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Combining Ability Analysis of Early Maturing Quality Protein Maize (*Zea mays* L.) Lines and Heterosis of their F1 Hybrids

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ABSTRACT

The present investigation was carried out with 56 genotypes involving 10 parental inbred lines, their 45 F₁s hybrids and one check (HQPM-5) with an objective to identify the suitable parents and desirable hybrid combinations using diallel mating design (excluding reciprocals) during *Rabi* 2018-2019 and *Kharif* 2019 at Field Experimentation Centre, Department of Genetics and Plant Breeding, SHUATS, Prayagraj (Allahabad), U.P. Analysis of variance revealed that the mean sum of squares due to treatments, parents, hybrids and parent vs. hybrids showed significant differences for all traits studied at 1% level of significance except for Anthesis Silking Interval. The SCA variance were higher than GCA variances for traits *viz.*, anthesis silking interval, plant height and ear height, days to maturity and number of kernel per row indicating predominance of non-additive gene action of these traits. However, the low and moderate values were obtained in the remaining traits. The QPM inbred lines *viz.*, CM-600, HKI-34 (H2), POP-31Q-182Q11 and TMT-TROP (QPM) which exhibited good general combiner for at least one trait can be used as donor parents for the accumulation of favourable genes and crosses TARUN-83-1-32 X JP-25-W95 and TMT-TROP-(QPM) X CM-138-1 showed highest positive significant SCA effects for grain yield per plant. These hybrids probably have potential as parents of hybrid varieties, as well as for inclusion in breeding programmes. POP-31Q-182Q11 X HKI-193-1, POP-31Q-182Q11 X TARUN-83-1-32 exhibited positive significant economic heterosis for grain yield and other yield attributing characters over check indicating the possibility of increasing yield by exploiting heterotic potential of these maize genotypes.

Keywords

Diallel, Heterosis,
GCA, SCA, Inbred,
Quality Protein
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Introduction

Maize (*Zea mays* L.) crop has been subjected to pervasive genetic studies than any other crops because of its cross pollinating nature and extremely large genetic variability, which enables it to prosper in tropical, subtropical, and temperate climates. It plays a very important role in human and animal nutrition and its kernel contains 80 % carbohydrates, 10% protein, 4.5% oil, 3.5% fiber and 2% minerals (Jugenheimer, 1976). It is a good source of calcium and phosphorous. Several hundred million people rely on maize as their principal daily food, for weaning babies, and for feeding livestock. Unfortunately maize (corn) has two significant flaws; it lacks the full range of amino acids, namely lysine and tryptophan, needed to produce proteins, and has its niacin (vitamin B₃) bound in an indigestible complex. Maize has suboptimal amounts of the essential amino acids tryptophan and lysine, which accounts for its lower status as a protein source (United Nations Food and Agriculture Organization, 1992). The normal maize protein is of poor nutritional quality due to a deficiency in two essential amino acids (lysine and tryptophan) and high leucine-isoleucine ratio. However, the breakthrough in maize production is obtained after the discovery of opaque-2 mutant maize which alters the amino acid composition and enhances the grain tryptophan and lysine content in maize (Mertz *et al.*, 1964). It promotes evolution of new Quality Protein Maize (QPM) composites such as Ratna, Shakti and Protina. QPM produces 70–100% more of lysine and tryptophan than the most modern varieties of tropical maize. These two amino acids allow the body to manufacture complete proteins, thereby eliminating wet-malnutrition. In addition tryptophan can be converted in the body to Niacin, which theoretically reduces the incidence of Pellagra. Therefore, it is desirable to replace the present maize hybrids

with QPM hybrids which are similar in cultivation, grain yield, potentiality, and tolerance to biotic and abiotic stresses with that of normal maize hybrids.

Development of hybrid variety is the effort that could be considered to increase QPM yield per unit area. Therefore, heterosis and combining ability are the useful parameter for breeding Sugiharto *et al.*, (2018). The magnitude of heterosis provides a basis for genetic diversity and acts as a guide in choosing desirable lines and cross combinations. Heterotic responses can be obtained in the positive and negative directions (+ve and –ve). Heterosis in negative direction was considered for days to 50% tasseling, days to 50% silking, anthesis-silking interval, days to maturity, cob height and plant height and other traits in positive direction of heterosis is desirable. Combining ability of an inbred line depend on its ability to produce superior hybrids in combination with other inbreds and it is one of the powerful tools in identifying the good inbred lines as best combiners that may be used in breeding program either to exploit heterosis or to accumulate productive genes. This approach has been used in identifying suitable maize genotypes for improvement of grain yield and other agronomic traits (Castilo and Goodman, 1989 and Fasahat *et al.*, 2016). It also helps to understand the genetic architecture of various characters that enable the breeder to design effective breeding plan for the future improvement of the existing materials. Therefore, the present study was conducted to estimate the magnitude of heterosis, the GCA effect of parents, SCA effect of hybrids and nature of gene action to explore suitable heterotic hybrid combinations in QPM.

Materials and Methods

The present investigation was undertaken with ten parental lines *viz.*, HKI-193-1 (P₁), JP-25-

W95 (P₂), CM-600 (P₃), CM-138-1 (P₄), DMR-N₄ (P₅), TARUN-83-1-32 (P₆), LM-13 (P₇), HKI-34 (H2) (P₈), POP-31Q-182Q11 (P₉), TMT-TROP-(QPM) (P₁₀) which were crossed in diallel mating design (excluding reciprocals) to develop 45 F₁'s hybrids at Field Experimentation Centre, Department of Genetics and Plant Breeding, SHUATS, Prayagraj, Uttar Pradesh during *Rabi* 2018-2019 and *Kharif* 2019 under Randomized Block Design (RBD) with three replications and the experimental field was divided into 3 blocks of equal size with plot with of 3m and Size of each bund 0.5 m, the row to row distance and Plant to plant distance 60 cm and 20 cm respectively and each line possesses single genotype.

Observations for all traits were recorded on five randomly selected competitive plants from each plot in each replication for all the characters viz. Days to first tassel emergence (50%), Days to first silk emergence (50%), Anthesis-silking interval (Days), Plant height (cm), Cob height (cm), Days to maturity, Cob length (cm), Cob girth (cm), Number of kernel rows per cob, Number of kernel per row, 100 kernel weight (g), Grain yield per plant (g/plant) except for days to 50 % silk emergence, days to 50 % tassel emergence and days to maturity where the observation will be recorded on plot basis.

The data recorded during the present investigation was subjected to following statistical analysis i.e. Analysis of variance (Fisher, 1963), Diallel analysis, Average heterosis (Turner, 1953), Heterobeltiosis (Foneska and Patterson, 1968) and Economic heterosis (Meredith and Bridges, 1972).

Results and Discussion

The present investigation revealed that the mean sum of squares due to treatments, parents, hybrids and parent vs. hybrids showed

significant differences for all traits studied at 1% level of significant except for anthesis-silking interval, which revealed that there is a wide range of variability among the genotypes suggesting that the genotypes were genetically variant for each other and provide the scope for breeding. Similar findings for analysis of variance for most of the characters in maize were also reported by Sofi and Rather (2006) (Darshan and Marker, 2019). Variances due to General Combining Ability (GCA) and Specific Combining Ability (SCA) were significant for all the characters except Anthesis Silking Interval. This study also revealed the significant differences of general combining ability (GCA) effects of parents and that of specific combining ability (SCA) effects of hybrids. Significant variance due to both GCA and SCA for all important yield attributing characters implied that both additive and non-additive genetic variances are important in controlling the expression of these characters. However, higher magnitude of SCA effects than GCA effects (GCA/SCA<1) were observed for anthesis silking interval, plant height and ear height, days to maturity and number of kernel per row. The relatively smaller proportion of GCA to SCA ratio indicated the predominance of non-additive genetic effects with respect to most of the traits in their inheritance, confirming the results of Aminu and Izge (2013), Patel *et al.*, (2016), Ram *et al.*, (2017) and Darshan and Marker (2019).

GCA effects

Results concluded (Table 1) that among 10 QPM inbred lines tested for their combining abilities pertaining to different characters under study, line CM-600 recorded significant *gca* effects in desirable direction for ten different characters viz., days to 50% tasseling, days to 50% silking, days to maturity, plant height, cob girth, cob length, kernel row per cob and number of kernel per

row, test weight, and grain yield per plant followed by HKI-34 (H2) for six characters viz., cob girth, cob length, number of kernel per row, number of kernel row per cob, 100 grain weight and grain yield per plant followed by POP-31Q-182Q11 for plant height, cob girth, number of kernel per row, number of kernel row per cob and grain yield per plant followed by TMT-TROP (QPM) for days to 50% tasseling, days to 50% silking, number of kernel per row and CM-138-1 for days to 50% tasseling, days to 50% silking and days to maturity.

Thus, the Quality Protein Maize inbred lines viz., CM-600, HKI-34 (H2), POP-31Q-182Q11 and TMT-TROP (QPM) which exhibited good general combiner for at least one trait can be used as donor parents for the accumulation of favourable genes (Scaria *et al.*, 2020).

Therefore these lines can be utilized in improvement of the respective traits in any breeding programme wherever hybridization is involved. Due to their good combining ability these lines can be utilized straightaway as parents for production of good hybrids by crossing with other divergent lines and can also be employed in the development of synthetic varieties. These findings are in conformity with the findings of Mostafavi *et al.*, (2012), Aminu *et al.*, (2014) and Scaria *et al.*, (2020).

SCA effects

The estimates of SCA effects (Table 2) indicated that twelve cross combinations showed negative significant SCA effects for days to 50% tasseling.

The highest SCA effects for days to 50% tasseling exhibited by crosses viz., TMT-TROP-(QPM) X HKI-193-1 (-4.78**), LM-13 X JP-25-W95 (-4.75**), HKI-34 (H2) X JP-

25-W95 (-4.33**), POP-31Q-182Q11 X HKI-34 (H2) (-4.19**) and POP-31Q-182Q11 X TARUN-83-1-32 (-4.00**).

The perusal of SCA effects indicated that eighteen cross combinations showed negative significant SCA effects for days to 50% silking and the highest SCA effects exhibited by crosses viz., POP-31Q-182Q11 X HKI-34 (H2) (-5.41**), POP-31Q-182Q11 X LM-13 (-5.05**), LM-13 X HKI-193-1 (-4.21**) and HKI-34 (H2) X HKI-193-1 (-3.91**). The perusal of SCA effects indicated that eleven cross combinations showed negative significant SCA effects for days to maturity.

The highest SCA effects for days to maturity exhibited by crosses viz., HKI-34 (H2) X HKI-193-1 (-4.13**), POP-31Q-182Q11 X HKI-34 (H2) (-4.08**), POP-31Q-182Q11 X LM-13 (-4.02**) and LM-13 X HKI-193-1 (-3.75**) indicating earliness. The highest SCA effects exhibited by crosses TARUN-83-1-32 X JP-25-W95 (62.21**) followed by TMT-TROP-(QPM) X CM-138-1 (55.51**), POP-31Q-182Q11 X CM-600 (49.09**), POP-31Q-182Q11 X HKI-34 (H2) (48.46**) and HKI-34 (H2) X CM-600 (30.52**).

These hybrids probably have potential as parents of hybrid varieties, as well as for inclusion in breeding programmes, since they may contribute superior alleles in new populations for high grain yield.

These results are in line with earlier independent studies of Kumar *et al.*, (1998) and Joshi *et al.*, (1998) who reported that maize grain yield and other traits were under the control of non-additive (SCA effects) type of gene action.

Similar results are also found by Junaidul *et al.*, (2015), Patel *et al.*, (2015), Matin *et al.*, (2016), Tulu *et al.*, (2016), Darshan and Marker (2019) and Solomon *et al.*, (2020).

Table.1 General combining Ability effects of parents for different parameters in Quality Protein Maize

S.No.	Notation	Genotype name	Days to 50% tasseling	Days to 50% silking	Anthesis-silking interval	Plant height (cm)	Cob height (cm)	Days to maturity	Cob girth (cm)	Cob length (cm)	Number of kernel per row	Number of kernel row per cob	100 seed weight (g)	Grain yield per plant (g/plant)
1	P ₁	HKI-193-1	1.10**	1.21**	-0.02	12.05**	-13.57**	-0.18	0.06	-0.05	-0.40	0.01	-1.49**	-8.19**
2	P ₂	JP-25-W95	-0.03	0.10	0.14	11.08 **	-4.13**	-0.15	-0.16 *	-0.22	-0.01	-0.06	1.51 **	5.46**
3	P ₃	CM-600	-0.95**	-1.09**	-0.27	23.42**	13.32**	-1.29**	0.20**	0.56*	2.42**	0.16*	0.75**	10.80**
4	P ₄	CM-138-1	-0.53**	-0.45**	0.36*	6.19**	0.09	-1.35**	-0.08	-0.49*	-0.20	0.06	-0.95 **	-3.35**
5	P ₅	DMR-N ₄	-0.01	0.10	0.03	-0.49	0.32	0.51*	-0.2**	-0.6**	-2.6**	-0.48**	0.98**	5.98**
6	P ₆	TARUN-83-1-32	0.272	0.32*	-0.10	-22.06**	1.78*	1.28**	-0.52**	0.15	-0.61*	-0.28**	0.62*	-4.34**
7	P ₇	LM-13	0.21	0.21	-0.21	10.90**	-4.46**	0.28	-0.15*	-0.20	-1.47**	-0.21*	-0.19	-5.81**
8	P ₈	HKI-34 (H2)	0.21	0.18	0.06	5.14 **	7.91**	0.78**	0.38**	0.51*	1.23**	0.57**	0.52*	8.88**
9	P ₉	POP-31Q-182Q11	0.18	-0.17	-0.10	-3.01*	-0.59	0.20	0.32**	0.26	0.91**	0.21**	-0.19	2.60*
10	P ₁₀	TMT-TROP-(QPM)	-0.47**	-0.40**	0.17	3.01*	-0.66	-0.10	0.19*	0.11	0.77**	0.07	-0.31	-0.11

**Significant at 1% and *Significant at 5% level

Table.2 Specific combining Ability effects of crosses for different parameters in Quality Protein Maize

S.N o.	Genotypes	Days to 50% tasseling	Days to 50% silking	Anthesis -silking interval	Plant height (cm)	Cob height (cm)	Days to maturity	Cob girth (cm)	Cob length (cm)	No. of kernel / row	No. of kernel row / cob	100 seed weight (g)	Grain yield / plant (g/plant)
1	JP-25-W95 X HKI-193-1	0.19	0.51	-0.45	-25.61**	-10.19	2.69**	-0.64*	-0.21	1.68	0.81**	-2.30**	-2.40
2	CM-600 X HKI-193-1	-0.83	-1.52**	0.10	-2.43	4.69	0.77	-0.19	-0.12	3.09**	-1.28**	-1.96*	-7.65*
3	CM-600 X JP-25-W95	-0.16	-0.41	0.71	7.05	-2.31	1.47*	0.04	-0.60	-1.64	-0.09	-2.55	-11.85**
4	CM-138-1 X HKI-193-1	-0.83	-1.55**	-0.01	-0.52	-0.67	1.61*	0.12	3.49**	2.67**	0.30	-0.15	5.65
5	CM-138-1 X JP-25-W95	-1.86**	0.22	0.93	-28.10**	-15.67**	-0.02	0.15	-1.99*	-3.26**	0.82**	-2.64**	-13.70**
6	CM-138-1 X CM-600	-0.50	-1.46**	-0.51	2.34	-0.83	0.38	0.37	-0.58	-2.18*	0.73**	0.86	-1.12
7	DMR-N ₄ X HKI-193-1	-0.83	1.00	-0.12	-3.56	2.36	-0.38	-1.74**	0.05	7.28**	0.90**	-0.09	22.32**
8	DMR-N ₄ X JP-25-W95	1.44**	-0.21	0.49	-20.13**	-16.24**	-0.02	1.61**	-0.11	-2.79**	0.23	2.64**	0.59
9	DMR-N ₄ X CM-600	-0.22	-1.91**	-0.62	0.50	-16.41**	-0.61	0.06	0.16	-0.24	0.94**	-1.75*	-4.05*
10	DMR-N ₄ X CM-138-1	-1.58**	-0.93	-0.06	4.48	-3.23	1.22	0.52	1.80*	2.26*	0.25	-0.21	-7.07
11.	TARUN-83-1-32 X HKI-193-1	-1.25*	0.07	0.07	10.87*	7.15	0.05	0.92**	-1.93*	-4.45**	-0.62*	8.35**	3.69
12.	TARUN-83-1-32 X JP-25-W95	0.38	0.35	0.35	19.42**	18.42**	-1.58*	-2.47**	2.39**	8.13**	1.33**	7.56**	62.21**
13.	TARUN-83-1-32 X CM-600	-1.28	0.90	0.90	1.80	-1.08	-1.16	0.73**	0.92	-0.78	-0.72*	2.06*	-6.11
14.	TARUN-83-1-32 X CM-138-1	0.02	-0.87	-0.87	-19.95**	-3.57	1.00	0.73**	1.80*	-0.47	0.32	-2.90*	-4.47**
15.	TARUN-83-1-32 X DMR-N ₄	-0.30	0.01	0.01	5.27	10.04 **	0.33	-0.63*	-1.05	-3.66**	-0.26	-0.42	-13.17**
16.	LM-13 X HKI-193-1	-0.36	-4.21**	1.07*	12.91**	21.45	-3.75**	-0.49	1.29	3.73**	-0.18	3.31**	22.99
17.	LM-13 X JP-25-W95	-4.73**	0.22	-0.98	12.40**	8.64**	-2.72**	0.10	-1.95*	-2.74**	-0.19	2.67**	-4.50
18.	LM-13 X CM-600	0.91	1.53**	0.90	9.44*	5.20	-0.63	-1.20**	0.27	3.40**	0.65*	1.32	17.40**
19.	LM-13 X CM-138-1	0.55	2.17**	-1.20*	9.15*	7.38*	-0.13	0.84**	-0.68	-1.61	0.76**	0.18	-3.51
20.	LM-13 X DMR-N ₄	1.88**	0.72	0.35	40.38 **	4.94	0.19	-0.25	1.43	4.78**	0.97**	-1.51	6.19
21.	LM-13 X TARUN-83-1-32	0.16	-0.71	0.21	0.08	13.20**	2.30	0.93**	0.38	-0.35	1.04	0.68	3.30
22.	HKI-34 (H2) X HKI-193-1	-0.55	-3.91**	0.37	26.82**	5.22	-4.13**	0.01	0.09	-0.82	1.26**	3.11**	16.43**
23.	HKI-34 (H2) X JP-25-W95	-4.33**	-0.13	-0.01	37.64**	15.62**	-1.11	0.72	-0.62	-0.76	-0.07	2.78**	5.42
24.	HKI-34 (H2) X CM-600	-0.66	-0.49	0.21	29.95**	15.18**	-0.02	0.86**	1.93*	2.51**	0.49	4.83**	30.52**
25.	HKI-34 (H2) X CM-138-1	-0.36	-0.52	1.10 *	43.06**	26.35**	-0.86	-2.33**	0.53	0.69	-0.58*	-3.54**	-18.25**
26.	HKI-34 (H2) X DMR-N ₄	-0.36	2.69**	-0.67	54.82**	37.58 **	1.80	0.07	1.31	6.89**	-0.24	1.38	19.27**
27.	HKI-34 (H2) X TARUN-83-1-32	2.24**	3.92**	0.18	14.32**	12.44**	1.25	-0.69*	1.88*	0.02	0.08	-2.65**	-11.57**
28.	HKI-34 (H2) X LM-13	1.52**	-3.85**	1.18 *	16.56**	5.80*	-2.55**	0.73**	1.07	1.88*	0.26	-1.22	-3.99
29.	POP-31Q-182Q11 X HKI-193-1	-3.61 **	3.89**	-0.70	21.49**	-15.45**	2.38	0.35	-0.38	-4.18**	-0.11	-0.10	-12.15**
30.	POP-31Q-182Q11 X JP-25-W95	3.41 **	-0.99	0.57	-6.88	-12.05**	0.75	0.52	-0.61	-2.39*	1.21**	0.34	-3.07
31.	POP-31Q-182Q11 X CM-600	-0.91	1.64**	0.46	5.96	-0.63	0.83	0.25	2.69**	5.35**	0.85**	6.54**	49.09**
32.	POP-31Q-182Q11 X CM-138-1	0.05	-1.05*	-0.31	35.87**	12.08**	0.66	0.38	0.65	3.59**	-0.36	2.41**	15.97**

33.	POP-31Q-182Q11 X DMR-N ₄	-0.61	-3.82**	1.24 *	39.76**	26.90 **	-2.33**	-1.73**	-0.84	2.00*	-0.15	0.43	0.63
34.	POP-31Q-182Q11 X TARUN-83-1-32	-4.00**	-1.27*	-0.23	23.40**	2.89	-0.22	-0.82**	-0.60	-1.93	0.17	3.21**	-2.17
35.	POP-31Q-182Q11 X LM-13	-0.72	-5.05**	0.10	18.03**	10.72 **	-4.02**	-0.08	2.49**	-1.07	1.15**	-0.93	-3.14**
36.	POP-31Q-182Q11 X HKI-34 (H2)	-4.19**	-5.41**	-0.92	-1.91	-7.83 **	-4.08 **	0.83	1.93*	4.63**	1.53**	5.37**	48.46**
37.	TMT-TROP-(QPM) X HKI-193-1	-4.78**	0.44	-0.20	9.42*	4.45	-1.25	0.13	1.31	-1.32	-0.85**	-3.66**	-16.88**
38.	TMT-TROP-(QPM) X JP-25-W95	0.94	-1.43**	-0.59	18.45 **	7.11 *	-1.55*	-0.41	0.02	-3.33**	-2.46**	-0.85	-19.62**
39.	TMT-TROP-(QPM) X CM-600	-1.41 **	-1.80**	-0.70	-15.63**	10.47**	-2.80**	1.11**	-2.34**	-4.52**	0.11	1.43	-6.00
40.	TMT-TROP-(QPM) X CM-138-1	-1.08*	-1.82**	-0.48	28.73 **	10.12**	0.36	1.09**	-1.43	4.85**	1.36**	8.86**	55.51**
41.	TMT-TROP-(QPM) X DMR-N ₄	-0.47	-0.60	-0.92	31.03 **	4.47	-1.30	1.33**	-0.11	0.12	0.43	3.87**	17.74**
42.	TMT-TROP-(QPM) X TARUN-83-1-32	-1.86**	-2.05**	-0.39	6.13	-12.26**	-1.52*	-0.28	-0.03	1.92*	1.97**	3.30**	7.62*
43.	TMT-TROP-(QPM) X LM-13	-0.33	-0.49	-0.06	28.23**	-0.10	1.00	0.05	1.36	2.17*	0.28	-1.24	0.22
44.	TMT-TROP-(QPM) X HKI-34 (H2)	-0.58	-1.18*	0.24	-36.65**	-21.53**	2.27**	0.50	-0.33	-0.51	-0.54	1.41	3.9
45.	TMT-TROP-(QPM) X POP-31Q-182Q11	2.497**	3.28**	0.49	14.44**	16.25**	-0.19	0.58*	0.11	0.66	0.48	-2.35**	-4.84

**Significant at 1% and *Significant at 5% level

Table.3 Economic heterosis (Hc) for Quantitative traits in Quality Protein Maize

S.N o.	Genotypes	Days to 50% tasseling	Days to 50% silking	Anthesis-silking interval	Plant height (cm)	Cob height (cm)	Days to maturity	Cob girth (cm)	Cob length (cm)	No. of kernel / row	No. of kernel row / cob	100 seed weight (g)	Grain yield / plant (g/plant)
1	JP-25-W95 X HKI-193-1	-8.19**	-8.84**	-41.67*	-9.49*	-24.08**	-0.36	-5.60	-14.42	-6.55	6.52	-4.81	2.06
2	CM-600 X HKI-193-1	-7.60**	-9.39**	-16.67	10.44**	-4.39	-0.72	1.68	-14.34	-15.94**	3.26	-1.98	1.38
3	CM-600 X JP-25-W95	-9.94**	-11.60**	-25.00	8.28*	3.91	-1.79	-1.41	-12.21	-0.87	-7.61*	0.24	3.55
4	CM-138-1 X HKI-193-1	-10.53**	-10.50 **	-50.00*	3.29	-7.26	-1.79	0.43	-17.25*	-25.55**	6.52	14.27*	4.76
5	CM-138-1 X JP-25-W95	-8.19**	-8.29 **	-16.67	-18.61**	-35.17**	-2.87*	-1.90	-28.06**	-30.13**	4.35	-5.81	-22.88**
6	CM-138-1 X CM-600	-9.94**	-11.60 **	-33.33	0.26	-17.30**	-1.43	-3.21	6.73	-11.14*	-1.09	5.43	1.51
7	DMR-N ₄ X HKI-193-1	-9.36**	-9.39 **	-41.67*	-10.93**	-17.46**	-0.36	-2.50	-4.08	-17.03**	-10.87**	3.66	-2.61
8	DMR-N ₄ X JP-25-W95	-9.94**	-11.05**	-50.00*	-4.08	-18.42**	-1.79	-1.36	-10.08	-16.38**	-5.43	-0.24	2.62
9	DMR-N ₄ X CM-600	-7.60**	-8.84 **	-25.00	-20.42**	-28.39**	-1.79	-5.60	-13.55	-25.76**	-7.61*	17.21**	0.23
10	DMR-N ₄ X CM-138-1	-5.85**	-7.18**	-33.33	-7.79*	-6.22	-2.51*	5.92	-13.42	6.77	6.25	3.66	28.10**
11.	TARUN-83-1-32 X HKI-193-1	-8.19**	-9.39 **	-33.33	-4.58	4.15	-1.08	-9.95**	-25.63**	-40.17**	-10.87**	8.28	-32.47**
12.	TARUN-83-1-32 X JP-25-W95	-8.19**	-9.39**	-58.33**	-12.56**	-19.62**	-1.43	-11.85**	-9.30	-32.53**	-5.43	-1.46	-21.87**
13.	TARUN-83-1-32 X CM-600	-7.60**	-8.29**	-8.33	8.89*	-1.83	-3.23**	-8.59**	-10.34	-24.67**	-7.61*	25.57**	-2.73
14.	TARUN-83-1-32 X CM-138-1	-9.94**	-11.60**	-25.00	14.26**	11.32*	-4.30**	2.07	-2.39	3.49	6.25	48.25**	88.22**
15.	TARUN-83-1-32 X DMR-N ₄	-8.19**	-8.29 **	-25.00	12.63**	-2.23	-2.87*	0.98	-31.58**	-38.21**	-10.87**	51.48**	-1.53
16.	LM-13 X HKI-193-1	-9.94**	-10.50**	-16.67	8.51*	5.90	-1.79	-0.27	-20.42**	-27.95**	2.17	11.97*	-6.85
17.	LM-13 X JP-25-W95	-8.19**	-7.73**	-16.67	19.14**	-2.23	-3.23**	-3.59	-8.34	-4.59	3.26	-6.11	-0.28
18.	LM-13 X CM-600	-5.26**	-5.52**	-58.33**	7.75*	-6.78	-4.66**	-6.41	-24.46**	-28.38**	2.17	4.04	-16.67*
19.	LM-13 X CM-138-1	-7.60**	-6.63**	0.00	17.02**	5.42	-4.66**	5.54	-13.55	-3.06	7.61*	12.84*	35.53**
20.	LM-13 X DMR-N ₄	-7.02**	-9.39**	-50.00*	14.07**	-0.64	-7.53**	-4.67	-29.71**	-24.24**	-2.17	15.82**	-5.77
21.	LM-13 X TARUN-83-1-32	-18.13**	-17.13**	8.33	17.59**	14.59**	-8.96**	3.21	-9.56	-3.49	-3.26	18.29**	30.55**
22.	HKI-34 (H2) X HKI-193-1	-16.96**	-17.68**	0.00	31.43**	12.60*	-8.96**	-0.43	-7.99	-4.15	1.09	1.85	6.99
23.	HKI-34 (H2) X JP-25-W95	-7.02**	-3.87**	-33.33	26.36**	20.81**	-2.87*	-2.88	-3.78	-18.12**	-4.35	4.23	-7.92
24.	HKI-34 (H2) X CM-600	-5.26**	-5.52**	-58.33**	37.10**	52.63**	-1.43	-2.83	-2.22	10.92*	-5.43	15.79**	39.62**
25.	HKI-34 (H2) X CM-138-1	-9.94**	-11.05**	-16.67	36.7**	31.74**	-5.38**	-1.25	-9.60	-12.23**	-7.61*	-5.59	-17.53*
26.	HKI-34 (H2) X DMR-N ₄	-9.94**	-11.05**	-33.33	38.43**	33.17**	-3.94**	6.28	4.17	2.62	7.61*	37.64**	75.51**
27.	HKI-34 (H2) X TARUN-83-1-32	-10.53**	-11.0**	-41.67*	38.16**	23.52**	-5.73**	-5.87	-14.12	-9.17	0.00	24.47**	29.52**
28.	HKI-34 (H2) X LM-13	-18.13**	-17.68 **	-25.00	35.25**	11.00*	-9.32**	-0.71	-10.43	-9.83*	9.78**	25.49**	41.68**
29.	POP-31Q-182Q11 X HKI-193-1	-18.13**	-19.34**	-58.33**	23.71**	-8.77	-9.32**	6.63*	-0.61	5.46	10.87**	44.88**	96.80**
30.	POP-31Q-182Q11 X JP-25-W95	-16.37**	-17.68**	-16.67	25.26**	-2.39	-9.32**	2.34	-3.87	-21.83**	6.52	6.78	0.41
31.	POP-31Q-182Q11 X CM-600	-9.36**	-10.50**	-33.33	24.51**	-11.48*	-3.23**	1.14	-25.11**	-32.53**	-5.43	35.74 **	-1.96

32.	POP-31Q-182Q11 X CM-138-1	-14.62**	-14.36**	0.00	21.56**	18.98**	-4.66**	-13.48**	-21.46**	-13.10**	-6.52	14.87*	4.49
33.	POP-31Q-182Q11 X DMR-N ₄	-8.77**	-9.94**	-41.67*	25.68**	-6.22	-2.51 *	-6.09	-13.99	-10.70*	-7.61*	26.33**	24.81**
34.	POP-31Q-182Q11 X TARUN-83-1-32	-7.60**	-5.52**	-16.67	17.81**	-6.62	-1.79	4.02	3.95	3.93	8.70*	49.37**	94.89**
35.	POP-31Q-182Q11 X LM-13	-9.36**	-10.50**	-16.67	5.90	-30.46**	-2.51*	-3.91	-19.20*	-22.49**	8.70*	16.47**	9.25
36.	POP-31Q-182Q11 X HKI-34 (H2)	-2.92*	-2.76*	-41.67*	25.23**	-34.61**	-1.08	-11.03**	-18.68*	-28.82**	-3.26	13.79*	-8.04
37.	TMT-TROP-(QPM) X HKI-193-1	-1.75	-1.10	-16.67	-3.52	-12.12*	-3.94**	-10.11**	-16.55*	-16.81**	1.09	-2.55	-9.17
38.	TMT-TROP-(QPM) X JP-25-W95	-8.77**	-10.50**	-33.33	-9.11*	-36.44**	-2.51 *	1.79	-14.29	-12.66**	-5.43	11.78	11.59
39.	TMT-TROP-(QPM) X CM-600	-7.60**	-8.29**	-25.00	17.93**	-26.63**	-3.94**	-4.29	-10.17	-12.45 **	0.00	-8.98	-14.68
40.	TMT-TROP-(QPM) X CM-138-1	-9.36**	-9.94**	-41.67*	1.59	-40.91**	-4.66**	-8.37*	-20.33**	-21.18 **	9.78**	-9.56	-7.62
41.	TMT-TROP-(QPM) X DMR-N ₄	-6.43**	-7.18**	-58.33**	3.48	-19.14**	-3.58**	-1.09	-15.60	-20.52**	-1.09	16.91**	9.54
42.	TMT-TROP-(QPM) X TARUN-83-1-32	-7.60**	-9.39**	-50.00*	8.51*	-19.86**	-2.87*	10.16**	-26.50**	-7.86	7.07*	42.66**	62.75**
43.	TMT-TROP-(QPM) X LM-13	-8.19**	-9.39**	-50.00*	-7.56*	-4.63	-5.73**	-2.99	-27.76**	-29.69**	3.26	10.78	-5.87
44.	TMT-TROP-(QPM) X HKI-34 (H2)	-7.60**	-9.39**	-50.00*	7.15	-18.82**	-5.02**	5.87	-13.94	-26.86**	-20.65**	-3.53	-35.03**
45.	TMT-TROP-(QPM) X POP-31Q-182Q11	-5.26**	-6.63**	-33.33	5.26	-22.09**	-5.02**	4.51	-6.52	-20.74**	-8.70*	-17.43**	-34.99**

**Significant at 1% and *Significant at 5% level

Heterosis

Cross POP-31Q-182Q11 X HKI-193-1 exhibited highest negative significant economic heterosis (Table 3) for traits viz., days to 50% tasseling (18.13%), days to 50% silking (19.34%) and Anthesis Silking Interval (58.33%). Crosses viz., POP-31Q-182Q11 X JP-25-W95, POP-31Q-182Q11 X HKI-193-1 and HKI-34 (H2) X LM-13 recorded highest negative significant heterosis for days to maturity. These crosses can be exploited further in breeding program for developing early maturing varieties. Genotypes which showed early maturity can be of immense use in future breeding program. These findings are in conformity with the findings of Shah *et al.*, (2016) and Matin *et al.*, (2016). The desirable crosses combination POP-31Q-182Q11 X HKI-193-1 and POP-31Q-182Q11 X TARUN-83-1-32 showed high magnitude of heterosis over the check variety HQPM-5 for grain yield along with other yield attributing characters. The study of heterotic response revealed that we can adopt the option of developing single cross QPM hybrids from the materials under study that belong to high Quality Protein Maize Remtluangpuii *et al.*, (2020), Darshan and Marker (2019), Solomon *et al.*, (2020).

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