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Heterosis studies for grain yield and yield components in maize (*Zea mays* L.)

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Abstract
Heterosis studies in maize revealed that eighteen out of hybrids recorded significantly negative heterosis over better parent for days to 50% flowering. Nine hybrids showed significantly negative heterosis over better parent for days to silking and anthesis silking interval. Twenty five hybrids recorded significantly negative standard heterosis for days to maturity. Ten hybrids recorded significantly positive Standard heterosis while, ten hybrids recorded significantly negative standard heterosis for plant height. For ear girth, better-parent heterosis ranged from -21.18% (PFSR-73×PFSR-127) to 17.95% (BML-10×ML-14). Better-parent heterosis for number of kernel rows per ear ranged from -27.61% (MGC-49×BPDT-5009) to 16.67% (ML-14×PFSR-92). Five hybrids recorded significantly positive heterosis over the better parent for the trait. Better-parent heterosis for number of kernels per row varied from -39.60% (ML-14×BPDT-5009) to 50.70% (PFSR-73×PFSR-92) for number of kernels per row. Better-parent heterosis for grain yield per plant ranged from -55.52% (MGC-49×BPDT-5009) to 44.65% (PFSR-73×ML-14).

Keywords: Maize, yield, standard heterosis, better parent heterosis

Introduction
Maze (*Zea mays* L.) is an important food crop that plays an important role in various industries like food, fodder and Industrial utilization. It belongs to the family, Poaceae, tribe Maydeae. Th crop has high potentiality and wider adaptability due to highly cross-pollinated nature and greater diversity. It is widely cultivated in an area of 193.7 m ha with a production of 1147.6 MT while, productivity was 5920 kg ha^{-1} globally. In India, it was grown in an area of 9.72 m ha with the production and productivity levels of 28.64 MT and 2965 kg ha^{-1}, respectively (FAO, 2020) [1].

Materials and Methods
The present study was carried out during *Kharif,* 2021and *Rabi,* 2021- at the Agricultural Polytechnic College, Polasa, Jagtial. Agricultural Polytechnic College, Polasa, Jagtial is located at a height of 243.4 m above mean sea level on 18º49'40" N latitude and 78º56'45" 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 experimental material consisted 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. These inbred lines were crossed in Half-diallel, Method-II, Model-I mating design and generated 28 hybrids and single cross hybrids 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.

Estimation of Heterosis
Estimates of heterosis was calculated according to Fonseca and Patterson (1968) [2].

Heterosis over mid parent: Heterosis was expressed as percent increase or decrease observed in the F$_1$ over the mid-parent as per the following formula.

$$\text{Heterosis (\%) } (h_1) = \frac{\overline{F_1} - \overline{MP}}{\overline{MP}} \times 100$$

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Where,

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

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

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

Heterobeltiosis % (h_2) = $\dfrac{\overline{F_1} - \overline{BP}}{\overline{BP}}$ x100

Where,
$\overline{BP}$ = Mean of better parent

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

Standard heterosis % (h_3) = $\dfrac{\overline{F_1} - \overline{SC}}{\overline{SC}} \times 100$

Where,
$\overline{sc}$ = 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 (σ^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 heterosisand 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 percent and 1 percent level of significance (0.05 and 0.01 level of probability) respectively.

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

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

EMS = Error mean of squares

r = Number of replications

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

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

Least significance difference (critical difference) for heterosis: The significance of the difference between two estimates of heterosis was tested by computing the least significant difference (LSD) by multiplying the SE m with the appropriate student t value of respective error degrees of freedom at the desired level of probability.

CD = SE m x 't' table value at error degrees of freedom

Results and Discussion

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 the commercial exploitation of heterosis.

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. The results are presented under Table.1 and Table.2.

Days to 50 percent anthesis

Mid-parent heterosis for 50 percent 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 Agarwal *et al*. (2021) [3] for the trait clearly indicating the possibility of exploiting heterosis for earliness.

Days to 50 percent 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 Agarwal *et al*. (2021) [3] and Tulu *et al.* (2021) [4].

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 Nandhitha et al. (2018) [5].

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 Upreti et al. (2020) [6].
Generally, significantly negative heterosis for days to 50 percent anthesis, days to 50 percent 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.

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 Chaurasia et al. (2021) [7] reported significantly negative standard heterosis for this trait.

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 Suresh et al. (2021) [8] reported positive standard heterosis for ear height.

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) [5].

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 Tello (2021) [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 Tello (2021) [9] for significantly positive standard heterosis.

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) [6] and standard heterosis by Tello (2021) [9].

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) [5] for Better-parent heterosis, Chaurasia *et al*. (2021) [7] and Tello (2021) [9] for standard heterosis.

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 Upreti *et al.* (2020) [6] and Chaurasia *et al*. (2021) [7].

Table 1: 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		
Heterosis	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

Crosses	Days to 50% anthesis			Days to 50% silking			Anthesis silking interval		
Heterosis	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

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**

Crosses	Days to maturity			Plant height (cm)			Ear height (cm)		
Heterosis	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

Crosses	Ear length (cm)			Ear girth (cm)			Number of kernel rows per ear		
Heterosis	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**

Crosses	Ear length (cm)			Ear girth (cm)			Number of kernel rows per ear		
Heterosis	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

Crosses	Number of kernels per row			100-kernel weight (g)			Grain yield (g/plant)		
Heterosis	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

Crosses	Number of kernels per row			100-kernel weight (g)			Grain yield (g/plant)		
Heterosis	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 2: 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 percent 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 percent 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**

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**

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.

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