reported that the inbred line, Sk5008/27 had desirable *gca* effects for earliness; Sk5010/54 for number of ears per plant; Sk5010/57 for ear position and Sk5008/31 for grain yield. Based on the specific combining ability studies the best hybrids identified were Sk5007/27 \times Sk11 for earliness; Sk5010/58 \times Sk11 for number of ears per plant; Sk5010/44 \times Sk11 for ear position and Sk5008/31 \times Gz658 for grain yield.

Suresh *et al.* (2021) evaluated 64 hybrids which were produced by crossing 32 inbred lines with 2 testers in line \times tester mating design and concluded that the inbred lines, GPM-688, GPM-759, GPM-648, CI-4, GPM-4, GPM-38 and GPM-608 were identified as good general combiners for days to 50% silking and days to 50% tasseling while, GPM-606, GPM-27, GPM-30 and GPM-18 were found to be the good general combiners for grain yield. The hybrids, GH-1813 and GH-1834 showed significant *sca* effects for number of kernels per rows, ear girth, ear length, GH-1852 and GH-1819 for 100 grain weight while, GH-1852, GH-1829, GH-1862 and GH-1843 for grain yield.

2.2 Heterosis

Heterosis is a fundamental method for improving crop productivity through the production of F_1 hybrids. Heterosis is defined as superiority of F_1 hybrids in one or more characters over its parents. It provides superiority of hybrids in adaptation, yield, quality, disease resistance, maturity and general vigour over its parents. Heterosis exploited more in cross pollinated crops than in self-pollinated crops. The negative and positive heterosis is useful for crop improvement. Heterosis is estimated in three different ways, viz., average heterosis, heterobeltiosis and standard heterosis. Average heterosis is estimated over mid-parent *i.e.*, mean value. Heterobeltiosis is estimated over the superior or better parent while, Standard heterosis is estimated over the commercial check. Standard heterosis is of direct practical relevance in plant breeding.

Over dominance hypothesis of heterosis was proposed by East and Shull in 1908. According this theory heterosis is the result of superiority of heterozygote over its both homozygous parents. Superiority of heterozygote may arise due to production of superior hybrid substance in heterozygote and cumulative action of divergent alleles.

Gazala *et al.* (2017) carried out an experiment to study heterosis in 27 hybrids which were produced in NCD II design by using 9 females and 3 males. The standard heterosis values ranged from -50 % to 75 % for anthesis silking interval, -25.62 % to

20.34 % for plant height and -13.01 % to 67.13 % for grain yield per plant.

Sharma *et al.* (2017) conducted an experiment to study heterosis for grain yield and quality traits in 63 hybrids which were developed by crossing 9 inbred lines with 7 testers in line x tester mating design and concluded that the better parent heterosis values ranged from 16.24 % to 128.73 % for grain yield, -17.82 % to -1.79 % for days to 50% tasseling and -13.22 % to 2.38 % for days to 50% silking.

Gami *et al.* (2018) estimated heterosis for yield and yield attributing traits in 40 hybrids which were developed by crossing 8 lines with 5 testers in line x tester mating design and revealed that the hybrid, BLD 266 × BLD 47 showed heterobeltiosis for plant height, ear height, ear girth, 100-kernel weight and grain yield per plant and the hybrids, BLD 206 × BLD 328, BLD 266 × BLD 328 showed heterobeltiosis for days to silking and days to tasseling.

Karim *et al.* (2018) carried out an experiment with seven inbred lines in half diallel mating design and reported that the heterosis for grain yield ranged from -65.83% to 21.26%, for days to 50% silking, the values ranged from -17.85% to 8.22%; for plant height values varied from -43.73% to 60.74% and for ear height the values ranged from -58.86% to 69.58%.

Nandhitha *et al.* (2018) conducted an experiment to study heterosis in 50 hybrids which were generated by crossing ten lines with five testers in line x tester mating design and concluded that most of crosses exhibited significantly negative standard heterosis for anthesis silking interval. The hybrids, N44 × UMI 1221 and E.No.15 × UMI 1210 showed positive significant standard heterosis for cob length and the hybrid, N10-65-3×E.No.8 showed significantly positive standard heterosis for grain yield.

Reddy *et al.* (2018) conducted an experiment to study heterosis for grain yield in 30 hybrids and concluded that the mid-parent heterosis ranged from -11.82% to 2.58% for days to tasseling, -58.82% to 31.25% for days to 50% silking and -4.55% to 7.63% for days to maturity, respectively. Relative heterosis values ranged from -54.84% to 40.74% for anthesis silking interval.

Shrestha *et al.* (2018) estimated heterosis in maize hybrids and concluded that standard heterosis for grain yield ranged from -0.03% to 73.4%. The hybrids, RL-165/RL-17 (in Test Cross) and RL-36/RL-197, RL-13-1/NML-1, RML-19/ NML-2 (in Diallel Cross) recorded more than 15% standard heterosis for grain yield.

Hussain *et al.* (2019) conducted an experiment to study heterosis in 15 hybrids which were produced by crossing six inbred lines in half diallel mating design and revealed that the heterosis for kernel yield ranged from -117.46% to 65.63%. Seven out

15 hybrids showed positive and significant heterosis for kernel yield.

Kanchavo *et al.* (2020) conducted an experiment to study the heterosis in 724 hybrids which were developed by 28 temperate and 23 tropical maize inbred lines and revealed higher heterosis except for the traits, plant height and hundred grain weight.

Upreti *et al.* (2020) studied heterosis in maize hybrids and reported that the mid-parent heterosis ranged from -42.05% to 13.85% for anthesis silking interval, -12.48% to -20.06% , -5.81% to 39.54% and 134.83% to 466.91% values for days to maturity, plant height and grain yield, respectively. The mid and better parent heterosis was significant and positive for ear length, ear girth, number of kernel rows per ear and number of kernels per row.

Abdulazeez *et al.* (2021) studied heterosis for yield and yield related traits in 21 hybrids which were generated by crossing seven inbred lines with three testers in line x tester mating design and estimated that mid-parent heterosis for grain yield ranged from 4.89% to 103.73% . They reported that 8 hybrids, L1×T1, L2×T2, L1×T2, L5×T2, L5×T3, L6×T2 and L5×T1 showed positive and significant heterosis for grain yield.

Agarwal *et al.* (2021) evaluated 28 hybrids which were generated by crossing eight inbred lines in half diallel mating design and revealed that the average heterosis for days to 50% anthesis and days to 50% silking ranged from -12.579% to 0.935% and -13.07% to 0.606% respectively. The hybrid, DQL 2159 (Q3) × 70160 (Q5) showed positive and significant average heterosis and heterobeltiosis for grain yield.

Chaurasia *et al.* (2021) concluded that the cross, P5 x P7 had positive and significant standard heterosis for 1000-grain weight and grain yield per plant and the hybrids, P3×P4, P2×P7, P2×P3 and P3×P7 showed negative significant heterosis for plant height. Among all the hybrids except P4×P6 showed significantly negative standard heterosis for days to 50% silking and days to 50% tasseling.

EI-Zaher (2021) estimated standard heterosis and revealed that the hybrids, P5 × P7, P6 × P7 and P5 × P6 showed significantly negative standard heterosis for silking and tasseling. The hybrids, P2 × P6, P4 × P6, P1 × P6 and P1 × P2 exhibited significantly negative standard heterosis among the tested hybrids for plant height and ear height.

Gemechu *et al.* (2021) studied 26 crosses which were developed by crossing 13 inbred lines and 2 testers in line x tester analysis. The highest positive significant mid-parent heterosis was reported for L4 × T2 (616.49%) followed by L10 × T2 (553.46%), L12 × T2 (436.3%) and L1 × T2 (394.86%) for grain yield, while the cross, L6 × T2 (164.92%) identified with the lowest positive and significant mid-parent heterosis. The cross, L10 XT2 (334.21%) recorded positive and significant heterosis over the standard

check for grain yield.

Habiba *et al.* (2021) studied heterosis for yield and its related traits in six hybrids and estimated that the hybrid, P2 x P5 showed the highest significantly positive mid-parent heterosis for plant height and number of leaves per plant. The better parent heterosis for plant height ranged from 41.3% to 52.2%.

Nyombayire *et al.* (2021) estimated heterosis in 45 hybrids which were generated by crossing 10 inbred lines in half diallel mating design and reported that mid-parent heterosis values ranged from 36.4 % to 267.7% for grain yield while, better parent heterosis ranged from 33.2% to 236% for grain yield.

Pawar *et al.* (2021) estimated heterosis for yield and its related traits in 56 hybrids and concluded that the standard heterosis ranged from 5.52 % to 37.42 %; mid-parent heterosis ranged from -10.96 % to 10.12 % while, better parent heterosis ranged from -8.61 % to 18.89 % for days to 50% silking. Mid, better and standard heterosis values for days to 50% tasseling ranged from -10.95 % to 10.43 %, - 9.85 % to 18.39 % and - 12.11 % to 16.32 % respectively. The values for mid, better and standard heterosis for grain yield varied from -35.39 % to 130.70 %, -51.76 % to 112.99 % and -65.12% to 38.35%, respectively.

Qin *et al.* (2021) estimated heterosis for yield and its related traits and revealed that mid-parent heterosis ranged from 7.03% to 216.55% and heterobeltiosis ranged from 6.57% to 68.41% for yield.

Ramadan *et al.* (2021) evaluated 20 hybrids for yield and its related traits. The results revealed that the cross, ART-B-17 x Zm-5 recorded the highest value of heterosis for grain yield per plant (47.48%).

Suresh *et al.* (2021) studied 64 hybrids which were produced by crossing 32 inbred lines and 2 testers in line x tester mating design and revealed that the hybrid, GH-1857 showed significant and negative heterosis for days to 50% tasselling and days to 50% silking. Thirteen (13) out of 64 hybrids showed positive significant heterosis for plant height and 22 hybrids showed positive significant heterosis for ear height.

Tello (2021) evaluated 64 hybrids which were developed by crossing 32 lines with 2 testers and inferred that the highest standard heterosis values reported in the cross, L17xT1 (61.75%) and (41.46%) over the two different checks. The characters, ear length, ear girth, number of kernel rows per ear, number of kernels per row, ear per plant and hundred grain weight showed positive standard heterosis.

Tesfaye and Sime (2021) carried out an experiment to study heterotic pattern in 48 crosses that were developed by Line x Tester mating design. The mid-parent heterosis

for number of kernels row ranged from 21.4 % to 68.4% and for better parent these values ranged from 13.6% to 57.4%. Mid and better parent heterosis values for 1000 kernel weight ranged from -101.1 % to 47.4%, -35.4 % to 21.3%, respectively while, for days to maturity the values ranged from -5 % to 13.9% and -5 % to 105%, respectively.

Tulu *et al.* (2021) evaluated 48 crosses produced by 12 inbred lines and 4 testers in line x tester mating design and reported that standard heterosis ranged from - 4.08% (L2 ×T3) to 6.95% (L2 × T4) and - 2.91% (L2 ×T3) to 8.25% (L2×T4) over standard checks, Jibat and Kolba, respectively for days to 50% silking (DS). Standard heterosis (SH) ranged from -66.17% (L8 ×T1) to 6.86% (L11 × T4) over Kolba and -64.39 % (L8 ×T1) to 12.49% (L11×T4) over the other check, Jibat for grain yield.

Viqar-Un-Nisa *et al.* (2021) reported 22.3% heterosis for CML-470 × KDM-914 A to -3.5% for KDM-916A × V-335 for 100- grain weight while, it ranged from 61.9% (CML-470 ×× K DM-914 A) to 9.3% (KDM916A x V-335) for grain yield per plant.

Yadav and Gangwar (2021) conducted heterotic studies in 21 hybrids which were developed through half diallel mating design and revealed that the crosses, P3 × P4, P5 × P7, P2 × P5, P1 × P2, P1 × P6, P2 × P7 and P3 × P5 showed desirable heterosis that ranged from -14.69 % to 49.55 % for grain yield.

Mideksa *et al.* (2022) carried out an experiment to estimate heterosis for yield and its attributing traits in 36 hybrids and reported that mid-parent heterosis varied from 111.2% to 386.6% for grain yield while, the better parent heterosis values ranged from 72.2% to 288.9%.

2.3 Correlation analysis

Correlation is measure of degree and direction of association between two or more variables. The concept of correlation was proposed by Sir Francis Galton in 1894. Grain yield is complex trait which depends on the number of yield attributing characters. The observable association between two variables is called phenotypic correlation. It is the resultant of both genotypic and environmental effects which generally varies under varied environmental conditions. The heritable or inherent association between two variables is genotypic correlation. Genotypic correlation is definitely more stable and play an important role in genetic improvement of one character by selecting other character or set of characters which are genetically linked. Association between the variables forms the basis of selection index which provides the useful information to the plant breeder in crop improvement programmes.

Ghimire and Timsina (2015) estimated correlation in fourteen maize genotypes and reported number of kernels per cob, plant height, ear girth, ear height, number of

kernels per row showed significantly positive correlation with grain yield. Grain yield showed significantly negative correlation with days to 50% silking and days to 50% anthesis and days to maturity.

Raut *et al.* (2017) carried out an experiment to study the correlation in fourteen genotypes and revealed that number of kernels per row (0.709), number of kernel rows per ear (0.700) had positive significant correlation with grain yield. Ear girth (0.587) and number of kernel rows per ear showed high positive significant correlation with grain yield.

Kandel *et al.* (2018) evaluated 20 inbred lines in alpha lattice design to study correlation and reported that ear length (0.857), ear girth (0.896), number of kernels per row (0.917), number of kernel rows per ear (0.941), shelling percentage (0.917), silk receptivity (0.980) had significantly positive correlation with grain yield while, grain yield had significantly negative correlation with anthesis silking interval (-0.726) and leaf area index (-0.692).

Ahmed *et al.* (2020) studied correlation for yield and its attributing traits in 32 exotic and local hybrids and revealed that the traits ear girth (0.508), ear length (0.388), number of kernels per ear (0.546) and number of kernel rows per ear (0.551) showed significantly positive correlation with yield. Days to 50% silking registered significantly negative correlation with ear girth, number of kernel rows per ear and number of kernels per row. Days to maturity showed significantly negative correlation with ear height. They also reported that plant height showed significantly positive correlation with ear height. Ear height exhibited significantly positive correlation with days to 50% silking, days to 50% anthesis and plant height while, ear length and ear girth exerted significantly positive correlation with number of kernel rows per ear and number of kernels per row. In addition, number of kernel rows per ear showed significantly positive correlation with days to maturity, ear length, ear girth and number of kernels per row. Finally, number of kernels per row showed significantly positive correlation with ear length, days to maturity, ear girth and number of kernel rows per ear.

Aman *et al.* (2020) reported that plant height, number of kernel rows per ear, ear height and 100 grain weight had significantly positive correlation with grain yield.

Chaurasia *et al.* (2020) studied 31 hybrids to study association between different variables that influence yield which were produced by crossing seven inbred lines in half diallel mating design. The results revealed that ear height (0.724), plant height (0.789), ear girth (0.833), ear length (0.875), 1000-grain weight (0.324) and grains per plant (0.898) showed positive and significant correlation with grain yield while the characters

like days to silking, days to anthesis, anthesis silking interval showed significantly negative correlation with grain yield. However, number of kernels per row exhibited significantly positive correlation with plant height, ear height, ear length, ear girth and number of kernels per row. They also concluded that number of kernel rows per ear recorded significantly positive correlation with ear height, ear length, ear girth and plant height while, ear girth showed positive and significant correlation with plant height, ear height and ear length. Finally, they inferred that ear length showed significantly positive correlation with plant height and ear height while, ear height showed significantly positive correlation with plant height.

Chavan *et al.* (2020) estimated correlation in 25 sweet corn inbred lines and reported that ear length (0.7153), ear height (0.4062), number of kernels per row (0.0393), number of kernel rows per ear (0.699) and cob weight without husk showed significantly positive correlation with cob weight with husk.

Dash *et al.* (2020) conducted an experiment to study the correlation for yield and yield attributing traits and revealed that ear height (0.395), ear girth (0.574), plant height (0.558), number of kernel rows per ear (0.272), 100-grain weight (0.459) and number of kernels per row (0.701) exhibited positive and significant correlation with grain yield.

Devasree *et al.* (2020) conducted correlation studies in 60 maize hybrids and revealed that ear height (0.841), ear weight (0.994), plant height (0.882), 100-grain weight (0.830) and number of kernels per rows (0.897) showed significantly positive correlation with grain yield.

Kumawat *et al.* (2020) carried out character association studies in 55 maize hybrids and reported that number of kernel rows per ear (0.5255), number of kernels per row (0.6623), ear length (0.6526), plant height (0.3855), ear height (0.3037), ears per plant (0.3107) and field weight (0.6579) showed significantly positive correlation with yield per plant.

Singh *et al.* (2020) carried out correlation studies in 25 genotypes and estimated that grain yield had positive and significant association with ear height (0.1544), plant height (0.2846), ear length (0.5434), ear girth (0.3719), number of kernels per row (0.1392) and number of kernel rows per ear (0.4624). The trait, ear height showed significantly positive correlation with number of kernels per row, plant height showed significantly positive association with ear height while, ear length recorded significantly positive association with ear girth and number of kernels per row, ear girth showed significantly positive correlation with number of kernels per row while, number of kernels per ear showed significantly positive association with number of kernels per row.

Verma *et al.* (2020) conducted correlation studies in 30 inbred lines and reported that number of seeds per cob (0.89), seed yield per cob, biological yield per plant (0.97) and shelling percentage (0.31) registered positive and significant correlation with seed yield per plant. Days to 50% silking showed positive and significant association with days to 50% tasseling. Plant height exhibited positive and significant correlation with number of kernel rows per cob, biological yield per plant.

Damtie *et al.* (2021) reported that ear height, number of ears and plant height had positive correlation with grain yield. They also revealed that plant height had significantly positive correlation with ear height, days to 50% silking while, days to 50% anthesis had significantly negative correlation with grain yield.

Gokulakrishnan *et al.* (2021) revealed that ear height (0.331), plant height (0.274), ear length (0.644), 100-grain weight (0.347) and biological yield per plant (0.975) had the highest positive correlation with grain yield per plant in 20 maize inbred lines.

Hadi *et al.* (2021) evaluated 30 three-way maize crosses and reported that grain yield exhibited significantly positive correlation with number of kernels rows per ear, number of kernels per row, ear length, leaves number and leaf area.

Ramesh Kanna *et al.* (2021) conducted correlation studies in nine genotypes and revealed that grain yield per plant had significantly positive correlation with days to 50% anthesis (0.765), ear height (0.519), days to 50% silking (0.764), days to 100% dry husk (0.092), number of kernels per row and leaf area.

Khan and Mahmud (2021) studied 35 genotypes and reported that grain yield per plant had positive and significant correlation with ear length (0.956), plant height (0.774), number of kernels per row (0.703) and 100 grain weight (0.365).

Krishna *et al.* (2021) reported that grain yield showed positive and significant correlation with ear height (0.97), plant height (0.03), ear length (0.91), ear girth (0.98), number of kernels per row (0.63), number kernel rows per ear (0.87) and 1000 grain weight (0.90). Number of kernel rows per ear showed significantly positive correlation with number of kernels per row and 100-grain weight.

Jagadev *et al.* (2021) carried out correlation studies in 50 quality protein maize inbred lines and concluded that grain yield had positive and significant correlation with plant height (0.347), ear height (0.293), leaf length (0.347), leaf breadth (0.380), 100-grain weight (0.376) and number of kernels per row (0.502).

Lenka and Tripathy (2021) carried out character association studies in 49 maize inbred lines and reported that grain yield had positive correlation with plant height (0.646), ear length (0.632) and number of kernels per row (0.589).

Magar *et al.* (2021) estimated correlation for growth and yield and reported that grain yield had significantly positive correlation with ear length, ear girth, number of rows per ear and test weight.

Shahrokhi *et al.* (2021) conducted an experiment to study the correlation in 24 super sweet maize inbred lines under normal and drought conditions. They reported that grain yield had significantly positive correlation with ear girth, number of kernel rows per ear, number of kernels per row and stem diameter in normal conditions while, grain yield had significantly positive correlation with plant height and number of kernel rows per ear under drought conditions.

Shrestha *et al.* (2021) carried out correlation studies among 16 maize hybrids and revealed that days to 50% tasseling (0.41), days to 50% anthesis (0.39), ear girth (0.49), number of kernel rows per ear (0.38) and plant height (0.37) showed significantly positive correlation with grain yield.

Yahaya *et al.* (2021) conducted correlation studies and reported that grain yield exhibited positive correlation with ear length (0.727), plant height (0.907), ear girth (0.687) and 1000-grain weight (0.758).

Gautham *et al.* (2022) reported that days to tassel initiation had significantly positive correlation with days to anthesis, days to silking and days to maturity. They reported that the traits, ear length and number of kernels per row recorded positive and significant correlation with grain yield.

Sayed *et al.* (2022) carried out an experiment to evaluate 36 hybrids which were developed by crossing nine inbred lines in half diallel mating design and revealed that grain yield had significantly positive correlation with ear height (0.650) and plant height (0.739).

2.4 Path analysis

Path analysis is a standardized partial regression coefficient which splits the correlation coefficient into the measures of direct and indirect effects and also direct and indirect contribution of each independent variable on the dependent variable. Path analysis reveals whether the association of independent characters on dependent character is due to their direct effects or the consequence of their indirect effects through other component characters.

The concept of path coefficient analysis was originally developed by Wright in 1921, but this technique was first used for plant selection by Dewey and Lu (1959) in crested cross.

Matin *et al.* (2017) conducted the experiment and revealed that the characters like anthesis silking interval, ear girth, ear length and plant height showed direct positive effect on yield whereas, the traits like days to 50% silking, days to 50% tasseling, days to maturity and ear height showed negative indirect effect on yield. They also revealed that days to 50% silking showed negative indirect effect on grain yield through anthesis silking interval and ear girth while, days to maturity registered negative indirect effects on grain yield through days to 50% silking.

Ahmed *et al.* (2020) indicated that number of kernels per ear and days to tasseling had the highest positive direct effect on the yield whereas, ear height and days to silking showed the highest direct negative effects on yield.

Chaurasia *et al.* (2020) conducted an experiment to study path analysis for yield and yield components in 31 hybrids which were developed by crossing seven inbred lines in half diallel mating design and revealed that days to 50% silking, ear height, ear length, grains per plant, 1000-grain weight, ear girth and number of kernel rows per ear exhibited positive direct effects on grain yield.

Chavan *et al.* (2020) reported that days to 50% silking registered direct positive effect on cob weight with husk followed by plant height, cob weight without husk and number of kernel rows per ear had direct effect on cob weight with husk while, ear length, days to 50% tasseling, ear girth, ear height and number of kernel rows per plant had direct negative effects on cob weight with husk.

Dash *et al.* (2020) carried out an experiment and concluded that ear height, plant height, 100 grain weight and number of rows per ear had direct positive effect on grain yield per plant whereas anthesis silking interval had direct negative effect on grain yield per plant.

Kumawat *et al.* (2020) conducted path analysis studies in 55 maize hybrids and revealed that ear length, number of kernels per row and number of kernel rows per ear had the highest direct positive effect on yield per plant.

Shikha *et al.* (2020) carried out path analysis studies in 49 genotypes and revealed that ear width, green fodder weight/plot, plant height, days to silking, number of kernels per row and ear length registered the highest direct positive effect on cob yield.

Singh *et al.* (2020) conducted path analysis experiment in 25 genotypes. The results revealed that the traits ear length, days to 75 % brown husk, days to 75% tasseling, ear girth and ear height showed the highest direct positive effect on grain yield.

Verma *et al.* (2020) studied 30 maize inbred lines and reported that days to 50% tasseling, days to 50% silking, ear weight, ear length, 100-seed weight, number of seed

per ear, seed yield per ear, number of ears per plant had positive direct effect on the seed yield per plant.

Atiq *et al.* (2021) reported that days to silking, ear height, plant height, number of kernels per row, number of kernel rows per ear, 1000-grain weight had positive direct effects on grain yield per plant while, days to tasseling showed positive indirect effect through plant height, number of kernel rows per ear, number of kernels per row, 100-grain weight, ear height on grain yield per plant. They also revealed that ear length exhibited positive indirect effect on grain yield through ear height, ear girth, number of kernel rows per ear, number of kernels per row, plant height and 100-grain weight. Finally, they reported that ear girth registered indirect positive effect on grain yield through plant height, ear height and number of kernels per row.

Damtie *et al.* (2021) conducted path analysis studies among 23 maize inbred lines and reported that days to 50% silking registered negative direct effect on grain yield while, plant height had desirable indirect effect on grain yield through ear weight.

Gokulakrishnan *et al.* (2021) conducted path analysis studies in 20 maize inbred lines and reported that biological yield per plant, ear height, ear length, ear girth, harvest index had positive direct effects on grain yield per plant.

Hadi *et al.* (2021) carried out path coefficient analysis in 30 three-way crosses. They revealed that number of kernel rows per ear, days to silking and leaf number showed direct positive effects on grain yield.

Jagadev *et al.* (2021) carried out an experiment to study path analysis in 50 maize inbred lines and revealed that days to 50% tasseling, number of kernel rows per ear, number of kernels per row and number of kernels per ear had direct positive effects on grain yield.

Krishna *et al.* (2021) conducted path coefficient studies in 39 maize hybrids that were generated by line x tester mating design and revealed that days to 50% silking, ear height, ear girth, ear length, number of kernels per row, number of kernel rows per ear and 100-grain weight had the highest positive direct effects on grain yield. They also revealed that plant height had indirect positive effect on grain yield through ear length, ear girth, ear height, number kernels per row and 100-grain weight. Finally, they concluded that ear height showed indirect positive contribution on grain yield via days to 50% anthesis and anthesis silking interval.

Muliadi *et al.* (2021) reported that plant height, ear girth, ear length, shelling percentage and days to 50% silking had direct positive effects on grain yield. Where, ear length and days to 50% anthesis showed negative direct effects on grain yield.

Ramesh Kanna *et al.* (2021) carried out an experiment to study path analysis among maize genotypes and reported that days to 50% silking, plant height, ear girth, ears per plant, days to 100% dry husk and harvest index showed direct positive effects on grain yield whereas, ear height and days to 50% anthesis had direct negative effects on grain yield.

Shahrokhi *et al.* (2021) carried out an experiment to study the path analysis in 24 super sweet inbred lines and concluded that number of kernel rows per ear had the highest direct positive effect on grain yield in normal condition whereas, plant height had positive direct effect on grain yield under drought conditions.

Yahaya *et al.* (2021) conducted an experiment to study the path analysis for grain yield and inferred that plant height had direct effect on grain yield followed by 1000-grain weight. The traits, ear length and ear girth had the highest indirect effects on grain yield.

2.5 Screening for charcoal rot

Charcoal rot was caused by *Macrophomina phaseolina*. It was reported that estimated yield loss due to Charcoal rot will be accounting for 63.5% especially in drier regions of India (Desai and Hedge, 1991). Charcoal rot is prevalent under high soil temperature and moisture stress. The disease is characterized by the development of minute, numerous black sclerotia on vascular bundles and inside rind of the stalk giving greyish black appearance (Mughogho and Pande, 1984). The standard screening technique followed for charcoal rot is tooth pick method.

Harleen *et al.* (2010) evaluated 20 inbred lines for charcoal rot under artificial epiphytotic conditions. The results revealed that the line, E-10 (LET DR99 × Ent 49-2) showed resistance and five genotypes (E2, E1, E15, E8 and E9) showed moderate resistance to charcoal rot.

Mahuku (2010) reported that various biotic and abiotic factors will be drastically affecting the maize production in the world and also in Asia among which losses due to the diseases have been accounting for 12-80%.

Krishna *et al.* (2013) carried out the experiment on inheritance of disease resistance by crossing Resistant x Susceptible genotypes and concluded that the resistance was governed by the dominant effects.

Kumar *et al.* (2013) screened 17 QPM inbred lines against charcoal rot and revealed that the inbred lines, DQL 2071 and DQL 2015 showed moderate resistance.

Murali *et al.* (2013) reported the role of epistatic effects (additive x additive, additive x dominant and dominant x dominant) as well as non-additive gene action in governing charcoal rot resistance in maize.

Mir *et al.* (2018) evaluated the hybrids produced by crossing the resistant and susceptible inbreds in half diallel mating design and observed the significance of GCA and SCA variances and indicated that both additive and non-additive gene actions were important in governing the charcoal rot resistance. Higher Baker ratio revealed the importance of additive gene action over non-additive gene action in governing the resistance.

Shoaib *et al.* (2019) reported that the lines, FH-1225, FH-1228 and FH-1025 showed moderate resistance, FH-1042 and FH-1231 exhibited moderate susceptibility while, FH-1232, FH-963, FH-1226, FH-929, FH1217, FH-1224 and FH-1046 showed susceptibility to charcoal rot.

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Chapter III

MATERIAL AND METHODS

The present research programme entitled “Genetic analysis for yield and evaluation of hybrids for charcoal rot resistance in Maize (*Zea mays* L.)” was carried out during *Kharif*, 2021 and *Rabi*, 2021-2022 to study the *gca* and *sca* effects, heterosis, correlation, direct and indirect effects of various yield component traits on grain yield at the Agricultural Polytechnic College, Polasa, Jagtial. Screening of the experimental hybrids for charcoal rot resistance was taken up at the Maize Research Centre, ARI, Hyderabad during *Rabi*, 2021-2022.

The material utilized and the methodologies adopted in the investigation to achieve the desired objectives have been described under the following sub-headings

3.1 Location of the experiment

3.2 Experimental material

3.3 Experimental methods

3.4 Observations recorded

3.5 Statistical procedures

3.1 Location of the experiment

Agricultural Polytechnic College, Polasa, Jagtial is located at a height of 243.4 m above mean sea level on 18°49'40" N latitude and 78°56'45" E longitude in Northern Telangana Zone of Telangana state. The fields are uniformly fertile, with a consistent texture and topography. In addition, the fields are near to an irrigation channel to provide adequate, quick and timely irrigation. The Maize Research Centre, Rajendranagar, Hyderabad is situated at 17°19' N Latitude and 79°23' E Longitude and 542.6 m altitude, where screening for charcoal rot resistance was conducted.

3.2 Experimental material

The experimental material used in the present investigation consists of eight inbred lines i.e., PFSR-73, PFSR-127, PFSR-151, BML-10, MGC-49, ML-14, PFSR-92, BPDT-5009 and the resultant 28 hybrids. Among the inbred lines, PFSR-73, PFSR-127, PFSR-151 and MGC-49 were resistant to charcoal rot while, BML-10 was moderately resistant, ML-14 was moderately susceptible and the remaining two inbred lines *viz.*, PFSR-92 and BPDT-5009 were highly susceptible to charcoal rot.

All the above inbred lines were collected from Maize Research Centre, ARI, Hyderabad which were proven as good combiners with varied levels of charcoal rot resistance.

3.3 Experimental methods

3.3.1 Generation of hybrids

Eight inbred lines were crossed in Half-diallel, Method-II, Model-I mating design and 28 hybrids were developed at Agricultural Polytechnic College, Polasa, Jagtial during *kharif*, 2021.

3.3.2 Crossing programme

The selected inbred lines were sown in three staggerings at five-day intervals during *Kharif*, 2021 to achieve synchrony in flowering and also for the continuous availability of sufficient quantity of pollen to complete the desired crosses in the study. All the cultural operations were taken up in the similar way as a regular maize crop. Hybridization programme was carried out by tassel bag method. The ear shoots of maize emerging from the leaf sheath were covered two days prior to silk emergence with butter paper cover to prevent cross-pollination. A kraft bag cover was placed over the tassel the day before pollination to collect pollen. To avoid contamination over the pollinated ear, the pollen collected in the tassel bag was dusted over the silk and immediately pinned the pollinated ear to avoid contamination. Hand pollination was done between 9:00 A.M. to 11:00 P.M. for thirty days. Parents were also selfed simultaneously using the tassel bag method to collect pure parental seeds for further evaluation. At maturity, the 28 hybrids and parents were harvested.

Table 3.1. List of Maize inbred lines used in the present investigation

S. No	Inbred line	Characters	Source of collection
1	PFSR-73	Good combiner, resistant to charcoal rot	Maize Research Centre, ARI, Hyderabad
2	PFSR-127	Good combiner, resistant to charcoal rot	Maize Research Centre, ARI, Hyderabad
3	PFSR-151	Good combiner, resistant to charcoal rot	Maize Research Centre, ARI, Hyderabad
4	BML-10	Good combiner, moderately resistant to charcoal rot	Maize Research Centre, ARI, Hyderabad
5	MGC-49	Good combiner, resistant to charcoal rot	Maize Research Centre, ARI, Hyderabad
6	ML-14	Good combiner, moderately susceptible to charcoal rot	Maize Research Centre, ARI, Hyderabad
7	PFSR-92	Good combiner, highly susceptible to charcoal rot	Maize Research Centre, ARI, Hyderabad
8	BPDT-5009	Good combiner, highly susceptible to charcoal rot	Maize Research Centre, ARI, Hyderabad

3.3.3 Field evaluation of hybrids along with parents and checks

Field evaluation was done with 28 experimental hybrids, eight parents and one check, DHM-117 which were sown in Randomized Block Design (RBD) replicated thrice by adopting a spacing of 75 × 20 cm during *Rabi* 2021-22 at Agricultural Polytechnic College, Polasa, Jagtial.

The recommended doses of N, P and K fertilizers were applied in the ratio of 180: 60: 40 kg ha⁻¹. The complete dose of P and K and one-third of nitrogen was applied as basal, while, remaining quantity of the nitrogen was applied in two equal split doses at knee height and tasseling stages. Timely irrigation, weeding operations as well as necessary plant protection measures were carried out in accordance with the recommendations to protect the crop from pests and diseases and thereby ensuring a healthy crop growth during field evaluation.

3.4 Observations recorded

3.4.1 Biometrical observations

Various biometrical observations that have relevance to grain yield were recorded on five randomly selected plants per treatment in all the genotypes in each replication. To reduce the error due to border effect, the plants were selected from the middle rows. The characters and the procedure adopted for recording the observation have been detailed below:

1. Days to 50 per cent anthesis
2. Days to 50 per cent silking
3. Anthesis Silking Interval (ASI)
4. Days to maturity
5. Plant height (cm)
6. Ear height (cm)
7. Ear length (cm)
8. Ear girth (cm)
9. Number of kernel rows per ear
10. Number of kernels per row
11. 100-kernel weight (g)
12. Grain yield (g/plant)
13. Stay green/ non-stay green type

3.4.1.1 Days to 50 per cent anthesis: This phenological observation was recorded based on the total number of plants in the entry. The number of days taken from the date of

sowing to the date of 50 per cent plants with pollen shed was recorded as days to 50 per cent anthesis and was expressed in days.

3.4.1.2 Days to 50 per cent silking: This phenological observation was recorded based on the total number of plants in the entry. Number of days taken from the date of sowing to the date of 50 per cent of plants with silk emergence were recorded and expressed in days.

3.4.1.3 Anthesis Silking Interval (ASI): The time between the days to 50 per cent anthesis to 50 per cent silking is counted and expressed as anthesis silking interval which is measured in days.

3.4.1.4 Days to maturity: Number of days counted from the date of sowing to date of 75 per cent of the cobs attained brown husk.

3.4.1.5 Plant height (cm): Plant height was measured as the height from the base of a plant to tip of the same plant and is expressed in centimeters on five randomly selected plants.

3.4.1.6 Ear height (cm): Ear height was measured from the base of the plant to the node of the attachment of the upper most ear in centimeters on five randomly selected plants.

3.4.1.7 Ear length (cm): Thread was used to measure the ear length. Length of the ear was measured from the base to the tip of the ear in centimeters from randomly selected five plants.

3.4.1.8 Ear girth (cm): Ear girth was measured in centimeters by using ordinary string (thread) at a point of maximum diameter after dehusking of the ear from five randomly selected ears. The thread was wrapped around the middle of the ear and the length was measured in centimeters and recorded as the ear diameter.

3.4.1.9 Number of kernel rows per ear: This observation was recorded by counting the number of rows per ear at the middle of the ear for the five randomly selected ears.

3.4.1.10 Number of kernels per row: From five randomly selected ears, the number of kernels per row were counted and recorded.

3.4.1.11 100-Kernel weight (g): A total of 100 kernels were counted from each entry in each replication weighted on electronic balance and recorded in grams.

3.4.1.12 Grain yield (g/plant): Grain yield was recorded in grams per plant after drying and shelling the grains from individual ears.

3.4.1.13 Stay green/ non-stay green type: The stay green character was recorded at physiological maturity stage. Ten competitive plants per entry were visually rated from 1 (highest) to 5 (lowest) to record the degree of stay green nature of genotypes.

Table 3.2. Scoring for stay green trait (Belicuas *et al.* 2014)

Score	Description
1	Plants with all leaves above the ear, at least two leaves below the ear, and the stalks green
2	Plants with all leaves above the ear and the stalks green
3	Plants with two leaves above the ear senescent and the others green regardless of the color of the stalks
4	Plants with two green leaves above the ear and senescent stalks
5	The plants with all the leaves and stalks senescent

3.4.2 Validation of parents and the identification of hybrids for charcoal rot resistance.

Another field trial was laid out at Maize Research Centre, ARI, Rajendranagar, Hyderabad during *Rabi*, 2021-2022 replicated twice with plot size of 2 rows of 4 m length and sown at a spacing of 75 × 20 cm for screening all the experimental hybrids (28) along eight parents and Kaveri-50 as a susceptible check. Artificial inoculation with Tooth pick method (Payak and Sharma, 1983) was used for this purpose.

3.4.2.1 Preparation of Potato dextrose agar (PDA) medium: The following components were used to make PDA medium for growing the fungi in the laboratory.

Potato (Peeled, washed and sliced) : 200 g
Dextrose : 20 g
Agar agar : 20 g
Distilled water : 1000 ml

Two hundred grams of potatoes were taken, peeled and cut into small pieces and boiled for 20 to 30 min. After boiling extract was filtered through muslin cloth. Dextrose and agar were added in equal amounts and boiled until properly dissolved. Sterilization was done at 121 °C for 15 min. Finally, 20 ml of each of the above medium was poured separately into Petri plates.

3.4.2.2 Screening for charcoal rot resistance: Tooth pick method was followed for inoculation of experimental hybrids of maize. For this purpose, round bamboo tooth picks about 6.5 cm long were boiled three times (about 1 hour each time) in tap water to remove toxic substances. After each boiling these were washed properly in fresh water and dried in the sun. After proper drying, tooth picks were loosely packed in bundles and put into the autoclavable glass jars/ bottles and enough potato dextrose broth was added to thoroughly moisten the toothpicks. After the potato dextrose agar was added, the jars with tooth picks were autoclaved immediately.

Sterilized toothpicks were inoculated with the culture of *Macrophomina phaseolina* pathogen aseptically. Growth of the fungal inoculum covering the toothpicks was used within 10 days for the purpose. Individual plants were inoculated by inserting the above tooth picks into the second internode (first elongated node) of the plant at tassel emergence. This was facilitated by making hole at 45° in the stalk with a jabber and then tooth picks were inserted into it. The Symptoms were recorded on 45 days after inoculation.

Disease symptoms were scored at harvest by longitudinal splitting the stalks of inoculated plants on 1-9 scale as per Payak and Sharma, 1983 (Table 3.3)

Table 3.3. Disease rating scale for maize charcoal rot disease (Payak and Sharma, 1983)

Disease score	Description
1	25% discolouration of the inoculated node
2	26-50% discolouration of the inoculated node
3	51-75 % discolouration of the inoculated node
4	76-100% discolouration of the inoculated node
5	Discolouration of the adjacent node, lesser than 50%
6	Discolouration of more than 50% of the adjacent node
7	Discolouration of more than three nodes
8	Discolouration of more than four nodes
9	Discolouration of five nodes or broken or lodged plant due to disease

Disease Score	Type of Reaction
1 – 3	Resistant
4 – 5	Moderately Resistant
6 – 7	Moderately Susceptible
8 – 9	Highly Susceptible

3.5 Statistical analysis

The mean values recorded individually for different observations and then subjected to the following statistical analysis.

3.5.1 Analysis of variance

3.5.1.1 RBD Analysis: The analysis of variance for each character was carried out as per standard statistical procedure described by Panse and Sukhatme (1985).

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

Where,

Y_{ij} = Performance of i^{th} genotype in j^{th} replication

μ = General mean

g_i = True effect of i^{th} genotype

v_j = True effect of j^{th} replication

e_{ij} = Random error associated with i^{th} genotype and j^{th} replication

Analysis of variance (ANOVA) was carried out for each character as indicated below:

Source of variation	d.f.	SS	MSS	F-ratio
Replications (r)	(r-1)	RSS	M_r	M_r/M_e
Treatments (t)	(t-1)	TSS	M_t	M_t/M_e
Error (e)	(r-1)(t-1)	ESS	M_e	
Total	(rt-1)			

Where,

r = Number of replications

t = Number of treatments (genotypes)

d.f. = Degrees of freedom

SS = Sum of squares

MSS = Mean sum of squares

M_r = Mean sum of squares due to replications

M_t = Mean sum of squares due to treatments

M_e = Mean sum of squares due to error

The significance of mean sum of squares for each character was tested against the corresponding error degrees of freedom using 'F' test given by Fisher and Yates (1967).

3.5.2 Estimation of combining ability

The data obtained from F_1 s and parents were analyzed as per Method II (F_1 s + parents) and Model -I (fixed effect) of Griffing (1956a) for combining ability. The mathematical model for combining ability is

$$X_{ij} = \mu + g_i + g_j + S_{ij} + \frac{1}{bc} \sum_k \sum_l e_{ijkl}$$

$i, j = 1, \dots, p$

$K = 1, \dots, b$

$L = 1, \dots, c$

Where,

- $b =$ Number of blocks
 $c =$ Number of observations on $(i,j)^{th}$ genotype in k^{th} block
 $\mu =$ Population mean
 $g_i =$ gca effect of the i^{th} parent
 $g_j =$ gca effect of the j^{th} parent
 $S_{ij} =$ sca effect of the cross between i^{th} and j^{th} parents such that
 $S_{ij} = S_{ji}$ and
 $e_{ijkl} =$ Environment effect pertaining to the $ijkl^{th}$ observation
 $ij^{th} =$ individual in k^{th} block

With i^{th} female parent and j^{th} male parent

The restrictions imposed on this model are

$$\sum e_i g_i = 0$$

$$e_j s_{ij} + s_{ii} = 0 \quad (\text{for each } i)$$

Analysis of variance

Source	d.f.	SS	MSS	Expected mean square
General Combining Ability	$(P - 1)$	S_g	M_g	$\sigma^2 e + (P+2) (1/P-1) \sum_i g_i^2$
Specific Combining Ability	$P(P - 1) / 2$	S_s	M_s	$\sigma^2 e + \frac{2}{P(P-1)} \sum_i \sum_j s_{ij}^2$
Error	M	S_e	M_e	$\sigma^2 e$

$$S_g = \frac{1}{(P+2)} \left[\sum_i (x_i + x_{ii})^2 - \frac{4}{P} x^2 \dots \right]$$

$$S_s = \sum_i \sum_j s_{ij}^2 - \frac{1}{(P+2)} \sum_i (x_i + x_{ii})^2 + \frac{2}{(P+1)(P+2)} x^2 \dots$$

Where,

- $S_g =$ Sum of square due to GCA
 $S_s =$ Sum of square due to SCA
 $P =$ Number of parents
 $x_i =$ Total of the array involving i^{th} parent
 $x_{ii} =$ Mean value of i^{th} parent
 $X =$ Grand total of $\frac{1}{2} (p) (p-1)$ progenies
 $X_{ij} =$ Progeny mean value in the diallel table
 $M =$ Degree of freedom for error

Mean square GCA to SCA variance ratio was calculated to know the type of gene action in the inheritance of that particular trait.

$$\sigma^2 \text{GCA} = \frac{M_g - M'_e}{n + 2}$$

$$\sigma^2 \text{SCA} = M_s - M'_e$$

i) General combining ability effects i^{th} parent with restriction $\sum g_i = 0$

$$\hat{g}_i = \frac{1}{(P + 2)} [\Sigma(x_i + x_{ii}) - \frac{2}{P} x \dots]$$

ii) Specific combining ability effects of ij^{th} cross: with restriction $\sum s_{ij} + s_{ii} = 0$

$$\hat{s}_{ij} = X_{ij} - \frac{1}{(P+2)} (x_i + x_{ii} + x_j + x_{jj}) + \frac{2}{(P+1)(P+2)} x \dots$$

Where,

P , x_{ij} , x_i , x_{ii} and $x..$ denotes the same term as mentioned earlier.

Standard Errors

$$\text{S. E. } \hat{g}_i = \sqrt{\frac{(P - 1)}{(P + 2)} \sigma_e^2}$$

$$\text{S. E. } \hat{s}_{ii} = \sqrt{\frac{P(P - 1)}{(P + 1)(P + 2)} \sigma_e^2}$$

$$\text{S. E. } \hat{s}_{ij} = \sqrt{\frac{P^2 + P + 2}{(P + 1)(P + 2)} \sigma_{e(i\#j)}^2}$$

Each *gca* and *sca* value was tested against zero for its significance by 't' test.

$$t = (g^{\wedge} - e) / \text{SE}(g_i) \text{ or } t = (\hat{s}_{ij} = 0) / \text{SE}(s_{ij})$$

3.5.3 Estimation of Heterosis

Estimates of heterosis was calculated according to Fonseca and Patterson (1968).

Heterosis over mid parent: Heterosis was expressed as per cent increase or decrease observed in the F_1 over the mid-parent as per the following formula.

$$\text{Heterosis (\%)} (h_1) = \frac{\bar{F}_1 - \overline{MP}}{\overline{MP}} \times 100$$

Where,

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

$$\overline{MP} = \text{Mean of mid parents}$$

Heterosis over better parent: Heterobeltiosis was expressed as per cent increase or decrease observed in F_1 over the better parent.

$$\text{Heterobeltiosis \% (h}_2\text{)} = \frac{\overline{F_1} - \overline{BP}}{\overline{BP}} \times 100$$

Where,

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

Heterosis over standard checks: Standard heterosis was expressed as per cent increase or decrease observed in F_1 over standard checks.

$$\text{Standard heterosis \% (h}_3\text{)} = \frac{\overline{F_1} - \overline{SC}}{\overline{SC}} \times 100$$

Where,

$$\overline{SC} = \text{mean of standard check}$$

Test of significance of heterosis: To test the significance for different types of heterosis needs computation of standard error (SEm). For relative heterosis and heterobeltiosis, SEm were calculated based on Error Mean Squares (EMS) from the ANOVA tables consisting parents and crosses, whereas, EMS from the RBD ANOVA ($\sigma^2 e$) table based on all treatments (parents, crosses and check) was used for standard heterosis.

The significance of heterosis *viz.*, heterosis over mid parent, better parent heterosis and standard heterosis was then tested by comparing the calculated 't' value with the tabulated student's 't'-value for appropriate error degrees of freedom at 5 per cent and 1 per cent level of significance (0.05 and 0.01 level of probability) respectively.

$$t'_{\text{cal}} \text{ for Heterosis and heterobeltiosis} = \frac{\overline{F_1} - \overline{MP} \text{ or } \overline{BP}}{\text{SEm}} \times 100$$

$$\text{Where, SEm} = \sqrt{2\text{EMS} / r}$$

EMS = Error mean of squares

r = Number of replications

$$t'_{\text{cal}} \text{ for Standard heterosis} = \frac{\overline{F_1} - \overline{SC}}{\text{SEm } \overline{SC}}$$

$$\text{Where, SE m } \overline{SC} = \sqrt{2\sigma e^2 / r}$$

Least significance difference (critical difference) for heterosis: The significance of the difference between two estimates of heterosis were tested by computing the least significant difference (LSD) by multiply the SEm with the appropriate students t value of respective error degrees of freedom at desired level of probability.

$$\text{CD} = \text{SE m} \times \text{'t' table value at error degrees of freedom}$$

3.5.4 Estimation of correlation coefficients

Correlation coefficients were calculated at genotypic and phenotypic level using the formulae suggested by Falconer (1964).

$$\text{Genotypic coefficient of correlation } (r_g) = r(x_i, x_j)_g = \frac{\text{Cov. } (x_i, x_j)_g}{\sqrt{V(x_i)_g \cdot V(x_j)_g}}$$

Where,

$r(x_i, x_j)_g$ is genotypic correlation between i^{th} and j^{th} characters

$\text{Cov. } (x_i, x_j)_g$ is genotypic covariance between i^{th} and j^{th} characters

$V(x_i)_g$ is genotypic variance of i^{th} character

$V(x_j)_g$ is genotypic variance of j^{th} character

$$\text{Phenotypic coefficient of correlation } (r_p) = r(x_i, x_j)_p = \frac{\text{Cov. } (x_i, x_j)_p}{\sqrt{V(x_i)_p \cdot V(x_j)_p}}$$

Where,

$r(x_i, x_j)_p$ is phenotypic correlation between i^{th} and j^{th} characters

$\text{Cov. } (x_i, x_j)_p$ is phenotypic covariance between i^{th} and j^{th} characters

$V(x_i)_p$ is phenotypic variance of i^{th} character

$V(x_j)_p$ is phenotypic variance of j^{th} character

Test of significance for correlation of coefficient: If 'r' is the observed correlation coefficient in a sample of 'n' pairs of observations from a bivariate normal population, then proved that under the null hypothesis

$$H_0: \rho=0$$

The variable x, y follows a bivariate normal distribution. If the population correlation coefficient of x and y is denoted by ρ , then it is often of interest to test whether ρ is zero or different from zero, on the basis of observed correlation coefficient 'r'. Thus if 'r' is the sample correlation coefficient based on a sample of 'n' observations, then the appropriate test statistic for testing the null hypothesis $H_0: \rho=0$ against the alternative hypothesis $H_1: \rho \neq 0$ is

$$t = \frac{r\sqrt{(n-2)}}{\sqrt{1-r^2}}$$

t follows student t distribution with (n-2) d.f.

if calculated value of $t >$ table value of t with (n-2) d.f. at specified level of significance, then the null hypothesis is rejected. That is, there may be significant correlation between the two variables. Otherwise, the null hypothesis is accepted.

3.5.5 Path coefficient analysis

The direct and indirect effects at both the genotypic and phenotypic levels were calculated by considering seed yield as dependent variable, using path coefficient analysis suggested by Wright (1921) and Dewey and Lu (1959). For estimating various direct and indirect effects, the following equations were used for the purpose.

$$r_{1y} = P_{1y} r_{11} + P_{2y} r_{12} + P_{3y} r_{13} \dots \dots \dots + P_{ny} r_{1n}$$

$$r_{2y} = P_{1y} r_{21} + P_{2y} r_{22} + P_{3y} r_{23} \dots \dots \dots + P_{ny} r_{2n}$$

$$r_{ny} = P_{1y} r_{n1} + P_{2y} r_{n2} + P_{3y} r_{n3} \dots \dots \dots + P_{ny} r_{nn}$$

Where,

1, 2, ... n = Independent variables

Y = Dependent variable

$r_{1y}, r_{2y}, \dots, r_{ny}$ = Coefficient of correlation between casual factors '1' to 'n' on dependent character, Y

$P_{1y}, P_{2y}, \dots, P_{ny}$ = Direct effect of character 1 to n on character, Y

The above equation can be written in matrix form as:

$$\begin{matrix}
 \text{A} & & \text{C} & & \text{B} \\
 r_{1y} & \left(\begin{matrix} 1 & r_{12} & r_{13} & \dots \dots \dots & r_{1n} \\ r_{21} & 1 & r_{23} & \dots \dots \dots & r_{2n} \\ \cdot & \cdot & \cdot & \cdot & \cdot \\ \cdot & \cdot & \cdot & \cdot & \cdot \\ \cdot & \cdot & \cdot & \cdot & \cdot \\ R_{ny} & r_{n1} & r_{n2} & r_{n3} & \dots \dots \dots & 1 \end{matrix} \right) & & \left(\begin{matrix} P_{1y} \\ P_{2y} \\ \cdot \\ \cdot \\ \cdot \\ P_{ny} \end{matrix} \right)
 \end{matrix}$$

Then,

$$B=[C]^{-1} A \text{ where } C^{-1} = \begin{pmatrix} c_{11} & c_{12} & c_{13} \dots & c_{1n} \\ c_{21} & c_{22} & c_{23} \dots & c_{2k} \\ \vdots & \vdots & \vdots & \vdots \\ \vdots & \vdots & \vdots & \vdots \\ c_{n1} & c_{n2} & c_{n3} \dots & c_{nn} \end{pmatrix}$$

Direct effects were as follows:

$$p_{1y} = \sum_{i=1}^k c_{1i} r_{iy}$$

$$p_{2y} = \sum_{i=1}^k c_{2i} r_{iy}$$

$$p_{ny} = \sum_{i=1}^k c_{ni} r_{iy}$$

Residual effect, which measures the contribution of characters not considered, was obtained as:

$$p_{ry} = \sqrt{1 - (p_{1y} r_{iy} + p_{2y} r_{iy} + \dots + p_{ny} r_{ny})}$$

Where, p_{ny} = Direct effect of x_n on Y

r_{iy} = Correlation coefficient of x_n on Y

Test of significance for path coefficient: when the empirical t value is larger than the critical value, then the coefficient is statically significant at a certain error probability.

The software used for the analysis of the data is Indostat software package.

Chapter IV

RESULTS AND DISCUSSION

Results of the present investigation entitled “Genetic analysis for yield and evaluation of hybrids for charcoal rot resistance in Maize (*Zea mays* L.)” have been presented under following heads:

- 4.1 Analysis of variance
- 4.2 Mean performance of parents and single cross hybrids
- 4.3 Heterosis
- 4.4 Combining ability analysis
- 4.5 Correlation analysis
- 4.6 Path analysis
- 4.7 Study on stay green trait
- 4.8 Screening for charcoal rot

4.1 Analysis of variance

The analysis of variance for yield and its attributing traits for all the genotypes (parents, hybrids and check) is presented in Table 4.1. The mean sum of squares of genotypes were found to be significant for all characters in the study indicating the presence of sufficient amount of variability in the material under study while, the mean sum of squares of replications were found to be non-significant for all the traits. Hence, there is a definite scope for the selection of good genotypes for various qualitative and quantitative characters for further development.

4.2 Mean performance of parents and single cross hybrids

Mean performance of the parents, hybrids along with one check, DHM-117 were evaluated for 12 yield and its attributing characters and are presented in Table 4.2.

4.2.1 Days to 50 per cent anthesis

Mean performance of the parents for days to 50 per cent anthesis was 74.50, and ranged from 71 days (BML-10) to 77 days (MGC-49 and PFSR-92). Among the hybrids, the mean value was 66.67 days and ranged from 62 days to 77 days while, mean value for the check (DHM-117) was 77 days. The inbred lines, BML-10 and PFSR-151 were found to be the earliest among the parents while, BML-10×BPDT-5009, PFSR-73×ML-14, ML-14×PFSR-92 and MGC-49×PFSR-92 were the earliest

among hybrids. The results indicated that hybrids (66.67) attained days to 50% anthesis earlier than parents (74.50) and also the check, DHM-117 (77).

4.2.2 Days to 50 per cent silking

Mean value for days to 50 per cent silking for parents was 76.50 days and ranged from 72 (BML-10) to 80 days (PFSR-92 and MGC-49) and for hybrids the mean value was 69.46 days that varied from 65 to 79 days. Mean value for the check was 80 days. The inbred line, BML-10 was the earliest among parents for days to 50 per cent silking. The crosses, MGC-49 × PFSR-92, PFSR-73×ML-14, ML-14×PFSR-92 and BML-10×BPDT-5009 were the earliest (65 days) among the hybrids. In general, the hybrids (69.46) attained days to 50% silking earlier than their parents (76.50) and also the check, DHM-117 (80).

4.2.3 Anthesis silking interval (ASI)

Mean value for the trait among parents was 2.12 days which varied from 1(PFSR-151) to 3 days (PFSR-92 and MGC-49) and in case of hybrids mean value was 2.82 days that ranged from 1 day (PFSR-73×PFSR-92) to 4 days (PFSR-151×MGC-49 and ML-14×BPDT-5009) while, check DHM-117 showed 3 days anthesis silking interval.

4.2.4 Days to maturity

Mean value for the trait among the parents was 113.87 days that ranged from 106 days (BML-10) to 119 days (PFSR-92). Among the hybrids mean value was 103.17 days that ranged from 96 days (PFSR-73× ML-14) to 111 days (PFSR-151×PFSR-92). The check attained maturity in 113.66 days.

4.2.5 Plant height (cm)

Mean value for plant height among the parents was 177.45 cm ranging from 124.53 cm (BML-10) to 213.11 cm (PFSR-73) and for hybrids the mean value was 231.66 cm ranging from 191.83 cm (BML-10× MGC-49) to 265.58 cm (PFSR-151×BPDT-5009). Plant height for the check (DHM-117) was 222.80 cm. five among the 28 hybrids attained the plant height above 250 cm.

4.2.6 Ear height (cm)

In general, lower ear height is desirable to resist against high velocity winds. Mean value for ear height was 56.41 cm for parents, ranging from 37.42 cm (BML-10) to 77.85 cm (PFSR-73), while, mean value for the hybrids was 68.68 cm, that ranged from 51.20 cm (PFSR-151×ML-14) to 85.14 cm (PFSR-73×MGC-49) whereas, the check, DHM-117 recorded ear height of 88.66 cm.

Table 4.1. Analysis of variance for yield and yield attributing traits among the selected maize genotypes

Character	Mean sum of squares		
Source of variation	Replications	Genotypes	Error
d.f	2	36	72
Days to 50% anthesis	0.56	92.182**	0.19
Days to 50% silking	0.48	82.229**	0.25
Anthesis Silking Interval	0.06	1.481**	0.07
Days to maturity	2.49	117.488**	0.46
Plant height (cm)	0.73	2966.608**	10.76
Ear height (cm)	5.52	401.988**	4.13
Ear length (cm)	0.54	15.373**	0.07
Ear girth (cm)	0.08	4.506**	0.05
No. of kernel rows per ear	0.160	4.385**	0.08
No. of kernels per row	15.77	91.787**	4.73
100-kernel weight (g)	1.15	64.201**	1.37
Grain yield (g/plant)	4.793	4069.800**	19.20

**Significance at 1% level

4.2.7 Ear length (cm)

Mean value of the parents for ear length was 14.09 cm, that ranged from 11.71 cm (BPDT-5009) to 16.42 cm (PFSR-73) and in case of hybrids the mean value was 18.30 cm, that varied from 14.96 cm (ML-14×BPDT-5009) to 20.98 cm (PFSR-127×ML-14). Ear length was 14.82 cm for the check, DHM-117.

4.2.8 Ear girth (cm)

Mean value for the trait ear girth was 12.27 cm among parents that ranged from 11.34 cm (PFSR-127) to 13.58 cm (BML-10) while, mean value among the hybrids was 14.11 cm, that ranged from 11.71 cm (PFSR-73×PFSR-151) to 15.81 cm (MGC-49×PFSR-92). The check, DHM-117 recorded the ear girth of 14.40 cm.

4.2.9 Number of kernel rows per ear

Mean value of the parents for number of kernel rows per ear was 12 that ranged from 10 (PFSR-127 and ML-14) to 14 (BML-10 and MGC-49) and hybrids recorded the mean value of 14, that ranged from 10 to 14. The hybrids, PFSR-73×MGC-49, PFSR-73×ML-14, PFSR-127×BML-10, PFSR-127×ML-14, PFSR-127×MGC-49, PFSR-151×MGC-49, PFSR-151×PFSR-92, BML-10×MGC-49, BML-10×PFSR-92, BML-10×BPDT-5009, MGC-49×BPDT-5009 and ML-14×BPDT-5009 had 14 kernel rows per ear which are similar with the check, DHM-117.

4.2.10 Number of kernels per row

Mean value of the parents for number of kernel rows per ear was 22.70 which ranged from 16.26 (MGC-49) to 30.26 (PFSR-92), among the hybrids mean value was 32.02, that ranged from 23.80 (PFSR-73×PFSR-127) to 38.33 (PFSR-73×ML-14). The check, DHM-117 recorded 30.46 number of kernels per row. Nineteen (19) among the 28 hybrids showed a higher number of kernels per row than the check, DHM-117.

4.2.11 100-kernel weight (g)

Mean performance of parents for 100-kernel weight was 23.05 g that ranged from 16.94 g (BPDT-5009) to 29.53 g (BML-10). Among hybrids, maximum kernel weight was recorded by PFSR-73×PFSR-92 (35.53 g) and minimum kernel weight was recorded by PFSR-151×PFSR-92 (23.73 g) while, the check, DHM-117 recorded 31.94 g. The hybrids recorded the highest mean value of 29.55 g compared to the parents (23.05 g).

Table 4.2. Mean performance of parents, crosses and standard check for yield and yield attributing traits of maize genotypes

Source	Days to 50% anthesis	Days to 50% silking	Anthesis silking interval	Days to maturity	Plant height (cm)	Ear height (cm)	Ear length (cm)	Ear girth (cm)	Number of kernel rows per ear	Number of kernels per row	100-kernel weight (g)	Grain yield (g/plant)
Parents												
PFSR-73	74	76	2.00	116	213.11	77.85	16.42	12.27	12	24.80	25.15	59.66
PFSR-127	76	78	2.00	113	198.09	63.44	14.28	11.34	10	20.00	23.51	44.33
PFSR-151	72	73	1.00	114	215.19	53.69	14.65	12.89	12	25.20	17.81	66.66
BML-10	71	72	2.00	106	124.53	37.42	11.83	13.58	14	18.66	29.53	77.66
MGC-49	77	80	3.00	118	137.73	40.05	14.31	13.16	14	16.26	21.19	59.33
ML-14	75	77	2.00	115	197.38	67.18	14.55	11.38	10	19.46	31.89	76.66
PFSR-92	77	80	3.00	119	176.50	56.07	14.96	11.40	12	30.26	18.36	61.33
BPDT-5009	74	76	2.00	110	157.01	55.53	11.71	12.10	12	26.93	16.94	59.00
Mean of parents	74.50	76.50	2.12	113.87	177.45	56.41	14.09	12.27	12	22.70	23.05	63.08
Range	71-77	72-80	1.00-3.00	106-119	124.53-213.11	37.42-77.85	11.71-16.42	11.34-13.25	10-14	16.26-30.26	16.94-29.53	44.3-77.66
Hybrids												
PFSR-73 × PFSR-127	75	77	2.00	106	215.04	64.80	16.18	12.44	12	23.80	27.58	106.00
PFSR-73 × PFSR-151	66	69	3.00	97	258.58	74.61	18.66	11.71	10	32.93	27.25	83.00
PFSR-73 × BML-10	77	79	2.00	106	214.32	76.62	17.84	12.56	12	25.53	28.50	106.33
PFSR-73 × MGC-49	67	69	3.00	109	234.58	85.14	18.70	15.64	14	35.13	28.30	143.66
PFSR-73 × ML-14	62	65	3.00	96	235.25	82.94	19.84	14.04	14	38.33	26.44	125.66

Table 4.2 (cont.).

Source	Days to 50% anthesis	Days to 50% silking	Anthesis silking interval	Days to maturity	Plant height (cm)	Ear height (cm)	Ear length (cm)	Ear girth (cm)	Number of kernel rows per ear	Number of kernels per row	100-kernel weight (g)	Grain yield (g/plant)
PFSR-73 × PFSR-92	72	73	1.00	105	240.34	76.24	18.92	13.95	12	31.26	35.53	153.33 *
PFSR-73 × BPDT-5009	72	74	2.00	103	233.52	71.88	18.22	13.63	12	35.86	24.47	98.33
PFSR-127 × PFSR-151	72	75	3.00	107	253.98	58.36	19.02	13.63	12	32.06	25.02	106.00
PFSR-127 × BML-10	64	67	3.00	97	230.21	70.89	18.57	14.86	14	28.00	30.45	133.00
PFSR-127 × MGC-49	63	66	3.00	97	233.85	64.98	18.11	14.64	14	33.06	32.39	164.66*
PFSR-127 × ML-14	63	66	3.00	101	253.57	81.86	20.98	15.29	14	37.73	35.36	187.33*
PFSR-127 × PFSR-92	72	74	2.00	105	216.36	63.92	15.73	12.22	12	27.40	28.66	93.33
PFSR-127 × BPDT-5009	72	75	3.00	110	229.42	63.86	18.34	14.88	14	29.20	33.25	156.66*
PFSR-151 × BML-10	62	65	3.00	101	234.90	51.46	18.87	15.26	12	29.40	32.11	149.66*
PFSR-151 × MGC-49	72	76	4.00	109	252.97	67.46	17.74	14.34	14	32.00	31.90	153.66*
PFSR-151 × ML-14	63	66	3.00	102	226.42	51.20	18.03	14.06	12	34.60	25.92	114.33
PFSR-151 × PFSR-92	74	77	3.00	111	232.02	67.58	18.10	14.04	14	30.13	23.73	131.00
PFSR-151 × BPDT-5009	63	65	2.00	100	265.58	78.32	20.88	13.57	12	37.86	32.29	157.66*
BML-10 × MGC-49	67	70	3.00	109	191.83	57.34	18.92	14.50	14	33.20	29.89	136.33
BML-10 × ML-14	63	66	3.00	97	246.22	65.15	18.19	14.07	12	29.80	31.48	138.33
BML-10 × PFSR-92	63	66	3.00	102	206.44	63.42	16.89	15.10	14	33.20	31.73	161.33*
BML-10 × BPDT-5009	62	65	3.00	104	206.75	56.08	16.16	13.40	14	32.80	27.79	116.33

Table 4.2 (cont.).

Source	Days to 50% anthesis	Days to 50% silking	Anthesis silking interval	Days to maturity	Plant height (cm)	Ear height (cm)	Ear length (cm)	Ear girth (cm)	Number of kernel rows per ear	Number of kernels per row	100-kernel weight (g)	Grain yield (g/plant)
MGC-49 × ML-14	63	66	3.00	106	249.61	75.00	18.62	14.22	12	31.53	25.73	108.00
MGC-49 × PFSR-92	62	65	3.00	98	214.19	67.26	18.56	15.81	12	36.46	30.72	144.66
MGC-49 × BPDT-5009	64	67	3.00	104	233.10	72.04	19.10	14.91	14	32.60	29.27	151.00*
ML-14 × PFSR-92	62	65	3.00	102	236.70	73.57	18.97	14.00	12	31.80	33.33	140.66
ML-14 × BPDT-5009	67	71	4.00	104	201.00	68.08	14.96	14.33	14	25.73	27.19	99.66
PFSR-92 × BPDT-5009	63	66	3.00	101	239.70	73.14	19.39	13.95	12	36.46	31.22	143.00
Mean of hybrids	66.67	69.46	2.82	103.17	231.66	68.68	18.30	14.11	14	32.02	29.55	132.25
Range	62-77	65-79	1.00-4.00	96-111	191.83-265.58	51.20-85.14	14.96-20.98	11.71-15.81	10-14	23.80-38.33	23.73-35.53	83.00-187.33
Grand mean	68.41	71.02	2.66	105.55	219.700	66.57	17.30	13.72	12.84	30.00	28.21	117.54
Check (DHM-117)	77.00	80.00	3.00	113.66	222.80	88.66	14.82	14.40	14.00	30.46	31.94	141.66
S. Ed	0.25	0.29	0.15	0.39	1.89	1.17	0.15	0.13	0.16	1.05	0.67	2.53
CD (0.05)	0.72	0.82	0.43	1.11	5.34	3.30	0.44	0.38	0.47	3.54	1.90	7.13
CV (%)	0.64	0.70	10.08	0.64	1.49	3.05	1.57	1.71	2.26	7.25	4.14	3.72

*Significance at 5% level

4.2.12 Grain yield (g/plant)

Mean value of the parents for grain yield was 63.08 g, that ranged from 44.33 g (PFSR-127) to 77.66 g (BML-10). Among the hybrids, the mean value was 132.25 g, which varied from 83 g (PFSR-73×PFSR-151) to 187.33 g (PFSR-127×ML-14). The check, DHM-117 recorded the grain yield of 141.66 g. Nine out of 28 hybrids recorded significantly superior grain yield per plant over the check, DHM-117.

4.3 Heterosis

Heterosis has proven to be the most important genetic tool for increasing production potential of crop plants. Identification of a specific parental combination capable of creating higher levels of heterotic effects in F_1 is crucial for commercial exploitation of heterosis.

The degree of heterosis in the present study varied from cross to cross and character to character. For a given character, there was significant high heterotic effects in some crosses and low heterotic effects in others, indicating that the nature of gene action differed depending on the genetic constitution of the parents.

In present investigation heterosis over mid parent (Mid-parent heterosis/average heterosis), over better parent (Better-parent heterosis) and over standard check (standard heterosis) was estimated in the 28 hybrids for twelve (12) traits in order to find the best combination of parents resulting in a high degree of useful heterosis and to characterise the parents for further use in future breeding programmes.

Negative heterotic values for days to 50% anthesis, days to 50% silking and days to maturity is desirable for the development of early maturing genotypes. For other yield attributing characters, positive estimates are considered as desirable. The results of heterosis, Better-parent heterosis and standard heterosis were presented in Table 4.3.

4.3.1 Days to 50 per cent anthesis

Mid-parent heterosis for 50 per cent anthesis ranged from -12.00% (PFSR-73×MGC-49) to 18.09% (PFSR-151×BML-10). Sixteen (16) out of 28 hybrids were showed significantly negative heterosis over the mid-parent. Better-parent heterosis ranged from -16.89% (PFSR-73×MGC-49) to 17.26% (PFSR-127×PFSR-92). Eighteen out of 28 hybrids recorded significantly negative better parent heterosis.

Standard heterosis ranged from -17.70% (BML-10×ML-14) to 2.21% (PFSR-73×PFSR-151, ML-14×BPDT-5009, PFSR-92×BPDT-5009). Twenty four (24) out of 28 hybrids were showed significantly negative standard heterosis.

Similar findings were also reported by Gami *et al.* (2018), Kanchao yu *et al.* (2020), Abdulazeez *et al.* (2021) and Agarwal *et al.* (2021) for the trait clearly indicating the possibility of exploiting heterosis for earliness.

4.3.2 Days to 50 per cent silking

Mid-parent heterosis for days to 50% silking ranged from -11.51% (PFSR-73×MGC-49) to 17.26% (PFSR-151×BML-10). Among the 28 hybrids, sixteen hybrids showed significantly negative mid parent heterosis. Better-parent heterosis ranged from -14.45% (PFSR-127 ×PFSR-92) to 16.08 (PFSR-151×BML-10). Among 28 hybrids, eighteen hybrids were recorded significantly negative heterosis over better parent.

Standard heterosis ranged from -16.38% (BML-10×ML-14) to 3.88% (PFSR-92×BPDT-5009). Twenty-three hybrids recorded significantly negative heterosis over the check, DHM-117.

Similar findings were also reported by Kanchao yu *et al.* (2020), Abdulazeez *et al.* (2021), Agarwal *et al.* (2021) and Tulu *et al.* (2021).

4.3.3 Anthesis silking interval

Mid-parent heterosis for anthesis silking interval ranged from -42.86% (PFSR-127×MGC-49) to 83.33 (PFSR-151×ML-14). Seven out of 28 hybrids showed significantly negative heterosis over mid-parent.

Better-parent heterosis for the character ranged from -50.00% (PFSR-73×ML-14, PFSR-127×MGC-49, MGC-49×PFSR-92 and MGC-49×BPDT-5009) to 66.67% (PFSR-92×BPDT-5009). Nine out of 28 hybrids showed significantly negative heterosis over better parent. Standard heterosis ranged from -75.00% (PFSR-73×ML-14) to 0.00% (PFSR-127×BPDT-5009).

The results for anthesis silking interval are in accordance with the earlier findings of Gazala *et al.* (2017), Karim *et al.* (2018), Nandhitha *et al.* (2018) and Reddy *et al.* (2018).

4.3.4 Days to maturity

Mid-parent heterosis for days to maturity ranged from -10.67% (BML-10×ML-14) to 8.09% (PFSR-151×BML-10). Fifteen out of the 28 hybrids showed significantly negative heterosis. Better-parent heterosis ranged from -14.58% (BML-10×ML-14) to 4.21% (PFSR-92×BPDT-5009). Eighteen out of the 28 hybrids recorded significantly negative heterosis over the better parent.

Standard heterosis ranged from -16.52% (PFSR-73×MGC-49) to 3.77% (PFSR-92×BPDT-5009). Twenty five out of the 28 hybrids recorded significantly negative

standard heterosis. Similar findings were also reported by Reddy *et al.* (2018), Kanchaoyu *et al.* (2020) and Upreti *et al.* (2020).

Generally, significantly negative heterosis for days to 50 per cent anthesis, days to 50 per cent silking, anthesis silking interval and days to maturity reveals the earliness of a genotype which is very important trait to suit well for the multiple cropping systems.

4.3.5 Plant height (cm)

Mid-parent heterosis for plant height ranged from -39.63% (ML-14×PFSR-92) to 36.53% (PFSR-73×BPDT-5009). Twenty one out of 28 hybrids recorded significantly positive heterosis and four hybrids were recorded significantly negative heterosis over the mid parent. Better-parent heterosis varied from -42.13% (ML-14×PFSR-92) to 20.73% (BML-10×MGC-49). Sixteen out of the 28 hybrids showed significantly positive heterosis while, seven hybrids were recorded significantly negative heterosis over the better parent.

Standard heterosis ranged from -45.91% (ML-14×PFSR-92) to 15.37% (PFSR-151×MGC-49). Ten out of 28 hybrids recorded significantly positive Standard heterosis while, ten hybrids recorded significantly negative standard heterosis.

The similar findings were also reported by Upreti *et al.* (2020), Habiba *et al.* (2021) for significant positive mid parent heterosis for plant height. Karim *et al.* (2018) and Chaurasia *et al.* (2021) reported significantly negative standard heterosis for this trait.

4.3.6 Ear height (cm)

Mid-parent heterosis for ear height ranged from -38.07% (ML-14 ×PFSR-92) to 40.85% (PFSR-73×BML-10). Twenty out of the 28 hybrids showed significantly positive heterosis over mid parent. Better-parent heterosis ranged from -44.29% (ML-14 ×PFSR-92) to 31.38% (PFSR-73×BML-10). Seventeen out of the 28 hybrids showed significantly positive heterosis over the better parent.

Standard heterosis ranged from -47.21% (ML-14 ×PFSR-92) to 20.10% (PFSR-73×BML-10). Among 28 hybrids, nine hybrids exhibited significantly positive Standard heterosis.

Significantly negative Better-parent heterosis for the trait was also reported by Gami *et al.* (2018) and Karim *et al.* (2018). Kanchao yu *et al.* (2020) and Suresh *et al.* (2021) reported positive standard heterosis for ear height.

4.3.7 Ear length (cm)

Mid-parent heterosis for ear length ranged from -18.97% (ML-14 ×PFSR-92) to 36.38% (PFSR-73×BPDT-5009). Among the 28 hybrids, twenty-five hybrids showed

significantly positive heterosis over mid parent, in which PFSR-73×BPDT-5009 (36.38) and BML-10×BPDT-5009 (36.11) recorded higher heterosis.

Better-parent heterosis varied from -19.24% (ML-14×PFSR-92) to 29.58% (MGC-49×ML-14). Among the 28 hybrids, fourteen hybrids showed significantly positive heterosis over the better parent.

Standard heterosis ranged from -36.29% (ML-14×PFSR-92) to 12.96% (PFSR-127×BML-10). Six out of 28 hybrids recorded significantly positive standard heterosis. These results are in accordance with the earlier findings of Nandhitha *et al.* (2018), Abdulazeez *et al.* (2021) and Tello (2021).

4.3.8 Ear girth (cm)

Mid-parent heterosis for ear girth ranged from -16.28% (PFSR-127×MGC-49) to 20.99% (PFSR-73×BML-10). Among the 28 hybrids, eighteen hybrids showed significantly positive heterosis over mid parent. Better-parent heterosis ranged from -21.18% (PFSR-73×PFSR-127) to 17.95% (BML-10×ML-14). Among the 28 hybrids, twelve hybrids recorded significantly positive heterosis over the better parent.

Standard heterosis ranged from -23.69% (MGC-49×BPDT-5009) to 6.42% (BML-10×ML-14). Among 28 hybrids, four hybrids recorded significantly positive heterosis over the check.

Significantly positive Mid-parent heterosis was also reported by Kanchaoyu *et al.* (2020), Better-parent heterosis by Gami *et al.* (2018) and standard heterosis by Tello (2021).

4.3.9 Number of kernel rows per ear

Mid-parent heterosis for number of kernel rows per ear varied from -25.00% (MGC-49×BPDT-5009) to 25.00% (ML-14×PFSR-92). Eleven out of the 28 hybrids showed significantly positive heterosis over mid parent. Better-parent heterosis ranged from -27.61% (MGC-49×BPDT-5009) to 16.67% (ML-14×PFSR-92). Among 28 hybrids, five hybrids recorded significantly positive heterosis over the better parent.

Standard heterosis ranged from -29.91% (MGC-49×BPDT-5009, PFSR-73×PFSR-127) to 0.93% (PFSR-127×BML-10, PFSR-127×BPDT-5009). None of the crosses showed significantly positive standard heterosis for this character.

These findings exhibited parallelism with earlier results of Upreti *et al.* (2020) for significantly positive mid and better parent heterosis and Tello (2021) for significantly positive standard heterosis.

Table 4.3. Estimates of heterosis over mid parent, better parent and standard check for yield and yield attributing traits in maize hybrids

Crosses	Days to 50% anthesis			Days to 50% silking			Anthesis silking interval		
	MH	BH	SH	H	HB	SH	MH	BH	SH
PFSR-73 × PFSR-127	-4.33**	-11.56**	-11.95**	-3.48**	-9.96**	-10.34**	20.00*	0.00	-25.00**
PFSR-73 × PFSR-151	11.33**	2.67**	2.21**	10.23**	2.60**	2.16**	-20.00*	-33.33**	-50.00**
PFSR-73 × BML-10	-1.22*	-9.78**	-10.18**	-2.35**	-9.96**	-10.34**	20.00*	0.00	-25.00**
PFSR-73 × MGC-49	-12.00**	-16.89**	-17.26**	-11.51**	-15.15**	-15.52**	0.00	-25.00**	-25.00**
PFSR-73 × ML-14	-2.49**	-4.44**	-4.87**	-3.11**	-5.63**	-6.03**	-33.33*	-50.00**	-75.00**
PFSR-73 × PFSR-92	-4.66**	-4.87**	-4.87**	-4.54**	-4.74**	-4.74**	9.09	0.00	-50.00**
PFSR-73 ×BPDT-5009	-3.13**	-3.56**	-3.98**	-1.74**	-2.16**	-2.59**	50.00**	50.00**	-25.00**
PFSR-127 × PFSR-151	-0.26	-0.52	-15.93**	-0.25	-0.50	-14.22**	0.00	0.00	-25.00**
PFSR-127 × BML-10	0.80	-0.52	-15.93**	0.76	-0.50	-14.22**	0.00	0.00	-25.00**
PFSR-127 × MGC-49	10.49**	8.00**	-4.42**	7.77**	4.72**	-4.31**	-42.86**	-50.00**	-50.00**
PFSR-127 × ML-14	6.14**	0.00	-4.42**	7.40**	2.74**	-3.02**	50.00**	0.00	-25.00**
PFSR-127× PFSR-92	-10.31**	17.26**	-17.26**	-9.26**	-14.45**	-15.52**	28.57**	0.00	-25.00**
PFSR-127× BPDT-5009	4.35**	-3.14**	-4.42**	6.76**	0.00	-1.29*	60.00**	33.33**	0.00
PFSR-151 × BML-10	18.09**	16.84**	-1.77**	17.26**	16.08**	-0.43	0.00	0.00	-25.00**
PFSR-151 × MGC-49	-3.08**	-5.50**	-16.37**	-4.62**	-7.55**	-15.52**	-33.33**	-41.67**	-41.67**
PFSR-151 × ML-14	-1.48**	-7.41**	-11.50**	0.96	-3.65**	-9.05**	83.33**	22.22**	-8.33

Table 4.3 (cont.).

Crosses	Days to 50% anthesis			Days to 50% silking			Anthesis silking interval		
	MH	BH	SH	MH	BH	SH	MH	BH	SH
PFSR-151 × PFSR-92	-9.13**	-16.35**	-16.37**	-8.58**	-15.07**	-15.09**	14.29	-11.11	-33.33**
PFSR-151 × BPDT-5009	-8.47**	-15.25**	-16.37**	-7.48**	-13.54**	-14.66**	20.00*	0.00	-25.00**
BML-10 × MGC-49	-1.55**	-5.00**	-15.93**	-2.21**	-6.13**	-14.22**	-14.29*	-25.00**	-25.00**
BML-10 × ML-14	-7.46**	-13.89**	-17.70**	-6.28**	-11.62**	-16.38**	33.33**	-11.11	-33.33**
BML-10 × PFSR-92	6.80**	-15.04**	-15.04**	-5.85**	-13.34**	-13.36**	28.57**	0.00	-25.00**
BML-10 × BPDT-5009	-8.56**	-16.14**	-17.26**	-7.55**	-14.41**	-15.52**	20.00*	0.00	-25.00**
MGC-49 × ML-14	-9.13**	-12.50**	-16.37**	-8.12**	-9.59**	-14.66**	20.00*	-25.00**	-25.00**
MGC-49 × PFSR-92	4.69**	-1.33**	-1.33**	3.15**	-1.05*	-1.29*	-29.41**	-50.00**	-50.00**
MGC-49 × BPDT-5009	8.27**	2.69**	1.33**	6.58**	2.62**	1.29*	-33.33**	-50.00**	-50.00**
ML-14 × PFSR-92	-4.07**	-6.19**	-6.19**	-4.66**	-7.39**	-7.33**	25.00	0.00	-58.33**
ML-14 × BPDT-5009	5.24**	3.59**	2.21**	6.70**	4.37**	3.02**	77.78**	33.33**	-33.33**
PFSR-92 × BPDT-5009	2.90**	2.52**	2.21**	4.56**	3.97**	3.88**	81.82**	66.67**	-16.67**
Range (lowest)	-12.00	-16.89	-17.70	-11.51	-14.45	-16.38	-42.86	-50.00	-75.00
Range (highest)	18.09	17.26	2.21	17.26	16.08	3.88	83.33	66.67	0.00

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

MH: Mid-parent heterosis, BH: Better-parent heterosis, SH: Standard heterosis over the check, DHM-117

Table 4.3 (cont.).

Crosses	Days to maturity			Plant height (cm)			Ear height (cm)		
Heterosis	MH	BH	SH	MH	BH	SH	MH	BH	SH
PFSR-73 × PFSR-127	-2.95**	-6.92**	-14.20**	16.15**	12.32**	6.31**	9.97**	5.25*	3.27*
PFSR-73 × PFSR-151	1.77**	-0.31	-8.12**	-2.90**	-5.34**	-6.90**	32.10**	18.24**	8.09**
PFSR-73 × BML-10	3.33**	2.52**	-5.51**	11.23**	9.09**	1.90	40.85**	31.38**	20.10**
PFSR-73 × MGC-49	-8.72**	-9.43**	-16.52**	13.09**	9.40**	2.19	24.83**	21.83**	17.00**
PFSR-73 × ML-14	-4.39**	-7.87**	-8.41**	11.73**	11.69**	4.40**	28.67**	17.64**	7.54**
PFSR-73 × PFSR-92	-6.49**	-10.14**	-10.14**	13.24**	8.59**	1.44	8.93**	7.01**	1.40
PFSR-73 × BPDT-5009	-1.08*	-2.74**	-7.25**	36.53**	18.11**	10.33**	-3.01	-9.95**	-17.68**
PFSR-127 × PFSR-151	-2.85**	-4.92**	-15.94**	2.42*	1.95	1.58	6.44**	-5.34**	-8.34**
PFSR-127 × BML-10	0.50	-2.88**	-11.88**	16.06**	10.15**	13.81**	28.94**	18.52**	15.48**
PFSR-127 × MGC-49	4.46**	0.96	-8.41**	0.35	-5.10**	-6.01**	-5.02**	-7.86**	-9.84**
PFSR-127 × ML-14	3.94**	-3.79**	-4.35**	3.02**	-0.34	-0.67	2.52	-8.96**	-9.91**
PFSR-127 × PFSR-92	-4.55**	-10.59**	-11.88**	9.87**	3.45	2.04	-25.45**	-26.40**	-27.40**
PFSR-127 × BPDT-5009	4.99**	-0.91	-5.51**	30.66**	13.54**	9.89**	6.72**	-3.87*	-4.84*
PFSR-151 × BML-10	8.09**	6.71**	-3.19**	7.13**	2.47*	0.78	25.98**	20.50**	-4.66
PFSR-151 × MGC-49	-2.59**	-3.83**	-12.75**	24.27**	17.30**	15.37**	31.32**	15.04**	10.49**
PFSR-151 × ML-14	0.93	-4.66**	-5.22**	-13.12**	-15.28**	-16.67**	9.33**	6.80*	-19.11**

Table 4.3 (cont.).

Crosses	Days to maturity			Plant height (cm)			Ear height (cm)		
	MH	BH	SH	MH	BH	SH	MH	BH	SH
PFSR-151 × PFSR-92	-10.15**	-13.37**	-15.36**	16.20**	8.75**	6.98**	10.07**	-3.02	-8.10**
PFSR-151 × BPDT-5009	-3.79**	-7.29**	-11.59**	7.68**	-8.82**	-10.33**	18.83**	14.20**	-10.54**
BML-10 × MGC-49	1.92**	1.92**	-7.54**	22.43**	20.73**	8.43**	20.80**	10.15**	5.79*
BML-10 × ML-14	-10.67**	-14.58**	-15.07**	1.53	-0.46	-6.96**	22.54**	19.93**	-5.12*
BML-10 × PFSR-92	-5.17**	-7.59**	-9.57**	15.36**	12.75**	1.26	16.88**	7.23**	1.62
BML-10 × BPDT-5009	-4.67**	-6.99**	-11.30**	30.14**	14.49**	2.82*	31.83**	31.18**	3.78
MGC-49 × ML-14	-7.93**	-11.95**	-12.46**	15.19**	11.39**	4.12**	20.13**	7.43**	3.18
MGC-49 × PFSR-92	5.78**	0.91	0.87	6.99**	6.02**	-7.43**	15.12**	14.35**	9.82**
MGC-49 × BPDT-5009	5.92**	3.34**	-1.45**	10.66**	-1.45	-13.95**	2.64	-6.82**	-10.51**
ML-14 × PFSR-92	-7.56**	-7.75**	-7.83**	-39.63**	-42.13**	-45.91**	-38.07**	-44.29**	-47.21**
ML-14 × BPDT-5009	5.65**	3.50**	2.90**	-25.99**	-35.99**	-40.17**	-26.66**	-27.88**	-43.50**
PFSR-92 × BPDT-5009	6.23**	4.21**	3.77**	-0.39	-10.58**	-23.33**	-8.61**	-16.53**	-20.90**
Range (lowest)	-10.67	-14.58	-16.52	-39.63	-42.13	-45.91	-38.07	-44.29	-47.21
Range (highest)	8.09	4.21	3.77	36.53	20.73	15.37	40.85	31.38	20.10

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

MH: Mid-parent heterosis, BH: Better-parent heterosis, SH: Standard heterosis over the check, DHM-117

Table 4.3 (cont.).

Crosses	Ear length (cm)			Ear girth (cm)			Number of kernel rows per ear		
	MH	BH	SH	MH	BH	SH	MH	BH	SH
PFSR-73 × PFSR-127	7.39**	0.47	0.21	-14.21**	-21.18**	-18.66**	-24.24**	-27.88**	-29.91**
PFSR-73 × PFSR-151	4.33**	-1.04	-3.91**	-5.26**	-10.71**	-15.48**	-0.53	-1.05	-12.15**
PFSR-73 × BML-10	15.62**	15.57**	0.68	20.99**	16.66**	5.25**	4.00*	-1.89	-2.80
PFSR-73 × MGC-49	27.40**	22.62**	6.82**	4.85**	-2.05	-5.52**	-0.50	-6.54**	-6.54**
PFSR-73 × ML-14	22.72**	16.93**	1.87	10.13**	8.22**	-6.10**	3.26	1.06	-11.21**
PFSR-73 × PFSR-92	18.57**	12.61**	-1.90	14.41**	9.53**	-8.25**	12.79**	3.19	-9.35**
PFSR-73 ×BPDT-5009	36.38**	17.55**	2.40*	11.08**	9.53**	-8.25**	-4.81**	-5.32**	-16.82**
PFSR-127 × PFSR-151	-1.04	-2.48*	-2.48*	1.27	-1.44	-0.41	7.54**	2.88	0.00
PFSR-127 × BML-10	20.78**	18.96**	12.96**	18.57**	16.66**	6.20**	2.86	1.89	0.93
PFSR-127 × MGC-49	-6.18**	-16.32**	-15.29**	-16.28**	-17.77**	-15.14*	-17.54**	-18.58**	-18.69**
PFSR-127 × ML-14	10.43**	-2.22	-1.22	7.28**	0.18	0.18	5.15**	-1.92	-4.67**
PFSR-127× PFSR-92	13.95**	2.63	1.62	12.21**	9.92**	6.02**	3.30	-9.62**	-12.15**
PFSR-127× BPDT-5009	17.15**	-5.51**	-4.49**	6.38**	-3.50**	-0.42	9.64**	3.85*	0.93
PFSR-151 × BML-10	5.85**	0.37	-2.55*	2.21	-0.19	-5.52**	5.47**	0.00	-0.93
PFSR-151 × MGC-49	26.59**	15.82**	12.46**	-4.41**	-5.30**	-8.66**	-10.89**	-15.71**	-15.89**
PFSR-151 × ML-14	15.81**	4.95**	1.90	7.62**	3.13*	-2.38	8.11**	5.26**	-6.54**

Table 4.3 (cont.).

Crosses	Ear length (cm)			Ear girth (cm)			Number of kernel rows per ear		
	MH	BH	SH	MH	BH	SH	MH	BH	SH
PFSR-151 × PFSR-92	11.66**	0.89	-2.05	10.58**	0.05	-5.29**	1.73	-7.37**	-17.76**
PFSR-151 × BPDT-5009	13.58**	-6.32**	-9.05**	15.41**	7.35**	1.62	5.32**	4.21*	-7.48**
BML-10 × MGC-49	19.61**	15.18**	0.25	2.52*	-0.79	-4.31**	-8.92**	-9.32**	-9.35**
BML-10 × ML-14	20.48**	14.85**	-0.04	20.25**	17.95**	6.42**	-1.02	-8.49**	-9.35**
BML-10 × PFSR-92	24.35**	18.14**	2.84*	20.30**	11.24**	0.36	14.13**	-0.94	-1.87
BML-10 × BPDT-5009	36.11**	17.36**	2.15	9.78**	4.43**	-5.79**	-4.52**	-10.38**	-11.21**
MGC-49 × ML-14	30.95**	29.58**	4.41**	2.50	-2.65	-6.10**	-5.58**	-11.32**	-13.08**
MGC-49 × PFSR-92	11.29**	9.76**	-11.56**	-4.56**	-14.37**	-17.41**	-2.70	-12.78**	-15.89**
MGC-49 × BPDT-5009	7.05**	-4.59**	-23.12**	-14.20**	-20.88**	-23.69**	-25.00**	-27.61**	-29.91**
ML-14 × PFSR-92	-18.97**	-19.24**	-36.29**	11.86**	5.33**	-8.61**	25.00**	16.67**	-1.87
ML-14 × BPDT-5009	8.57**	-2.32	-22.94**	5.36**	2.12	-11.40**	14.75**	12.90**	-1.87
PFSR-92 × BPDT-5009	13.96**	2.84	-19.42**	-2.87	-5.73**	-23.24**	-0.58	-8.60**	-20.56**
Range (lowest)	-18.97	-19.24	-36.29	-16.28	-21.18	-23.69	-25.00	-27.61	-29.91
Range (highest)	36.38	29.58	12.96	20.99	17.95	6.42	25.00	16.67	0.93

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

MH: Mid-parent heterosis, BH: Better-parent heterosis, SH: Standard heterosis over the check, DHM-117

Table 4.3 (cont.).

Crosses	Number of kernels per row			100-kernel weight (g)			Grain yield (g/plant)		
	MH	BH	SH	MH	BH	SH	MH	BH	SH
PFSR-73 × PFSR-127	27.16**	17.62**	-4.82	-6.08*	-10.51**	-14.55**	-30.54**	-37.59**	-41.41**
PFSR-73 × PFSR-151	-12.56*	-25.10**	-26.20**	6.55*	3.34	-10.64**	-3.48	-7.00*	-20.05**
PFSR-73 × BML-10	24.15**	7.11	1.54	2.24	1.86	-11.26**	29.24**	23.50**	8.02**
PFSR-73 × MGC-49	54.78**	48.96**	10.79*	-3.44	-4.12	-17.09**	22.20**	18.55**	-5.51
PFSR-73 × ML-14	27.62**	24.07**	-9.63	56.55**	28.83**	11.41**	77.61**	44.65**	15.29**
PFSR-73 × PFSR-92	65.79**	50.70**	3.66	-17.70**	-23.26**	-23.26**	7.66*	-7.23*	-26.07**
PFSR-73 × BPDT-5009	26.41**	19.06**	-7.32	12.38**	-9.29**	-21.56**	28.48**	0.00	-20.30**
PFSR-127 × PFSR-151	5.64	-4.39	-4.43	14.93**	6.37	1.57	33.15**	23.81**	16.24**
PFSR-127 × BML-10	24.12**	15.04**	9.06	21.44**	16.12**	10.88**	50.27**	40.85**	32.24**
PFSR-127 × MGC-49	1.99	-2.14	-20.81**	-0.56	-5.89	-10.14**	-19.77**	-29.82**	-34.12**
PFSR-127 × ML-14	9.77	4.29	-15.61**	37.77**	9.18**	4.25	56.93**	17.79**	10.59**
PFSR-127 × PFSR-92	23.88**	5.00	-15.03**	3.00	0.68	0.68	42.77**	12.53**	5.65**
PFSR-127 × BPDT-5009	16.50**	14.29*	-7.51	34.61**	4.75	0.02	60.07**	15.54**	8.47**
PFSR-151 × BML-10	-10.58*	-12.89*	-12.91*	-11.64**	-14.61**	-25.60**	13.58**	12.61**	-1.50
PFSR-151 × MGC-49	25.52**	10.21	9.44	21.61**	18.77**	1.25	47.35**	37.90**	18.55**
PFSR-151 × ML-14	11.04*	-4.01	-4.05	36.68**	15.32**	-6.29*	50.64**	19.24**	2.51

Table 4.3 (cont.).

Crosses	Number of kernels per row			100-kernel weight (g)			Grain yield (g/plant)		
	MH	BH	SH	MH	BH	SH	MH	BH	SH
PFSR-151 × PFSR-92	10.23	-13.87**	-13.87**	8.91**	-1.19	-1.30	44.85**	20.99**	4.01
PFSR-151 × BPDT-5009	7.91	-4.02	-4.05	48.08**	22.44**	-0.50	86.15**	41.11**	21.30**
BML-10 × MGC-49	7.74	-3.86	-8.86	-6.40*	-7.40*	-19.32**	0.00	-7.16*	-18.80**
BML-10 × ML-14	25.75**	11.18*	5.39	34.73**	10.56**	-3.68	58.11**	24.36**	8.77**
BML-10 × PFSR-92	24.74**	-0.61	-5.78	-1.90	-8.02**	-8.21**	56.48**	29.80**	13.53**
BML-10 × BPDT-5009	6.47	-3.05	-8.09	49.02**	19.94**	4.49	60.46**	20.92**	5.76*
MGC-49 × ML-14	43.19**	41.71**	5.39	38.72**	14.81**	-2.12	71.94**	43.48**	7.52**
MGC-49 × PFSR-92	9.73	-3.63	-28.32**	-14.88**	-20.17**	-21.15**	-32.33**	-40.13**	-55.14**
MGC-49 × BPDT-5009	-24.05**	-25.74**	-42.20**	6.56	-13.52**	-26.27**	-44.12**	-55.52**	-66.67**
ML-14 × PFSR-92	-16.42*	-25.93**	-46.05**	18.83**	-7.40*	-7.40	8.37	1.30	-41.60**
ML-14 × BPDT-5009	-37.60**	-39.60**	-52.99**	21.94**	18.95**	-33.56**	-5.57	-11.00	-55.39**
PFSR-92 × BPDT-5009	30.46**	12.38	-12.52*	-24.79**	-41.15**	-42.42**	-9.58*	-20.00**	-53.88**
Range (lowest)	-37.60	-39.60	-52.99	-24.79	-41.15	-42.42	-44.12	-55.52	-66.67
Range (highest)	65.79	50.70	10.79	56.55	28.83	11.41	86.15	44.65	32.24

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

MH: Mid-parent heterosis, BH: Better-parent heterosis, SH: Standard heterosis over the check, DHM-117

Table 4.4. Standard heterosis, Better-parent heterosis and Mid-parent heterosis for top five crosses for each trait in maize hybrids

Character/Cross	Standard heterosis	Better-parent heterosis	Mid-parent heterosis
Days to 50 per cent anthesis			
BML-10×ML-14	-17.70**	-13.89**	-7.46**
PFSR-73×MGC-49	-17.26**	-16.89**	-12.00**
BML-10×BPDT-5009	-17.26**	-16.14**	-8.56**
PFSR-151×PFSR-92	-16.37**	-16.35**	-9.13**
PFSR-151×BPDT-5009	-16.37**	-15.25**	-8.47**
Days to 50 per cent silking			
BML-10×ML-14	-16.38**	-11.62**	-6.28**
PFSR-73×MGC-49	-15.52**	-15.15**	-11.51**
PFSR-127×PFSR-92	-15.52**	-14.45**	-9.26**
BML-10×BPDT-5009	-15.52**	-14.41**	-7.55**
PFSR-151×MGC-49	-15.52**	-7.55**	-4.62**
Anthesis silking interval			
PFSR-73×ML-14	-75.00**	-50.00**	-33.33*
ML-14×PFSR-92	-58.33**	0.00	25.00
PFSR-127×MGC-49	-50.00**	-50.00**	-42.86**
MGC-49×BPDT-5009	-50.00**	-50.00**	-33.33**
MGC-49×PFSR-92	-50.00**	-50.00**	-29.41**
Days to maturity			
PFSR-73×MGC-49	-16.52**	-9.43**	-8.73**
PFSR-127×PFSR-151	-15.94**	-4.92**	-2.85**
PFSR-151×PFSR-92	-15.36**	-15.36**	-10.15**
BML-10×ML-14	-15.07**	-13.37**	-10.67**
PFSR-151×MGC-49	-12.75**	-3.83**	-2.59**
Plant height (cm)			
PFSR-151×MGC-49	15.37**	17.30**	24.27**
PFSR-73×BPDT-5009	10.33**	18.11**	36.53**
PFSR-127×BML-10	10.15**	13.81**	16.06**
PFSR-73×BPDT-5009	9.89**	13.54**	30.66**
BML-10×MGC-49	8.43**	20.73**	22.43**

Table 4.4 (cont.).

Character/Cross	Standard heterosis	Better-parent heterosis	Mid-parent heterosis
Ear height (cm)			
ML-14×PFSR-92	-47.21**	-44.29**	-38.07**
ML-14×BPDT-5009	-43.50**	-27.88**	-26.66**
PFSR-127×PFSR-92	-27.40**	-26.40**	-25.45**
PFSR-92×BPDT-5009	-20.90**	-16.53**	-8.61**
PFSR-151×ML-14	-19.11**	6.80*	9.33**
Ear length (cm)			
PFSR-127×BML-10	12.96**	18.96**	20.78**
PFSR-151×MGC-49	12.46**	15.82**	26.59**
PFSR-73×MGC-49	6.82**	22.62**	27.40**
MGC-49×ML-14	4.41**	29.58**	30.95**
BML-10×PFSR-92	2.84*	18.14**	24.35**
Ear girth (cm)			
BML-10×ML-14	6.42**	17.95**	20.25**
PFSR-127×BML-10	6.20**	16.66**	18.57**
PFSR-127×PFSR-92	6.02**	9.92*	12.21**
PFSR-73×BML-10	5.25*	16.66*	20.99**
PFSR-151×BPDT-5009	1.62	7.35**	15.41**
Number of kernel rows per ear			
PFSR-127×BPDT-5009	0.93	3.85*	9.64**
PFSR-127×BML-10	0.93	1.89	2.86
PFSR-127×PFSR-151	0.00	2.88	7.54**
PFSR-151×BML-10	-0.93	0.00	5.47**
ML-14×PFSR-92	-1.87	16.67**	25.00**
Number of kernels per row			
PFSR-73×MGC-49	10.79*	48.96**	54.78**
PFSR-127×BML-10	9.06	15.04**	24.12**
MGC-49×ML-14	5.39	41.71**	43.19**
BML-10×ML-14	5.39	11.18**	25.75**
PFSR-73×PFSR-92	3.66	50.70**	65.79**
100-kernel weight (g)			
PFSR-73×ML-14	11.41**	28.83**	56.55**
PFSR-127×BML-10	10.88**	16.12**	21.44**
BML-10×BPDT-5009	4.49	19.94**	49.02**
PFSR-127×ML-14	4.25	9.18**	37.77**
PFSR-127×PFSR-151	1.57	6.37	14.93**

Table 4.4 (cont.).

S. No	Character/Cross	Standard heterosis	Better-parent heterosis	Mid-parent heterosis
12	Grain yield per plant (g)			
1	PFSR-127×BML-10	32.24**	40.85**	50.27**
2	PFSR-151×BPDT-5009	21.30**	41.11**	86.15**
3	PFSR-151×MGC-49	18.55**	37.90**	47.35**
4	PFSR-127×PFSR-151	16.24**	23.81**	33.15**
5	PFSR-73×ML-14	15.29**	44.65**	77.61**

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

4.3.10 Number of kernels per row

Mid-parent heterosis for number of kernels per row ranged from -37.60% (ML-14×BPDT-5009) to 65.79% (PFSR-73×PFSR-92). Among the 28 hybrids, fifteen hybrids recorded significantly positive heterosis over the mid parent, among which PFSR-73×PFSR-92 (65.79%) and PFSR-73×MGC-49 (54.78%) recorded high Mid-parent heterosis.

Better-parent heterosis for number of kernels per row varied from -39.60% (ML-14×BPDT-5009) to 50.70% (PFSR-73×PFSR-92). Among 28 hybrids, nine hybrids recorded significantly positive heterosis over the better parent.

Standard heterosis ranged from -52.99% (ML-14×BPDT-5009) to 10.79% (PFSR-73×MGC-49). Only one out of the 28 hybrids recorded significantly positive heterosis over the check.

Similar findings of significantly positive mid and better parent heterosis were reported by Upreti *et al.* (2020) and standard heterosis by Tello (2021).

4.3.11 100-kernel weight (g)

Mid-parent heterosis for 100-kernel weight ranged from -24.79% (PFSR-92×BPDT-5009) to 56.55% (PFSR-73×ML-14). Among the 28 hybrids, sixteen hybrids recorded significantly positive heterosis, among which PFSR-73×ML-14 (56.55%), BML-10×BPDT-5009(49.02%) and PFSR-151×BPDT-5009 (48.08%) recorded high Mid-parent heterosis.

Better-parent heterosis ranged from -41.15% (PFSR-92×BPDT-5009) to 28.83% (PFSR-73×ML-14). Among the 28 hybrids, ten hybrids recorded significantly positive heterosis over the better parent.

Standard heterosis ranged from -42.42% (PFSR-92×BPDT-5009) to 11.41% (PFSR-73×ML-14). Among 28 hybrids, two hybrids recorded significantly positive standard heterosis.

These findings are in accordance with the earlier findings of Gami *et al.* (2018) for Better-parent heterosis, Chaurasia *et al.* (2021) and Tello (2021) for standard heterosis.

4.3.12 Grain yield (g/plant)

Mid-parent heterosis for grain yield ranged from -44.12% (MGC-49×BPDT-5009) to 86.15% (PFSR-151×BPDT-5009). Nineteen out of the 28 hybrids recorded significantly positive heterosis over mid parent.

Better-parent heterosis ranged from -55.52% (MGC-49×BPDT-5009) to 44.65% (PFSR-73×ML-14). Among 28 hybrids, seventeen hybrids registered significantly positive heterosis over better parent. The hybrids PFSR-73×ML-14 (44.65%), MGC-49×ML-14 (43.48%), PFSR-151×BPDT-5009 (41.11%) and PFSR-127×BML-10 (40.85%) were found superior among all the hybrids.

Standard heterosis ranged from -66.67% (MGC-49×BPDT-5009) to 32.24% (PFSR-127×BML-10). Thirteen among the 28 hybrids recorded significantly positive heterosis the over the check. The hybrids PFSR-127×BML-10 (32.24%), PFSR-151×BPDT-5009 (21.30%) and PFSR-151×MGC-49 (18.55%) were found superior among all the hybrids under study.

These findings on grain yield were also supported by Karim *et al.* (2018), Reddy *et al.* (2018), Upreti *et al.* (2020), Agarwal *et al.* (2021) and Abdulazeez *et al.* (2021) for average heterosis; Sharma *et al.* (2017) and Gami *et al.* (2018) for better parent heterosis; Gazala *et al.* (2017), Nandhitha *et al.* (2018), Chaurasia *et al.* (2021) and Gemechu *et al.* (2021) for standard heterosis.

In general, presence of significant heterosis, Better-parent heterosis and standard heterosis for grain yield per plant and other associated traits indicates the presence of high genetic diversity among the parents and crosses as well as the unidirectional distribution of allelic constitution contributing to desirable heterosis in the present material. Negative heterosis in number of crosses for variables like days to 50% anthesis, days to 50% silking, anthesis silking interval and days to maturity revealed that the hybrids were superior to their parents for these traits and heterotic effects were in the desired direction. Crosses with good heterotic expression in F₁ could be explored further in future generations to select superior transgressive segregants.

4.4 Combining ability analysis

The concept of combining ability was given by Sprague and Tatum (1942) which facilitates the partitioning of genotypic variation of hybrids into variation due to general combining ability (main effects) and specific combining ability (interaction effects). This analysis helps in determining the gene action controlling the trait and it helps breeders in identifying suitable parents for hybridization and superior cross combinations through General combining ability (*gca*) and Specific combining ability (*sca*) studies respectively.

The data recorded on 28 hybrids and eight parents along with one check were used for combining ability analysis using half diallel mating design. The results of the analysis are discussed under the following sub heads:

4.4.1 Analysis of variance for combining ability based on half diallel design

4.4.2 General combining ability effects and specific combining ability effects

4.4.3 GCA and SCA variance and gene action

4.4.1 Analysis of variance for combining ability based on half diallel design

The analysis of variance for combining ability of all the traits under present study has been presented in the Table 4.5.

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

4.4.2 General combining ability effects and specific combining ability effects

General combining ability (*gca*) is the average performance of an inbred in a series of hybrid combinations and is mainly attributed due to additive and additive \times additive gene effects and thus provides the measure of variance due to additive gene action. This analysis enables the breeder in identifying parents that have the ability to transmit their desirable traits to the offspring as additive gene effects prevail in the offspring.

According to Sprague and Tatum (1942), low *gca* estimates indicate that the inbred line or the value of its combination with other inbred lines do not differ from the average of all crosses while, the high and positive *gca* estimates are of interest when the aim is to increase the value of the trait of interest. The additive parental effects measured by *gca* effects in terms of fixable genetic variance are of practical use on account of their

response to selection and possibility of genetic enhancement of a genotype for specific attribute through normal selection procedure.

Specific combining ability (*sca*) is the performance of a parent in a specific cross in relation to *gca* and it gives the measure of variance due to non-additive gene action. The *sca* analysis used to identify promising hybrid combinations as non-additive gene effects prevail in these combinations.

The *sca* effects represent that dominance and epistatic components are more relevant for the improvement of cross-pollinated crops where commercial exploitation of heterosis is feasible. The specific crosses involving good general combiners having high *sca* effects may be utilized for hybrid breeding emphasizing the importance of *sca* effects.

The general combining ability effects of 8 parents and specific combining ability effects of the resultant 28 hybrid combinations were estimated as per the half diallel mating design. The trait wise results *gca* effects of parents have been presented in Table 4.6 and *sca* effects of hybrids are presented in Table 4.7.

4.4.2.1 Days to 50 per cent anthesis

***gca* effects**

For days to 50 per cent anthesis, *gca* effects among parents ranged from -3.58 (BML-10) to 3.21 (BPDT-5009). Among the parents, BML-10 (-3.58), PFSR-151 (-1.98), PFSR-127 (-1.78) and MGC-49 (-0.88) exhibited significant *gca* effect, implying that these lines are good general combiners for earliness, while, ML-14 (1.05), PFSR-92 (1.71), PFSR-73 (2.25) and BPDT-5009 (3.21) exhibited significantly positive effects and considered to be poor combiners for earliness.

The findings are in accordance with the earlier findings of Murtadha *et al.* (2018), Abd-Elaziz *et al.* (2021) and El-Gazzar (2021) who reported the importance of additive gene action for days to 50 per cent anthesis. Therefore, the identified lines are effective for generation of early maturing maize hybrids.

***sca* effects**

The *sca* effects for days to 50 per cent anthesis, ranged from -7.53 (PFSR-73×MGC-49) to 11.06 (PFSR-151×BML-10). Among the 28 hybrids, seventeen hybrids recorded significant negative *sca* effects. The hybrids, PFSR-73×MGC-49 (-7.53), PFSR-151×BPDT-5009 (-6.73), PFSR-127×PFSR-92 (-6.10), BML-10×BPDT-5009 (-5.80) and MGC-49×ML-14 (-5.66) showed negative and significant *sca* effect which is desirable for earliness.

These results are comparable with the findings of Murtadha *et al.* (2018), Abd-Elaziz *et al.* (2021) and El-Gazzar (2021) that revealed the importance of non-additive gene action for days to 50 per cent anthesis.

4.4.2.2 Days to 50 per cent silking

***gca* effects**

For days to 50 per cent silking, *gca* effects ranged from -3.40 (BML-10) to 3.39 (BPDT-5009). Among the 8 parents, four parents exhibited significant negative *gca* effects, among which the highest negative significant *gca* effect was recorded by BML-10 (3.40) followed by PFSR-151 (-1.77), PFSR-127 (-1.40) and MGC-49 (-0.70), indicating that these parents are good general combiners for earliness. However, the parents, ML-14 (0.59), PFSR-92 (1.45), PFSR-73 (1.85) and BPDT-5009 (3.39) recorded significant positive *gca* effects, indicating that these are poor general combiners for earliness.

Similar findings were also reported by Begum *et al.* (2018), Sandesh *et al.* (2018) and Sun *et al.* (2018) who reported the importance of additive gene action in governing days to 50 per cent silking.

***sca* effects**

The range of *sca* effects for days to 50 per cent silking varied from -6.93 (PFSR-73×MGC-49) to 11.06 (PFSR-151×BML-10). Among the 28 hybrids, sixteen hybrids exhibited significantly negative *sca* effects. The hybrid, PFSR-73×MGC-49 (-6.93) recorded the highest negative significant *sca* effect followed by PFSR-151×BPDT-5009 (-6.73), PFSR-127×PFSR-92 (-5.83), BML-10×BPDT-5009 (-5.77) and PFSR-151×PFSR-92 (-5.13).

None of the parent was a good general combiner in four crosses out of sixteen desirable crosses under the study indicating the predominance of non-additive (dominance × dominance) gene action while in the remaining crosses, at least one parent was a good general combiner, indicating the predominance of non-additive (additive × dominance) gene action in the inheritance of this character. Hence, heterosis breeding can be exploited in improvement of the trait.

These results are in accordance with the earlier findings of Sandesh *et al.* (2018) and Darshan and Marker (2019) who reported non-additive gene action for days to 50 per cent silking.

4.4.2.3 Anthesis silking interval

***gca* effects**

For anthesis silking interval, *gca* effects ranged from -0.42 (ML-14) to 0.27 (BML-10). Among the 8 parents, three parents showed negative significant *gca* effects, among which the highest negative significant *gca* effects were recorded by ML-14 (-0.42) followed by PFSR-73 (-0.29) and PFSR-92 (-0.29) and the remaining parents showed positive and significant *gca* effects. These results are in agreement with the findings of Patel (2022).

***sca* effects**

The *sca* effects for anthesis silking interval ranged from -1.10 (PFSR-127×MGC-49) to 1.25 (PFSR-151×ML-14). Among 28 hybrids, six hybrids showed significantly negative *sca* effect. The hybrid, PFSR-127×MGC-49 (-1.10) recorded the highest significant negative *sca* effect followed by PFSR-73×ML-14 (-0.94), MGC-49×BPDT-5009 (-0.90), PFSR-151×MGC-49 (-0.64), PFSR-73×PFSR-151 (-0.54) and MGC-49×PFSR-92 (-0.50).

Out of six desirable crosses, three crosses had neither of parents as good general combiners, implying that predominance of non-additive (dominance × dominance) gene action. In the remaining three desirable crosses, one cross had both the parents as good general combiners while the remaining two crosses had at least one parent as a good general combiner indicating that predominance of non-additive (additive × dominance) gene action in the later two crosses in the inheritance of this character and heterosis breeding is rewarding the improvement of this character.

4.4.2.4 Days to maturity

***gca* effects**

The *gca* effects for days to maturity ranged from -3.42 (PFSR-127) to 3.84 (BPDT-5009). Among the parents, five parents showed significantly negative *gca* effects. The parent PFSR-127 (-3.42) had the highest negative significant *gca* effect followed by PFSR-151 (-2.55), PFSR-73 (-1.45), BML-10 (-1.09) and MGC-49 (-0.42). Whereas, three parents showed significant and positive *gca* effect for the trait.

***sca* effects**

The *sca* effects for days to maturity ranged from -9.37 (BML-10×ML-14) to 9.32 (PFSR-151×BML-10). Fifteen hybrids showed significantly negative *sca* effects. The hybrid, BML-10×ML-14 (-9.37) showed the highest negative significant *sca* effect followed by PFSR-151×PFSR-92 (-8.40), PFSR-73×MGC-49 (-7.77), MGC-49×ML-14 (-7.04) and BML-10×BPDT-5009 (-6.40).

Two among the fifteen desirable crosses both the parents as good general combiners while the remaining thirteen crosses had at least one parent as a good general combiner indicating that predominance of non-additive (additive \times dominance) gene action.

Similar results were also reported by Yadav and Gangwar (2021) for additive and non-additive gene action governing the trait.

4.4.2.5 Plant height (cm)

***gca* effects**

For plant height, *gca* effects ranged from -20.00 (BPDT-5009) to 16.35 (PFSR-127). Three parents among eight showed significantly negative *gca* effects and considered to be good general combiners for dwarfness, while, the remaining five parents exhibited significantly positive *gca* effects. Similar results were reported by Hussain *et al.* (2019) and Sayed *et al.* (2022).

***sca* effects**

For plant height, *sca* effects ranged from -66.25 (ML-14 \times PFSR-92) to 41.96 (PFSR-73 \times BPDT-5009). Among 28 hybrids, ten hybrids showed significantly negative *sca* effects. The hybrid, PFSR-73 \times BPDT-5009 (41.96) recorded the highest positive significant *sca* effect followed by PFSR-127 \times BPDT-5009 (37.00), PFSR-151 \times MGC-49 (34.99), MGC-49 \times ML-14 (32.60) and PFSR-151 \times PFSR-92 (31.93). Similar kind of results were also reported by Sayed *et al.* (2022) for additive and non-additive gene action governing the trait.

4.4.2.6 Ear height (cm)

***gca* effects**

For ear height, *gca* effects ranged from -7.09 (ML-14) to 6.17 (PFSR-73). Four parents among eight showed significantly negative *gca* effects and considered to be good general combiners. while, the remaining four parents exhibited significantly positive *gca* effects

***sca* effects**

For ear height, *sca* effects ranged from -18.70 (ML-14 \times PFSR-92) to 11.19 (PFSR-73 \times ML-14). Among 28 hybrids, six hybrids showed significantly negative *sca* effects. The hybrid, ML-14 \times PFSR-92 (-18.70) recorded the highest negative significant *sca* effect followed by PFSR-127 \times PFSR-92 (-13.38) and ML-14 \times BPDT-5009 (-12.79). Similar kind of results were also reported by Yadav and Gangwar (2021) and Sayed *et al.* (2022) for additive and non-additive gene action governing the trait.

4.4.2.7 Ear length (cm)

***gca* effects**

For ear length, the *gca* effects ranged from -1.67 (BPDT-5009) to 0.92 (PFSR-127). Among all the parents, four parents showed significantly positive *gca* effect. The parent, PFSR-127 (0.92) recorded the highest significant positive *gca* effect followed by BML-10 (0.90), PFSR-151 (0.87) and PFSR-73 (0.72) and these are considered as good general combiners. Similar kind of results were also reported by Mesekal *et al.* (2021) and Mousa *et al.* (2021).

***sca* effects**

For ear length, *sca* effects ranged from -3.60 (PFSR-73×PFSR-127) to 2.76 (PFSR-151×MGC-49). Among all the hybrids, seventeen hybrids showed significantly positive *sca* effect. The hybrid, PFSR-151×MGC-49 (2.76) showed the highest significant and positive *sca* effect followed by PFSR-73×BPDT-5009 (2.59), BML-10×BPDT-5009 (2.37), MGC-49×ML-14 (2.18) and PFSR-73×MGC-49 (1.86). Similar kind of results were also reported by Mousa *et al.* (2021) and Suresh *et al.* (2021).

4.4.2.8 Ear girth (cm)

***gca* effects**

For this trait, *gca* effects ranged from -0.61 (BPDT-5009) to 0.74 (BML-10). The parents BML-10 (0.74), PFSR-127 (0.47), PFSR-151 (0.33) and ML-14 (0.23) recorded significantly positive *gca* effects and considered as good general combiners for this trait. The results are in agreement with the earlier findings of Ola *et al.* (2018).

***sca* effects**

For this trait, *sca* effects ranged from -2.14 (PFSR-73×PFSR-127) to 1.68 (PFSR-151×BPDT-5009). Among the 28 hybrids, fourteen hybrids recorded significantly positive *sca* effects, among which PFSR-73×PFSR-127 (1.68) showed the highest significant positive *sca* effect followed by PFSR-127×PFSR-92 (1.62), PFSR-73×BML-10 (1.13) and BML-10×PFSR-92 (1.01).

Among the fourteen desirable crosses, eight crosses had only one parent as a good general combiner showing the presence of non-additive gene action (additive × dominance) and remaining three crosses had neither of the parent as good general combiners indicating presence of non-additive gene action (dominance × dominance) while the other three crosses had both parents as good general combiners. The similar results were also reported by Mousa *et al.* (2021) and Suresh *et al.* (2021).

4.4.2.9 Number of kernel rows per ear

***gca* effects**

For this trait, *gca* effects ranged from -0.59 (PFSR-92) to 0.79 (BML-10). Four out of eight parents BML-10 (0.79), PFSR-127 (0.33), ML-14 (0.17) and PFSR-151 (0.13) showed significantly positive *gca* effects implying that these four parents are good general combiners for this character.

The similar findings were reported by Gazala *et al.* (2017), Sun *et al.* (2018), Ola *et al.* (2018), Diribu *et al.* (2019), Hussain *et al.* (2019), Yadav and Gangwar (2021) and Patel (2022).

***sca* effects**

For number of kernel rows per ear, *sca* effect ranged from -2.83 (PFSR-73×PFSR-127) to 1.61 (ML-14×PFSR-92). Eleven out of 28 hybrids recorded significantly positive *sca* effect, among which ML-14×PFSR-92 (1.61) recorded the highest positive significant *sca* effect followed by PFSR-127×BPDT-5009 (1.56), ML-14×BPDT-5009 (1.32), PFSR-73×MGC-49 (1.07) and PFSR-73×PFSR-92 (1.01).

Among the eleven desirable crosses, four crosses had one parent as a good general combiner showing the predominance of non-additive gene action (additive × dominance), four crosses had neither parent as good general combiner which is also implying the presence of non-additive gene action (dominance × dominance). For the remaining three crosses both parents as good general combiners. The similar findings were reported by Suresh *et al.* (2021) and Patel (2022).

4.4.2.10 Number of kernels per row

***gca* effects**

The *gca* effects for this character ranged from -2.95 (PFSR-92) to 3.11 (BML-10). The parent BML-10 (3.11) recorded the highest significant *gca* effect followed by PFSR-151 (2.21), PFSR-73 (0.88) and PFSR-127 (0.78) and thus these parents are considered as good general combiners for this trait.

These findings are in accordance with the earlier results of Diribu *et al.* (2019), Hussain *et al.* (2019) and Patel (2022).

***sca* effects**

The *sca* effects for number of kernels per row, ranged from -9.88 (ML-14×BPDT-5009) to 8.47 (MGC-49×ML-14). Twelve out of 28 hybrids recorded significantly positive *sca* effects. The hybrid MGC-49×ML-14 (8.47) registered high positive and significant *sca* effect followed by PFSR-73×PFSR-92 (7.95), PFSR-73×MGC-49 (7.66), PFSR-151×MGC-49 (5.87) and PFSR-92×BPDT-5009 (5.27).

Among the twelve desirable crosses, nine crosses had one parent as a good general combiner showing the presence of non-additive gene action (additive \times dominance), two crosses had no parent as good general combiner indicating the predominance of non-additive gene action (dominance \times dominance) and one cross had both the parents as good general combiners.

Similar kind of results were also reported by Mousa *et al.* (2021), Suresh *et al.* (2021) and Patel (2022).

Table 4.5. Analysis of variance for combining ability for yield and its attributing traits in maize genotypes

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

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

Table 4.6. Estimates of general combining ability (*gca*) effects of the parents for yield and its attributing traits

Source	Days to 50% anthesis	Days to 50% silking	Anthesis silking interval	Days to maturity	Plant height (cm)	Ear height (cm)	Ear length (cm)	Ear girth (cm)	Number of kernel rows per ear	Number of kernels per row	100-kernel weight (g)	Grain yield (g/plant)
PFSR-73	2.25**	1.85**	-0.29**	-1.45**	12.41**	6.17**	0.72**	-0.32**	-0.29**	0.88*	-0.22	-2.35**
PFSR-127	-1.78**	-1.40**	0.30**	-3.42**	16.35**	1.63**	0.92**	0.47**	0.33**	0.78*	2.88**	20.24**
PFSR-151	-1.98**	-1.77**	0.17**	-2.55**	6.65**	-1.77**	0.87**	0.33**	0.13**	2.21**	0.88**	17.24**
BML-10	-3.58**	-3.40**	0.27**	-1.09**	9.07**	4.10**	0.90**	0.74**	0.79**	3.11**	0.90**	18.70**
MGC-49	-0.88**	-0.70**	0.14**	-0.42**	4.32**	5.71**	-0.12**	-0.30**	-0.24**	-0.20**	-0.55**	-12.09**
ML-14	1.05**	0.59**	-0.42**	2.47**	-16.83**	-7.09**	-0.67**	0.23**	0.17**	-1.79**	-0.60**	-4.75**
PFSR-92	1.71**	1.45**	-0.29**	2.64**	-11.98**	-2.73**	-0.96**	-0.54**	-0.59**	-2.95**	0.11	-16.25**
BPDT-5009	3.21**	3.39**	0.10*	3.84**	-20.00**	-6.02**	-1.67**	-0.61**	-0.29**	-2.04**	-3.40**	-20.72**
Gi at 95%	0.18	0.20	0.11	0.27	1.34	0.82	0.10	0.09	0.11	0.86	0.47	1.77
Gi-Gj at 95%	0.27	0.31	0.16	0.42	2.02	1.24	0.16	0.14	0.17	1.30	0.71	2.68

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

Table 4.7. Estimates of specific combining ability (*sca*) effects of the hybrids for yield and its attributing traits

Source	Days to 50% anthesis	Days to 50% silking	Anthesis silking interval	Days to maturity	Plant height (cm)	Ear height (cm)	Ear length (cm)	Ear girth (cm)	Number of kernel rows per ear	Number of kernels per row	100-kernel weight (g)	Grain yield (g/plant)
PFSR-73 × PFSR-127	-2.63**	-2.23**	0.32*	-2.10**	10.19**	0.84	-3.60*	-2.14**	-2.83**	1.27	-3.51**	-51.76**
PFSR-73 × PFSR-151	8.23**	7.79**	-0.54**	4.02**	-24.36**	6.26**	-1.11**	-1.14**	-0.10	-7.55**	-0.26	-25.43**
PFSR-73 × BML-10	0.50*	-0.23	0.35*	5.55**	-6.52**	8.90**	-0.29*	1.52**	0.56**	1.15	-0.48	10.43**
PFSR-73 × MGC-49	-7.53**	-6.93**	0.49**	-7.77**	-1.09	5.09**	1.86**	0.96**	1.07**	7.66**	-0.87	23.23**
PFSR-73 × ML-14	-0.13*	-0.90**	-0.94**	-1.34**	25.15**	11.19**	1.49**	0.34**	-0.01	2.19	8.25**	43.57**
PFSR-73 × PFSR-92	-0.80**	-0.77**	-0.07	-3.50**	13.47**	2.48**	1.08**	0.79**	1.01**	7.95**	-3.52**	0.07
PFSR-73 × BPDT-5009	-1.63**	-1.03**	0.52**	-1.37**	41.96**	-7.75**	2.59**	0.87**	-0.34*	3.23**	0.54	12.20**
PFSR-127 × PFSR-151	-1.40**	-1.60**	-0.14	-3.00**	-8.77**	-0.83	-1.05**	0.13	1.00**	0.08	0.51	10.30**
PFSR-127 × BML-10	0.20**	0.03	-0.24	0.19	8.52**	10.17**	1.77**	0.37**	0.47**	3.85**	3.46**	31.50**
PFSR-127 × MGC-49	6.16**	4.99**	-1.10**	3.52**	-23.92**	-9.38**	-2.44**	-1.65**	-1.29**	-3.17**	-1.77**	-31.69**
PFSR-127 × ML-14	4.23**	4.69**	0.45**	5.29**	10.28**	3.36**	0.72**	0.47**	0.29	0.22	2.85**	24.30**
PFSR-127 × PFSR-92	-6.10**	-5.83**	0.32*	-3.54**	10.91**	-13.38**	1.53**	1.62**	-0.01	1.58	0.99	28.80**
PFSR-127 × BPDT-5009	2.06**	3.23**	0.92**	2.59**	37.00**	5.88**	1.11**	0.77**	1.56**	3.27**	4.31**	37.27**
PFSR-151 × BML-10	11.06**	11.06**	-0.10	9.32**	-3.33**	-0.69	-1.04**	-0.73**	0.40*	-5.17**	-6.17**	-21.83**
PFSR-151 × MGC-49	-2.63**	-3.30**	-0.64**	-2.34**	34.99**	8.42**	2.76**	-0.15	-0.69**	5.87**	3.85**	35.63**
PFSR-151 × ML-14	-0.90**	0.39	1.25**	3.42**	-17.60**	0.25	1.35**	0.24	0.23	2.79*	1.49*	6.97**

Table 4.7 (cont.).

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

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

4.4.2.11 100-kernel weight (g)

***gca* effects**

The *gca* effects for 100-kernel weight ranged from -3.40 (BPDT-5009) to 2.86 (PFSR-127). Three parents, PFSR-127 (2.88), BML-10 (0.90) and PFSR-151 (0.88) showed significantly positive *gca* effects. These parents were considered as good general combiners. Significantly positive *gca* effect was also reported by Hussain *et al.* (2019) Kumar *et al.* (2019) and Yadav and Gangwar (2021).

***sca* effects**

The *sca* effects for this character ranged from -6.45 (PFSR-92×BPDT-5009) to 8.25 (PFSR-73×ML-14). Eleven out of the 28 hybrids recorded significantly positive *sca* effects. The hybrid, PFSR-73×ML-14 (8.25) recorded the highest significant *sca* effect followed by BML-10×BPDT-5009 (7.71), PFSR-151×BPDT-5009 (6.14), PFSR-127×BPDT-5009 (4.31) and PFSR-151×MGC-49 (3.85).

Among the eleven desirable crosses, eight crosses had one parent as good general combiner and only one cross had both parents as good general combiners indicating that presence of non-additive gene action (additive × dominance). Two crosses had neither of parents as good general combiner implying that presence of non-additive gene action (dominance × dominance). As this trait is governed by non-additive gene action, it can be improved by heterosis breeding. The similar findings are also reported by Murtadha *et al.* (2018) and Suresh *et al.* (2021).

4.4.2.12 Grain yield (g/plant)

***gca* effects**

The *gca* effects for grain yield ranged from -20.72 (BPDT-50 09) to 20.24 (PFSR-127). Among the parents, three parents showed significantly positive *gca* effects. The parent, PFSR-127 (20.24) showed the highest significant positive *gca* effect followed by BML-10 (18.70) and PFSR-151 (17.24) indicating that these are good general combiners for this trait.

***sca* effects**

The *sca* effects for grain yield ranged from -51.76 (PFSR-73×PFSR-127) to 47.93 (PFSR-151 ×BPDT-5009). Among 28 hybrids, sixteen hybrids showed significantly positive *sca* effects. The hybrid, PFSR-151×BPDT-5009 (47.93) showed the highest significant *sca* effect followed by PFSR-73×ML-14 (43.57), PFSR-127×BPDT-5009 (37.27), PFSR-151×MGC-49 (35.63), BML-10×PFSR-92 (31.67) and PFSR-127 ×BML-10 (31.50).

The results are in agreement with the findings of Gazala *et al.* (2017), Begum *et al.* (2018), Murtadha *et al.* (2018), Ola *et al.* (2018), Sandesh *et al.* (2018), Diribu *et al.* (2019), El-Gazzar (2021), El-Shahed *et al.* (2021) and Patel (2022) for both *gca* and *sca* effects which were significantly positive.

4.4.3 GCA and SCA variance and gene action

The estimates of GCA and SCA variances and their ratios are presented in the Table 4.8. The GCA variance of parents and SCA variance of hybrids for the different traits are prerequisites for precise improvement in hybrid breeding. General combining ability due to is additive gene action and fixable while, specific combining ability is due to non-additive gene action i.e., dominance and epistasis and not fixable. The success of hybrid programmes based on the results of combining ability depends on the extent of genetic parameters remaining stable over environments and the presence of non-additive gene action is a very good prospect for the exploitation of desirable characters through hybrid breeding. A comparison of the magnitude of variance components due to *gca* and *sca* confirmed the gene action in controlling the expression of characters. The ratio of *gca* and *sca* variance is more than unity indicates additive gene action and less than unity indicating the preponderance of non-additive gene action.

In present investigation, the ratio between variance due to GCA and SCA was less than unity for all the characters *viz.*, for days to 50 per cent anthesis, days to 50 per cent silking, anthesis silking interval, days to maturity, plant height (cm), ear height (cm), ear girth (cm), ear length (cm), number of kernel rows per ear, number of kernel rows per row, 100 grain wight and grain yield (g/plant) indicating that these traits are controlled by non-additive gene action.

These findings are comparable with the earlier findings of Murtadha *et al.* (2018) Hussain *et al.* (2019) and Mousa *et al.* (2021).

Promising general and specific combiners for grain yield and other characters

Based on significant *gca* effect, the parents PFSR-127, BML-10 and PFSR-151 were identified as good general combiners for grain yield and its contributing traits like days to 50 per cent anthesis, days to 50 per cent silking, days to maturity, ear length, ear girth (Table 4.10).

Based on *sca* effects, the hybrids, PFSR-151×BPDT-5009, PFSR-73×ML-14, PFSR-127×BPDT-5009, PFSR-151×MGC-49 and PFSR-73×MGC-49 were identified as good specific combiners for yield and yield attributing traits (Table 4.11).

Table 4.9. Top five hybrids with high *sca* effects, *per se* performance and *gca* effects of parents for yield and its attributing traits in maize hybrids

Hybrid	<i>Per se</i> performance	<i>sca</i> effects	<i>gca</i> effects	
			parent 1	parent 2
Days to 50 per cent anthesis				
PFSR-73×MGC-49	68	-7.53**	2.25**	-0.88**
PFSR-151×BPDT-5009	63	-6.73**	-1.98**	3.21**
PFSR-127×PFSR-92	72	-6.10**	-1.78**	1.71**
BML-10×BPDT-5009	62	-5.80**	-3.58**	3.21**
MGC-49×ML-14	63	-5.66**	-0.88**	1.05**
Days to 50 per cent silking				
PFSR-73×MGC-49	69	-6.93**	1.85**	-0.75**
PFSR-151×BPDT-5009	65	-6.73**	-1.77**	3.39**
PFSR-127×PFSR-92	74	-5.83**	-1.40**	1.45**
BML-10×BPDT-5009	65	-5.77**	-3.40**	3.39**
PFSR-151×PFSR-92	77	-5.13**	-1.77**	1.45**
Anthesis silking interval				
PFSR-127×MGC-49	3	-1.10**	0.30**	0.14**
PFSR-73×ML-14	3	-0.94**	-0.29**	-0.42**
MGC-49×BPDT-5009	3	-0.90**	0.14**	0.10*
PFSR-151×MGC-49	4	-0.64**	0.17**	0.14**
PFSR-73×PFSR-151	3	-0.54**	-0.29**	0.17**
Days to maturity				
BML-10×ML-14	97	-9.37**	-1.09**	2.47**
PFSR-151×PFSR-92	111	-8.40**	-2.55**	2.64**
PFSR-73×MGC-49	109	-7.77**	-1.45**	-0.42**
MGC-49×ML-14	106	-7.04**	-0.42**	2.47**
BML-10×BPDT-5009	104	-6.40**	-1.09**	3.84**
Plant height (cm)				
PFSR-73×BPDT-5009	233.52	41.96**	12.41**	-20.00**
PFSR-127×BPDT-5009	229.42	37.00**	16.35**	-20.00**
PFSR-151×MGC-49	252.97	34.99**	6.65**	4.32**
MGC-49×ML-14	249.61	32.60**	4.32**	-16.83**
PFSR-151×PFSR-92	232.02	31.93**	6.65**	-11.98**

Table 4.9 (cont.).

Hybrid	<i>Per se</i> performance	<i>sca</i> effects	<i>gca</i> effects	
			parent 1	parent 2
Ear height (cm)				
ML-14×PFSR-92	73.57	-18.70**	-7.09**	-2.73**
PFSR-127×PFSR-92	63.92	-13.38**	1.63**	-2.73**
ML-14×BPDT-5009	68.08	-12.79**	-7.09**	-6.02**
PFSR-92×BPDT-5009	73.14	-11.11**	-2.73**	-6.02**
PFSR-127×MGC-49	64.98	-9.38**	5.71**	5.71**
Ear length (cm)				
PFSR-151×MGC-49	17.74	2.76**	0.87**	-0.12**
PFSR-73×BPDT-5009	18.22	2.59**	0.72**	-1.67**
BML-10×BPDT-5009	16.16	2.37*8	0.90**	-1.67**
MGC-49×ML-14	18.62	2.18**	-0.12**	-0.67**
PFSR-73×MGC-49	18.70	1.86**	0.72**	-0.12**
Ear girth (cm)				
PFSR-151×BPDT-5009	13.57	1.68**	0.33**	-0.61**
PFSR-127×PFSR-92	12.22	1.62**	0.47**	-0.54**
PFSR-73×BML-10	12.56	1.52**	-0.32**	0.74**
BML-10×ML-14	14.07	1.13**	0.74**	0.23**
BML-10×PFSR-92	15.10	1.01**	0.74**	-0.54**
Number of kernel rows per ear				
ML-14×PFSR-92	12	1.61**	0.17**	-0.59**
PFSR-127×BPDT-5009	14	1.56**	0.33**	-0.29**
ML-14×BPDT-5009	14	1.32**	0.17**	-0.29**
PFSR-73×MGC-49	14	1.07**	-0.29**	-0.24**
PFSR-73×PFSR-92	12	1.01**	-0.29**	-0.59**
Number of kernels per row				
MGC-49×ML-14	31.53	8.47**	-0.20**	-1.79**
PFSR-73×PFSR-92	31.26	7.95**	0.88*	-2.95**
PFSR-73×MGC-49	35.13	7.66**	0.88*	-0.20**
PFSR-151×MGC-49	32.00	5.87**	2.21**	-0.20**
PFSR-92×BPDT-5009	36.46	5.27**	-2.95**	-2.04**

Table 4.9 (cont.).

Hybrid	<i>Per se</i> performance	<i>sca</i> effects	<i>gca</i> effects	
			parent 1	parent 2
100-kernel weight (g)				
PFSR-73×ML-14	26.44	8.25**	-0.22	-0.60**
BML-10×BPDT-5009	27.79	7.71**	0.90**	-3.40**
PFSR-151×BPDT-5009	32.29	6.14**	0.88**	-3.40**
PFSR-127×BPDT-5009	33.25	4.31**	2.88**	-3.40**
PFSR-151×MGC-49	31.90	3.85**	0.88**	-0.55**
Grain yield per plant (g)				
PFSR-151×BPDT-5009	157.66	47.93**	17.24**	-20.72**
PFSR-73×ML-14	125.66	43.57**	-2.35**	-4.75**
PFSR-127×BPDT-5009	156.66	37.27**	20.24**	-20.72**
PFSR-151×MGC-49	153.66	35.63**	17.24**	-12.09**
BML-10×PFSR-92	161.33	31.67**	18.70**	-16.25**

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

Table 4.10. Promising general combiners for earliness, yield and its attributing traits

Parents	Characters
PFSR-127	Grain yield per plant, days to 50% anthesis, days to 50% silking, days to maturity, ear length, ear girth, number of kernels per ear, number of kernels per row and 100-kernel weight.
BML-10	Grain yield per plant, days to 50% anthesis, days to 50% silking, days to maturity, ear length, ear girth, number of kernels per ear, number of kernels per row and 100-kernel weight.
PFSR-151	Grain yield per plant, days to 50% anthesis, days to 50% silking, days to maturity, ear length, ear girth, number of kernels per ear, number of kernels per row and 100-kernel weight.

Table 4.11. Promising specific combiners for earliness, yield and its attributing traits

Hybrid	Characters
PFSR-151×BPDT-5009	Grain yield per plant, days to 50% anthesis, days to 50% silking, days to maturity, ear length, ear girth, number of kernel rows per ear, number of kernels per row and 100-kernel weight.
PFSR-73×ML-14	Grain yield per plant, days to 50% anthesis, days to 50% silking, anthesis silking interval, days to maturity, ear length, ear girth and 100-kernel weight.
PFSR-127×BPDT-5009	Grain yield per plant, ear length, ear girth, number of kernel rows per ear, number of kernels per row and 100-kernel weight.
PFSR-151×MGC-49	Grain yield per plant, days to 50% anthesis, days to 50% silking, anthesis silking interval, days to maturity, ear length, number of kernel rows per ear, number of kernels per row and 100-kernel weight.
BML-10×PFSR-92	Grain yield per plant, days to 50% anthesis, days to 50% silking, days to maturity, ear length, ear girth, number of kernel rows per ear, number of kernels per row and 100-kernel weight.
PFSR-73×MGC-49	Grain yield per plant, days to 50% anthesis, days to 50% silking, days to maturity, ear length, ear girth, number of kernel rows per ear, number of kernels per row and 100-kernel weight.

4.5 Correlation analysis

Correlation is the degree and direction of the association between two or more variables which provides useful tool in determining yield components and utilized for the genetic improvement of grain yield. Information on genotypic correlations reveals the existence of real associations, whereas, the phenotypic correlations are due to genotype \times environment interactions. Significant phenotypic correlations without significant genotypic associations are of no value. If the genotypic correlation is significant and phenotypic is not, it means that the existing real association is masked by environmental effect. This indicates the importance of genotypic correlation compared to phenotypic correlation.

Phenotypic and genotypic correlations were worked out on yield and yield attributing traits in 28 crosses and 8 parents are presented in Table 4.12. In general, phenotypic correlations provide the information on phenotypic expression of the traits at field level and hence the phenotypic correlations have been discussed hereunder.

4.5.1 Days to 50 per cent anthesis

Days to 50 per cent anthesis exhibited significantly negative association with grain yield per plant. It also exhibited significantly negative correlation with anthesis silking interval, plant height, ear girth, number of kernel rows per ear, number of kernels per row and 100-kernel weight and negative non-significantly correlated with ear height.

The results are in accordance with the findings of Ghimire and Timsina (2015) Chaurasia *et al.* (2020) and Damtie *et al.* (2021).

4.5.2 Days to 50 per cent silking

Significantly negative correlation of days to 50 per cent silking was observed for anthesis silking interval, plant height, ear length, number of kernel rows per ear, number of kernels per row and 100-kernel weight. This trait also showed significantly negative association with grain yield per plant.

These findings are in consonance with the findings of by Ghimire and Timsina (2015) and Chaurasia *et al.* (2020) for grain yield. Ahmed *et al.* (2020) reported significantly negative correlation of days to 50% silking with ear girth, number of kernel rows per ear and number of kernels per row.

Table 4.12. Phenotypic and genotypic correlation coefficients for yield and its attributing traits in maize genotypes

Character		DA	DS	ASI	DM	PH	EH	EL	EG	KRE	KPR	100KW	GY
DA	P	1.000	0.9895**	-0.3780**	0.8110**	-0.4418**	-0.1424	-0.5993**	-0.6136**	-0.2298*	-0.6170**	-0.4462**	-0.6041**
	G	1.000	0.9917**	-0.4063**	0.8184**	-0.4446**	-0.1472	-0.6061**	-0.6275**	-0.2379*	-0.6648**	-0.4577**	-0.6082**
DS	P		1.000	-0.2532**	0.8154**	-0.4214**	-0.1370	-0.5738**	-0.5898**	-0.1954*	-0.5894**	-0.4392**	-0.5758**
	G		1.000	-0.2911**	0.8236**	-0.4234**	-0.1414	-0.5825**	-0.6041**	-0.2010*	-0.6369**	-0.4516**	-0.5797**
ASI	P			1.000	-0.1968*	0.2199*	0.1041	0.3353**	0.4415**	0.3985**	0.3887**	0.1618	0.3866**
	G			1.000	-0.2192*	0.2418*	0.1038	0.3573**	0.4781**	0.4387**	0.4417**	0.1806	0.4237**
DM	P				1.000	-0.5008**	-0.2433*	-0.5873**	-0.4794**	-0.1438	-0.5708**	-0.5003**	-0.5819**
	G				1.000	-0.5071**	-0.2472*	-0.5952**	-0.4944**	-0.1448	-0.6109**	-0.5208**	-0.5890**
PH	P					1.000	0.6525**	0.8210**	0.3377**	-0.0508	0.6529**	0.4433**	0.6040**
	G					1.000	0.6699**	0.8334**	0.3462**	-0.0510	0.7037**	0.4574**	0.6064**
EH	P						1.000	0.5300**	0.1907*	0.0401	0.4786**	0.3756**	0.4114**
	G						1.000	0.5383**	0.2006*	0.0392	0.5237**	0.4000**	0.4260**
EL	P							1.000	0.5352**	0.1282	0.7327**	0.5225**	0.7255**
	G							1.000	0.5521**	0.1345	0.7933**	0.5382**	0.7403**
EG	P								1.000	0.7022**	0.5168**	0.5213**	0.8109**
	G								1.000	0.7302**	0.5564**	0.5470**	0.8260**
KRE	P									1.000	0.2060*	0.2425*	0.5182**
	G									1.000	0.2206*	0.2638*	0.5383**
KPR	P										1.000	0.3129**	0.6550**
	G										1.000	0.3377**	0.7030**
100KW	P											1.000	0.7729**
	G											1.000	0.7965**

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

DA: days to 50% anthesis, DS: days to 50% silking, ASI: anthesis silking interval, DM: days to maturity, PH: plant height, EH: ear height, EL: ear length, EG: ear girth, KRE: number of kernel rows per ear, KPR: number of kernels per row, 100 KW: hundred kernel weight and GY: grain yield per plant, P: phenotypic correlation coefficient and G: genotypic correlation coefficient

4.5.3 Anthesis silking interval

Anthesis silking interval exhibited significantly positive association with plant height, ear length, ear girth, number of kernel rows per ear and number of kernels per ear.

Anthesis silking interval showed positive and significant correlation with grain yield per plant. These findings are in consonance with the findings of Ahmed *et al.* (2020).

4.5.4 Days to maturity

Days to maturity showed significantly negative correlation with plant height, ear height, ear length, ear girth, 100-kernel weight and number of kernels per row. This trait exhibited significantly negative correlation with grain yield per plant and non-significant negative association with number of kernel rows per ear.

Significantly negative correlation of days to maturity with ear length was earlier reported by Chaurasia *et al.* (2020). Ahmed *et al.* (2020) reported significantly negative correlation with ear height.

4.5.5 Plant height (cm)

Plant height had significantly positive association with ear height, ear length, ear girth, number of kernels per row and 100-kernel weight and grain yield per plant.

The results are in accordance with the findings of Chaurasia *et al.* (2020) for ear height, ear length, ear girth, number of kernel rows per ear and number of kernels per row. Significant positive correlation of plant height with ear height was reported by Ahmed *et al.* (2020). Damtie *et al.* (2021) reported significantly positive correlation of plant height with ear height.

4.5.6 Ear height (cm)

Ear height recorded significant and positive association with ear length, ear girth, number of kernels per row and 100-kernel weight. This trait showed significantly positive correlation with grain yield per plant.

These results are in accordance with the findings of Chaurasia *et al.* (2020), Dash *et al.* (2020), Singh *et al.* (2020) and Gokulakrishnan *et al.* (2021) for grain yield. Significantly positive correlation of ear height with number of kernels per row also reported by Singh *et al.* (2020).

4.5.7 Ear length (cm)

Ear length exhibited significant and positive correlation with ear girth, 100-kernel weight and number of kernels per row. This trait showed significantly positive association with grain yield per plant. Ear length exhibited significantly positive correlation with number of kernels per row indicating that the longer ear length accommodates more number of kernels per row which ultimately results in higher grain yield per plant.

These results are in agreement with the findings of Kumawat *et al.* (2020), Singh *et al.* (2020) Khan and Mahmud (2021) for grain yield. Significant and positive correlation of ear length with number of kernel rows per ear and number of kernels per row was reported by Ahmed *et al.* (2020).

4.5.8 Ear girth (cm)

Ear girth recorded significantly positive correlation with number of kernel rows per ear, number of kernels per row and 100-kernel weight. This trait also showed significantly positive association with grain yield per plant. The positive and significant association was observed between ear girth and number of kernel rows per ear giving an indication that higher the ear girth more will be number of kernel rows per ear which is an important yield contributing trait.

These results were found similarity with the findings of Kandel *et al.* (2018) and Ahmed *et al.* (2020) for grain yield. Singh *et al.* (2020) reported significantly positive association of ear girth with number of kernels per row. Ahmed *et al.* (2020) reported significantly positive correlation of ear girth with number of kernel rows per ear and number of kernels per row.

4.5.9 Number of kernel rows per ear

Number of kernel rows per ear showed significantly positive correlation with number of kernels per row and 100-kernel weight. It also showed significantly positive association with grain yield per plant.

Similar kind of results were also reported by Ghimire *et al.* (2015), Raut *et al.* (2017) and Kandel *et al.* (2018) for grain yield. Ahmed *et al.* (2020) reported significantly positive correlation of number of kernel rows per ear with number of kernels per row. Krishna *et al.* (2021) reported significantly positive correlation of this trait with number of kernels per row and 100-kernel weight.

4.5.10 Number of kernels per row

Number of kernels per row showed significantly positive association with 100-kernel weight and with grain yield per plant. The findings are in accordance with the earlier findings of Krishna *et al.* (2021).

4.5.11 100-kernel weight (g)

The trait, 100-kernel weight recorded significantly positive correlation with grain yield per plant.

The results from the character association studies revealed that the traits *viz.*, ear length, ear girth, plant height, ear height, number of kernel rows per ear, number of kernels per row and 100-kernel weight exhibited significantly positive correlation with grain yield. Hence, improvement of these traits simultaneously results in the improved grain yield.

The traits, days to 50% anthesis, days to 50% silking and days to maturity exhibited negative and significant correlation with grain yield which is desirable in that direction. It is also desirable for the selection of early maturing inbred lines with more ear length, ear girth, number of kernel rows per ear, number of kernels per row, plant height and 100-kernel weight which ultimately results in the higher grain yield.

Character association among yield attributing traits with significantly positive correlation with grain yield is highly essential to formulate sound breeding strategy. Interrelationship between yield attributing traits revealed that days to 50% anthesis had positive significant association with days to 50% silking and days to maturity, days to 50% silking with days to maturity indicating the interdependency of these characters. Hence, these characters to be given a top most priority during selection process to bring about improvement of yield with early maturity in maize.

In addition, plant height showed positive and significant correlation with ear height, ear length, ear girth, number of kernels per row and 100-kernel weight; ear height with ear length, ear girth, number of kernels per row and 100-kernel weight; ear length with ear girth, number of kernels per row and 100-kernel weight; ear girth with number of kernel rows per ear, number of kernels per row and 100-kernel weight; number of kernels per row with 100-kernel weight; 100-kernel weight with grain yield. Therefore, inbred lines with these traits to be given priority during selection process for improving the respective characters which simultaneously improves the grain yield.

4.6 Path analysis

Path analysis is useful to determine the degree of direct and indirect effect of the independent variables on the dependent variable. The correlation provides information on trait association, their degree of linear relationship, whereas path coefficient analysis will partition the traits into components that measure the direct and indirect effects. This is helpful to recognize direct and indirect causes of correlation.

The results of phenotypic and genotypic path coefficient analysis on yield and yield attributing traits are presented in Table 4.13.

4.6.1 Days to 50 per cent anthesis

Days to 50 per cent anthesis exhibited a negative direct effect (-0.5336) on grain yield and it was significantly negatively correlated (-0.6041) with grain yield, which was mainly due to indirect negative contribution exerted through days to 50 per cent silking and days to maturity.

Similar kind of results were also reported by Muliadi *et al.* (2021). Positive indirect contribution of days to 50% anthesis on grain yield through the anthesis silking interval was supported by Matin *et al.* (2017).

4.6.2 Days to 50 per cent silking

Days to 50 per cent silking showed a positive direct effect (0.5901) on grain yield with a significantly negative correlation (-0.5758) that has been mainly attributed to the indirect negative contribution through the anthesis silking interval, plant height, ear height, ear length, ear girth, number of kernel rows per ear, number of kernels per row and 100-kernel weight.

Positive direct effect was reported by Chaurasia *et al.* (2020), Shikha *et al.* (2020), Atiq *et al.* (2021), Muliadi *et al.* (2021) and Ramesh Kanna *et al.* (2021). Matin *et al.* (2017) reported a negative indirect effect through the anthesis silking interval and ear girth.

4.6.3 Anthesis silking interval

Anthesis silking interval exhibited a direct negative effect (-0.0939) on grain yield with a significantly positive correlation (0.3886) which was due to indirect positive contribution through days to 50 per cent anthesis, days to 50 per cent silking and days to maturity. The results are in accordance with earlier findings of Dash *et al.* (2020).

4.6.4 Days to maturity

Days to maturity showed a negative direct effect (-0.0050) with grain yield and with a significantly negative correlation (-0.5819) which is mainly attributed due to indirect negative contribution through days to 50 per cent anthesis and days to 50 per cent silking. Similar kind of results were also reported by Matin *et al.* (2017).

4.6.5 Plant height

Plant height exhibited direct positive effect (0.1763) on grain yield with significantly positive correlation (0.6040) was mainly due to the indirect positive effects through anthesis silking interval, ear height, ear length, ear girth, number of kernels per row and 100-kernel weight.

These results are in accordance with Matin *et al.* (2017), Dash *et al.* (2020), Shikha *et al.* (2020), Ramesh *et al.* (2021) and Muliadi *et al.* (2021). Antiq *et al.* (2021) reported the positive indirect effect of plant height on grain yield which was attributed through the ear height and number of kernels per row.

4.6.6 Ear height

Ear height registered negative direct effect (-0.0760) on grain yield and it showed significantly positive correlation (0.4114) with grain yield which was attributed through the indirect positive effects through days to 50 per cent anthesis, days to 50 per cent silking and days to maturity. The results are in consonance with the earlier findings of Ahmed *et al.* (2020) and Krishna *et al.* (2021).

4.6.7 Ear length

Positive direct effect (0.0760) exhibited by ear length on grain yield and it exhibited significantly positive correlation (0.7255) with grain yield which was mainly due to indirect positive effects through plant height, ear height, ear girth, number of kernel rows per ear, number of kernels per row and 100-kernel weight.

These results are in accordance with Matin *et al.* (2017), Chaurasia *et al.* (2020), Kumawat *et al.* (2020), Shikha *et al.* (2020), Gokulakrishnan *et al.* (2021) and Muliadi *et al.* (2021).

4.6.8 Ear girth

Ear girth recorded direct positive effect (0.3063) on grain yield with significantly positive correlation (0.8109) which was due to positive indirect effect through anthesis silking interval, plant height, ear height, ear length, number of kernel rows per ear, number of kernels per row and 100-kernel weight.

Similar kind of results were also reported by Matin *et al.* (2017), Shikha *et al.* (2020), Gokulakrishnan *et al.* (2021), Ramesh Kanna *et al.* (2021) and Muliadi *et al.* (2021).

4.6.9 Number of kernel rows per ear

Number of kernel rows per ear had direct positive effect (0.1787) on grain yield with significantly positive correlation (0.5182) which was due to indirect positive effects

through anthesis silking interval, ear height, ear girth, ear length, number of kernels per row and 100-kernel weight.

Chaurasia *et al.* (2020), Dash *et al.* (2020), Shikha *et al.* (2020), Antiq *et al.* (2021), Hadi *et al.* (2021) and Shahrokhi *et al.* (2021) also reported similar kind of results.

4.6.10 Number of kernels per row

Number of kernels per row exhibited positive direct effect (0.2403) on grain yield with significantly positive correlation (0.6550) which was due to indirect positive contribution through anthesis silking interval, plant height, ear height, ear girth, ear length, number of kernels rows per ear and 100-kernel weight.

These results are in accordance with the findings of Kumawat *et al.* (2020), Shikha *et al.* (2020), Atiq *et al.* (2021) and Krishna *et al.* (2021).

4.6.11 100-kernel weight

Hundred kernel weight had positive direct effect (0.4391) on grain yield with significantly positive correlation (0.7229) which was due to indirect positive effects via anthesis silking interval, plant height, ear height, ear length, ear girth, number of kernel rows per ear and number of kernels per ear.

These results are in accordance with the earlier findings of Chaurasia *et al.* (2020), Dash *et al.* (2020), Atiq *et al.* (2021) and Krishna *et al.* (2021).

Table 4.13. Path coefficients for yield and its attributing traits in maize genotypes

Character		DA	DS	ASI	DM	PH	EH	EL	EG	KRE	KPR	100KW	GY
DA	P	-0.5336	-0.5280	0.2017	-0.4328	0.2358	0.0760	0.3198	0.3274	0.1226	0.3293	0.2381	-0.6041**
	G	-1.7364	-1.7220	0.7055	-1.4211	0.7719	0.2557	1.0524	1.0895	0.4130	1.1543	0.7948	-0.6082**
DS	P	0.5839	0.5901	-0.1494	0.4812	-0.2487	-0.0808	-0.3386	-0.3480	-0.1153	-0.3478	-0.2592	-0.5758**
	G	1.7823	1.7972	-0.5232	1.4802	-0.7609	-0.2541	-1.0468	-1.0858	-0.3612	-1.1447	-0.8116	-0.5797**
ASI	P	0.0355	0.238	-0.0939	0.0185	-0.0206	-0.0098	-0.0315	-0.0415	-0.0374	-0.0365	-0.0152	0.3866**
	G	0.1099	0.0788	-0.2706	0.0593	-0.0654	-0.0281	-0.0967	-0.1294	-0.1187	-0.1195	-0.0489	0.4237**
DM	P	-0.0041	-0.0041	0.0010	-0.0050	0.0025	0.0012	0.0029	0.0024	0.0007	0.0029	0.0025	-0.5819**
	G	0.0230	0.0232	-0.0062	0.0281	-0.0143	-0.0070	-0.0167	-0.0139	-0.0041	-0.0172	-0.0147	-0.5890**
PH	P	-0.0779	-0.0743	0.0388	-0.0883	0.1763	0.1150	0.1447	0.0595	-0.0090	0.1151	0.0781	0.6040**
	G	-0.0492	-0.0468	0.0268	-0.0561	0.1107	0.0741	0.0922	0.0383	-0.0056	0.0779	0.0506	0.6064**
EH	P	0.0108	0.0104	-0.0079	0.0185	-0.0496	-0.0760	-0.0403	-0.0145	-0.0030	-0.0364	-0.0286	0.4114**
	G	0.0171	0.0164	-0.0121	0.0287	-0.0778	-0.1161	-0.0625	-0.0233	-0.0045	-0.0608	-0.0464	0.4260**
EL	P	-0.0456	-0.0436	0.0255	-0.0447	0.0624	0.0403	0.0760	0.0407	0.0097	0.0557	0.0397	0.7255**
	G	-0.0149	-0.0143	0.0088	-0.0146	0.0205	0.0132	0.0245	0.0136	0.0033	0.0195	0.0132	0.7403**
EG	P	-0.1880	-0.1807	0.1353	-0.0468	0.1034	0.0584	0.1639	0.3063	0.2151	0.1583	0.1597	0.8109**
	G	-0.1925	-0.1854	0.1467	-0.1517	0.1062	0.0616	0.1694	0.3068	0.2240	0.1707	0.1678	0.8260**
KRE	P	-0.011	-0.0349	0.0712	-0.0257	-0.0091	0.0072	0.0229	0.1255	0.1787	0.0368	0.0433	0.5182**
	G	-0.0397	-0.0335	0.0732	-0.0241	-0.0085	0.0065	0.0224	0.1218	0.1667	0.0368	0.0440	0.5383**
KPR	P	-0.1483	-0.1416	0.0934	-0.1371	0.1569	0.1150	0.1760	0.1242	0.0495	0.2403	0.0752	0.6550**
	G	-0.2756	-0.2640	0.1831	-0.2532	0.2917	0.2171	0.3288	0.2307	0.0915	0.4145	0.1400	0.7030**
100KW	P	-0.1959	-0.1929	0.0710	-0.2197	0.1947	0.1649	0.2294	0.2289	0.1065	0.1374	0.4391	0.7729**
	G	-0.2324	-0.2293	0.0917	-0.2644	0.2322	0.2031	0.2733	0.2777	0.1339	0.1715	0.5077	0.7965**

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

DA: days to 50% anthesis, DS: days to 50% silking, ASI: anthesis silking interval, DM: days to maturity, PH: plant height, EH: ear height, EL: ear length, EG: ear girth, KRE: number of kernel rows per ear, KPR: number of kernels per row, 100 KW: hundred kernel weight and GY: grain yield per plant.

Residual effect

Residual factor is square root of $1-r^2$ (multiple r) from the regression analysis which is used to determine the path coefficient. In plant breeding, comprehensive knowledge on all component traits of yield is very important. The residual effect permits precise explanation about the pattern of interaction of other possible components of yield which were not included in the investigation. The residual effect in the present investigation was 0.2875 for phenotypic and 0.2052 for genotypic path coefficients. This residual effect provides the information about contribution of component traits that are studied on yield was 71.25% at phenotypic level and 79.48 % at genotypic level, the remaining 28.75% at phenotypic and 20.52% at genotypic was the contribution of other traits which were not included in the study and its association with the dependent variable, yield.

Path coefficient analysis revealed that days to 50 per cent silking (0.5901) showed the highest positive direct effect on grain yield followed by 100-kernel weight (0.4391), ear girth (0.3063), number of kernels per row (0.2403) and number of kernel rows per ear (0.1787) at phenotypic level. The highest positive direct effect was registered by days to 50 per cent silking (1.7972) on grain yield followed by 100-kernel weight (0.5077), number of kernels per row (0.4145), ear girth (0.3068) and number of kernel rows per ear (0.1667). Hence, these characters are to be given top most priority in development of high yielding genotypes in future breeding programmes.

4.7 Study on stay green trait

Stay green is a character which delays the senescence of leaf and stalk. In stay green genotypes, leaves and stalks remain green for longer period there by increasing the higher time period for carrying out photosynthetic activity which ultimately supplies higher quantity of carbohydrates to the leaves, stalks and roots that results in higher grain yield. The score for stay green/non-green trait is given in Table 4.14.

Table 4.14. Scoring of maize genotypes for stay green trait

S. No	Genotypes	Score	Stay green/non-stay green
1	PFSR-73	4	Non-stay green
2	PFSR-127	4	Non-stay green
3	PFSR-151	5	Non-stay green
4	BML-10	5	Non-stay green
5	MGC-49	1	Stay green
6	ML-14	4	Non-stay green
7	PFSR-92	3	Stay green
8	BPDT-5009	5	Non-stay green
9	PFSR-73 × PFSR-127	5	Non-stay green
10	PFSR-73 × PFSR-151	4	Non-stay green
11	PFSR-73 × BML-10	5	Non-stay green
12	PFSR-73 × MGC-49	4	Non-stay green
13	PFSR-73 × ML-14	4	Non-stay green
14	PFSR-73 × PFSR-92	5	Non-stay green
15	PFSR-73 × BPDT-5009	4	Non-stay green
16	PFSR-127 × PFSR-151	5	Non-stay green
17	PFSR-127 × BML-10	5	Non-stay green
18	PFSR-127 × MGC-49	3	Stay green
19	PFSR-127 × ML-14	4	Non-stay green
20	PFSR-127 × PFSR-92	4	Non-stay green
21	PFSR-127 × BPDT-5009	2	Non-stay green
22	PFSR-151 × BML-10	5	Non-stay green
23	PFSR-151 × MGC-49	3	Stay green
24	PFSR-151 × ML-14	4	Non-stay green

Table 4.14 (cont.).

S. No	Genotypes	Score	Stay green/non-stay green
24	PFSR-151 × ML-14	4	Non-stay green
25	PFSR-151 × PFSR-92	3	Stay green
26	PFSR-151 × BPDT-5009	4	Non-stay green
27	BML-10 × MGC-49	5	Non-stay green
28	BML-10 × ML-14	5	Non-stay green
29	BML-10 × PFSR-92	3	Stay green
30	BML-10 × BPDT-5009	5	Non-stay green
31	MGC-49 × ML-14	3	Stay green
32	MGC-49 × PFSR-92	2	Stay green
33	MGC-49 × BPDT-5009	4	Non-stay green
34	ML-14 × PFSR-92	5	Non-stay green
35	ML-14 × BPDT-5009	5	Non-stay green
36	PFSR-92 × BPDT-5009	4	Non-stay green

Perusal of the data (Table 4.14) indicated that the two parents, MGC-49 and PFSR-92 were identified as stay green types which recorded 1 and 3 scores respectively. However, the remaining parents (6) were of non-stay green types. Seven (7) out of the resultant hybrids (28) were also stay green type. Critical examination of the data revealed that 4 out of 7 experimental hybrids that were developed by crossing MGC-49 as one of the parents were found to be stay green type (57.1%) while, 2 out of 7 experimental hybrids that were developed by crossing PFSR-92 as one of the parent were also found to be stay green types (28.6%). The hybrid which was developed by crossing both the stay green parents (MGC-49 and PFSR-92) was found stay green type and the remaining 21 hybrids were identified as non-stay green types.

Two out of 5 superior hybrids (PFSR-127 × MGC-49 and BML-10 × PFSR-92) based on mean performance for grain yield per plant were found to be stay green types while, the remaining three top yielders were of non-stay green types. Further, investigations need to be carried out to understand the inheritance pattern of stay green character.

4.8 Screening for charcoal rot

Charcoal rot is a major destructive disease in maize and it is caused by *Macrophomina phaseolina*. Losses due to Charcoal rot is accounting for 63.5% especially in drier regions of India. It is prevalent under high soil temperature and moisture stress. The disease is characterized by the minute, numerous black sclerotia in vascular bundles and inside rind of the stalk giving greyish black appearance. Keeping in view the importance of the disease, studies were conducted to screen parents and hybrids for charcoal rot resistance at Maize Research Centre, Agricultural Research Institute, Hyderabad. Eight parents and 28 hybrids along with susceptible check (Kaveri-50) were screened for charcoal rot disease using tooth pick method. The disease scoring was done using 0-9 scale of Payak and Sharma, 1983. Accordingly, based on the disease scoring, the maize genotypes have been categorized as resistant, moderately resistant, moderately susceptible and highly susceptible types for charcoal rot (Table 4.15).

Table 4.15. Screening of maize genotypes for charcoal rot resistance using 0-9 scale (Payak and Sharma, 1983)

Genotypes	Disease score (0-9 scale)	Disease reaction
PFSR-73	2.7	Resistant
PFSR-127	2.3	Resistant
PFSR-151	3.1	Resistant
BML-10	4.1	Moderately resistant
MGC-49	3.5	Resistant
ML-14	6.2	Moderately susceptible
PFSR-92	8.1	Highly susceptible
BPDT-5009	8.2	Highly susceptible
PFSR-73 × PFSR-127	2.5	Resistant
PFSR-73 × PFSR-151	2.6	Resistant
PFSR-73 × BML-10	3.6	Resistant
PFSR-73 × MGC-49	3.5	Resistant
PFSR-73 × ML-14	6.7	Moderately susceptible
PFSR-73 × PFSR-92	3.7	Resistant
PFSR-73 × BPDT-5009	5.9	Moderately resistant
PFSR-127 × PFSR-151	2.4	Resistant
PFSR-127 × BML-10	4.5	Moderately resistant

Table 4.15 (cont.).

Genotypes	Disease score (0-9 scale)	Disease reaction
PFSR-127 × MGC-49	2.6	Resistant
PFSR-127 × ML-14	3.3	Resistant
PFSR-127 × PFSR-92	3.8	Resistant
PFSR-127 × BPDT-5009	4.1	Moderately resistant
PFSR-151 × BML-10	3.9	Resistant
PFSR-151 × MGC-49	3.4	Resistant
PFSR-151 × ML-14	4.8	Moderately resistant
PFSR-151 × PFSR-92	3.0	Resistant
PFSR-151 × BPDT-5009	3.7	Resistant
BML-10 × MGC-49	5.7	Moderately resistant
BML-10 × ML-14	6.7	Moderately susceptible
BML-10 × PFSR-92	7.1	Moderately susceptible
BML-10 × BPDT-5009	7.3	Moderately susceptible
MGC-49 × ML-14	6.9	Moderately susceptible
MGC-49 × PFSR-92	2.6	Resistant
MGC-49 × BPDT-5009	3.9	Resistant
ML-14 × PFSR-92	8.0	Highly susceptible
ML-14 × BPDT-5009	8.1	Highly susceptible
PFSR-92 × BPDT-5009	8.0	Highly susceptible
Kaveri-50	8.2	Highly susceptible

Altogether 8 parents were used to develop 28 hybrids. Among the parents 4 were found to be resistant to charcoal rot, one was moderately resistant, one was moderately susceptible and two parents were highly susceptible. Different combinations of crosses were affected during the investigation which included resistant × resistant, resistant × moderately resistant, resistant × susceptible, resistant × moderately susceptible, moderately resistant × susceptible, moderately susceptible × susceptible and susceptible × susceptible types.

All the seven hybrids were found resistant when both the parents were resistant. Two out of four hybrids were resistant and the remaining two hybrids were moderately resistant when the crossings were done between resistant and moderately resistant parents. Six out of eight hybrids were resistant and the remaining two hybrids were moderately resistant when the crosses were done involving one resistant and one

susceptible parent. Two out of three hybrids were moderately susceptible and the remaining one cross showed moderately resistant reaction when the hybrids were developed between resistant and moderately susceptible parents. All the two hybrids exhibited moderately susceptible reaction when the crosses were done between moderately resistant and susceptible parents. When the hybrid was developed between one moderately resistant and one moderately susceptible parent the resultant hybrid exhibited moderately susceptible reaction. All the two hybrids exhibited highly susceptible reaction when the crosses were done between moderately susceptible and susceptible parents. Finally, the hybrid showed highly susceptible reaction when the both the parents are highly susceptible.

Screening for charcoal rot resistance indicated that fifteen hybrids were resistant to charcoal rot, five hybrids showed moderately resistant, five hybrids were moderately susceptible and three hybrids recorded the highly susceptible reaction to charcoal rot.

Three out of five superior hybrids (PFSR-127 × ML-14, PFSR-127 × MGC-49 and PFSR-151 × BPDT-5009) based on mean performance for grain yield per plant were found to be resistant to charcoal rot, one hybrid recorded (PFSR-127 × BPDT-5009) was found to be moderately resistant and the remaining one hybrid (BML-10 × PFSR-92) showed moderately susceptible reaction to charcoal rot.

Table 4.16. Overall performance of the superior hybrids (top five high yielders) identified in the study

S. No	Name of the cross	<i>Per se</i> performance (g/plant)	<i>sca</i> effect for grain yield per plant	Stay green nature	Reaction to charcoal rot resistance
1	PFSR-127 × ML-14	187.33	24.30**	Non-stay green	Resistant
2	PFSR-127 × MGC-49	164.66	-31.69**	Stay green	Resistant
3	BML-10 × PFSR-92	161.33	31.67**	Stay green	Moderately susceptible
4	PFSR-151 × BPDT-5009	157.66	47.93**	Non-stay green	Resistant
5	PFSR-127 × BPDT-5009	156.66	37.27**	Non-stay green	Moderately resistant

Among the superior hybrids which recorded high grain yield per plant and *sca* effects it was found that two hybrids were resistant to charcoal rot among which one is non-stay green (PFSR-127 × ML-14) and the other one is stay green type (PFSR-127 × MGC-49). Hence further investigations have to be carried out with different resistant

sources over years and across the locations to develop high yielding varieties which are of stay green type and resistant to charcoal rot.

Chapter V

SUMMARY AND CONCLUSIONS

The present investigation “Genetic analysis for yield and evaluation of hybrids for Charcoal rot resistance in maize (*Zea mays* L.) was under taken with eight inbred lines. These eight inbred lines were crossed in half diallel mating design to develop 28 hybrids in *kharif*, 2021. The one complete set of the experimental hybrids (28) along with 8 parents and one commercial check, DHM-117 were evaluated for yield and its attributing traits at Agricultural Polytechnic College, Polasa, Jagtial during *Rabi*, 2021-2022 and other complete set of the experimental hybrids (28) along with 8 parents and one susceptible check, Kaveri-50 were used screened for charcoal rot resistance at Maize Research Centre, Agricultural Research Institute, Rajendranagar, Hyderabad during *Rabi*, 2021-2022. Data was collected on yield and its contributing traits and subjected to analysis for interpretation.

The analysis of variance of genotypes (treatments) for yield and its component traits revealed that mean sum of squares for replications were non-significant for all the characters while, the mean sum of squares due to treatments were significant for all the characters. This indicated the presence of sufficient amount variation in the breeding material.

(i) Mean performance and Heterosis

The inbred lines, BML-10 and PFSR-151 were found to be the earliest among the parents while, BML-10×BPDT-5009, PFSR-73×ML-14, ML-14×PFSR-92 and MGC-49×PFSR-92 were the earliest among hybrids. The results indicated that the hybrids attained days to 50% anthesis earlier than the parents. The inbred line, BML-10 recorded the lowest ear height which is highly desirable for resistance against high velocity winds. However, the lowest ear height was observed in the hybrid, PFSR-151×ML-14. The inbred line, BML-10 recorded the maximum 100-kernel weight and grain yield per plant. The hybrid, PFSR-73×PFSR-92 recorded the highest 100-kernel weight of 35.53 g. The hybrid, PFSR-127×ML-14 recorded highest grain yield per plant. Nine out of 28 experimental hybrids recorded significantly superior grain yield per plant over the check, DHM-117.

Twenty-four (24) out of 28 hybrids showed significantly negative standard heterosis for days to 50% anthesis which is desirable for the development of early maturing hybrids. Twenty-five out of the 28 hybrids recorded significantly negative

standard heterosis for days to maturity. Among 28 hybrids, four hybrids recorded significantly positive standard heterosis for ear girth. Only one out of 28 hybrids recorded significantly positive heterosis over the check for number of kernels per row. Two hybrids recorded significantly positive standard heterosis for 100-kernel weight. Standard heterosis for grain yield per plant ranged from -66.67% (MGC-49×BPDT-5009) to 32.24% (PFSR-127×BML-10). Thirteen among the 28 hybrids recorded significantly positive standard heterosis for the trait, grain yield per plant.

(ii) Combining ability

The analysis of variance for combining ability revealed that the parents showed significant differences for all the characters under study. The crosses also exhibited significant differences implying the varied performance of cross-combinations. The parent vs hybrids also showed significance for all the characters except number of kernel rows per ear. These results revealed that there exists sufficient amount variability in breeding material under study.

The estimates of combining ability revealed that mean SCA variance was greater in magnitude than GCA variance for days to 50% anthesis, days to 50% silking, anthesis silking interval, days to maturity, plant height, ear height, ear length, ear girth, number of kernel rows per ear, number of kernels per row, 100-kernel weight and grain yield per plant indicating that these characters were controlled by non-additive gene action.

Combining ability analysis revealed that among parents, PFSR-127, BML-10 and PFSR-151 were found good general combiners for grain yield per plant, days to 50% anthesis, days to 50% silking, days to maturity, ear length, ear girth, number of kernel rows per ear, number of kernels per row and 100-kernel weight. The hybrids, PFSR-151×BPDT-5009, PFSR-73×ML-14 and PFSR-127×BPDT-5009 were identified as specific combiners for earliness, yield and its attributing traits.

Based on *per se* performance, *sca* effects and standard heterosis, PFSR-127×ML-14, BML-10×PFSR-92 and PFSR-151×MGC-49 were identified as the best hybrids for yield and yield attributing traits.

(iii) Correlation and Path analysis

Correlation studies revealed that the significant negative correlation of grain yield with days to 50% anthesis, days to 50% silking and days to maturity while positive significant correlation with ear length, ear girth, ear height, plant height, number of kernel rows per ear, number of kernels per row and 100-kernel weight.

Studies on path coefficient revealed that days to 50% silking, 100-kernel weight, ear girth, number of kernels per row and number of kernel rows per ear showed the highest

positive direct effects on grain yield and hence these characters play a key role in the development of high yielding genotypes in further breeding programmes.

Among parents, MGC-49 and PFSR-92 were found stay green while, among the hybrids, PFSR-127×MGC-49, PFSR-151×MGC-49, PFSR-151×PFSR-92, BML-10×PFSR-92, MGC-49×ML-14 and MGC-49×PFSR-92 were also identified showed stay green character.

(iv) Screening for charcoal rot resistance

Screening for charcoal rot resistance indicated that fifteen hybrids were resistant to charcoal rot, five hybrids showed moderately resistant, five hybrids were moderately susceptible and three hybrids recorded the highly susceptible reaction to charcoal rot.

Three out of five superior hybrids (PFSR-127 × ML-14, PFSR-127 × MGC-49 and PFSR-151 × BPDT-5009) based on mean performance for grain yield per plant were found to be resistant to charcoal rot, one hybrid recorded (PFSR-127× BPDT-5009) was found to be moderately resistant and the remaining one hybrid (BML-10 × PFSR-92) showed moderately susceptible reaction to charcoal rot.

Among the superior hybrids which recorded high grain yield per plant and *sca* effects it was found that two hybrids were resistant to charcoal rot among which one is non-stay green (PFSR-127 × ML-14) and the other one is stay green type (PFSR-127 × MGC-49). Hence further investigations have to be carried out with different resistant sources for charcoal rot resistance and also sources for stay green trait and further testing are required over years and across the locations to develop high yielding hybrids which are of stay green type coupled with charcoal rot resistance.