The Pharma Innovation Journal 2022; 11(5): 535-541

www.ThePharmaJournal.com

The Pharma Innovation

ISSN (E): 2277-7695
ISSN (P): 2349-8242
NAAS Rating: 5.23
TPI 2022; 11(5): 535-541

www.thepharmajournal.com
Received: 01-03-2022
Accepted: 06-04-2022

Preeti Basser
Department of Genetics and Plant Breeding, Sam Higginbottom University of Agriculture Technology and Sciences, Prayagraj, Uttar Pradesh, India

Shailesh Marker
Department of Genetics and Plant Breeding, Sam Higginbottom University of Agriculture Technology and Sciences, Prayagraj, Uttar Pradesh, India

Ruchi Bishnoi
Department of Genetics and Plant Breeding, Sam Higginbottom University of Agriculture Technology and Sciences, Prayagraj, Uttar Pradesh, India

Rohitash Sharma
Department of Genetics and Plant Breeding, Sam Higginbottom University of Agriculture Technology and Sciences, Prayagraj, Uttar Pradesh, India

Anand Paul Bunga
Department of Genetics and Plant Breeding, Sam Higginbottom University of Agriculture Technology and Sciences, Prayagraj, Uttar Pradesh, India

Corresponding Author:
Preeti Basser
Department of Genetics and Plant Breeding, Sam Higginbottom University of Agriculture Technology and Sciences, Prayagraj, Uttar Pradesh, India

Per se performance and outbreeding enhancement in single crosses of quality protein maize (QPM) inbred lines adapted to Vindhyan region of eastern Uttar Pradesh

Preeti Basser, Shailesh Marker, Ruchi Bishnoi, Rohitash Sharma and Anand Paul Bunga

Abstract
Knowledge of per se performance of parental lines and heterosis or outbreeding enhancement plays a crucial role for the breeding programs to develop competitive hybrids. Hence, this research was planned to assess the performances of QPM inbred lines and their single crosses; and estimate the magnitudes of mid-parent and better parent heterosis for grain yield and its components. Ten Quality Protein Maize parental inbred lines were crossed to produce 45 single crosses by using diallel mating design (Griffing Method-I, Model-II). The experimental material comprising of 56 (10 parental inbred lines, one check and 45 crosses) were evaluated in Randomized Block Design (RBD) with three replications. Analysis of variance showed that mean squares due to genotypes and per se performances of parents were highly significant for most of the traits studied. On the basis of per se performance for grain yield per plant three parental genotypes *viz*., TMT-TROP-(QPM), JP-25-W95 and CM-600 were identified as high yielding genotypes and three high yielding single crosses identified as POP-31Q-182Q11 X HKI-193-1, POP-31Q-182Q11 X TARUN-83-1-32 and TARUN-83-1-32 X CM-138. The highest mid-parent and better-parent heterosis for grain yield were obtained from POP-31Q-182Q11 X HKI-193-1 and TMT-TROP-(QPM) X TARUN-83-1-32 respectively. The results obtained in this study showed the promising potentials of the identified inbred lines and hybrids for further breeding of QPM for Vindhyan region of Eastern Uttar Pradesh.

Keywords: Diallel, mid-parent heterosis, better-parent heterosis, inbred, per se and quality protein maize

Introduction
Maize (*Zea mays* L.) is the world's most extensively grown cereal and is the primary staple food in many developing countries (MALIK *et al*., 2004) [3]. It has emerged as world's foremost crop among the cereals with highest production and productivity (Kumar *et al*., 2016) [4] and it is a tactical crop in many parts of the developing world where livelihoods of millions of poor farmers depend on maize cultivation. In India, maize is third important food crop after wheat and rice. Maize 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 (Shah, 2016) [6]. It is a good source of calcium and phosphorous.

However, 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. A breakthrough came in the 1960s; with the discovery of the enhanced nutritional quality of the maize mutant opaque2 (Mertz *et al*. 1964). The protein quality of opaque2 maize is 43% higher than that of common maize and 95% of the value of casein (Mertz 1992). Due to maize being allogamous crop species, maintenance of heterozygosity is utmost important to suppress the undesirable effect of recessive alleles, therefore, grain productivity enhancement needs better exploitation of heterosis utilizing additive and non-additive gene actions. (Kumar *et al*., 2016) [4].

Heterosis is significant in maize breeding and is dependent on level of dominance and differences in gene frequency. The manifestation of heterosis depends on genetic divergence of the two parental varieties (Dufera Tulu *et al*.). It is manifested as an increase in vigor, size, growth rate, yield or some other characteristics. But in some cases, the hybrid may be inferior to the weaker parent, which is also considered as heterosis. That means heterosis can be positive or negative. The interpretation of heterosis depends on the nature of trait under study and the way it is measured. Generally, heterosis is an important trait used by breeders to evaluate the performance of offspring in relation to their parents. It estimates the enhanced performance of hybrids compared to their parents. Often the superiority of F1 is estimated over the average of the two parents, or the mid parent. Hence, generation of information on heterosis and per se performance of the new QPM inbred lines is necessary for a successful QPM hybrid variety development.

Thus, this study was conducted to estimate the magnitudes of heterosis for grain yield and yield related traits in QPM hybrids, and to evaluate the performance of newly developed QPM inbred lines.

Materials and Methods

The present investigation was undertaken with ten parental lines *viz*., HKI-193-1 (P_1), JP-25-W95 (P_2), CM-600 (P_3), CM-138-1 (P_4), DMR-N_4 (P_5), TARUN-83-1-32 (P_6), LM-13 (P_7), HKI-34 (H2) (P_8), POP-31Q-182Q11 (P_9), TMT-TROP-(QPM) (P_{10}) which were crossed in diallel mating design (excluding reciprocals) to develop 45 F_1'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).

Estimation of Heterosis

Better parent heterosis (BPH) and mid parent heterosis (MPH) in percent were calculated for those traits that showed statistically significant differences among genotypes as recommended by Falconer and Mackay (1996).

These were computed as percentage increase or decrease of the cross performances over the mid parent, best parent and best standard check as follows.

MPH (%) = $(F1-MP)\ MP*100$

BPH (%) = $(F1-BP)\ BP*100$

Where, *F1* = Mean value of a cross

MP = Mean value of the two parents

BP = Mean value of the better parent

Test of significance for heterosis was made using the t-test. The standard errors of the difference for heterosis were calculated as follows:

SE(d) for BPH= ± 2MSE/r

SE of mid parent heterosis = ± 3MSE/2r

Where, *SE (d)* is standard error of the difference, MSeis error mean square and r is number of replications and calculated t value was compared against the tabulated t-value at degree of freedom for error.

t (Better Parent) = F1- BP /SE(d), t (Mid Parent) = F1-MP /SE(d) and t (standard check) = F1 – SV/SE(d)

Results and Discussion

The data collected were analyzed and significance tests were performed for each trait at 5% and 1% probability levels. The results are presented and discussed below.

Analysis of Variance

The Analysis of Variance for different characters are presented and discussed in table 3. 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) [1].

Parents Perse performance and Mean Performance of QPM hybrids for different quantitative parameters

In this study the variability exploited in breeding programme is preferred from the naturally occurring variants and wild relative of main crop species as well as from strains and genetic stock artificially develop by human efforts and an attempt was made to assess the mean performance and extent of variability in QPM germplasm. The grand mean values, range, F ratio, Standard Error of mean (SE) and Critical Difference (CD) of parents and their crosses in F1 generation along with the checks for all the characters are presented in table 4.

The per se performances of the parents (10 inbred lines and 45 single crosses) is given in tables 4. Grain yield per plant varied among parents from 32.53 (DMR-N4) to 96.67 g/plant (POP-31Q-182Q11). Among the inbred lines POP-31Q-182Q11 had the highest yield (96.67 g/plant), followed by JP-25-W95 (68.23 g/plant) and CM-600 (57.20 g/plant). Higher grain yield per plant is desirable in maize, as it directly contribute for higher production. Hybrids *viz*., POP-31Q-182Q11 X HKI-193-1(134.28g/plant), POP-31Q-182Q11 X TARUN-83-1-32(132.98 g/plant) and TARUN-83-1-32 X CM-138-1 (128.42 g/plant) were found significantly superior with higher grain yield per plant among all genotypes.

Plant height ranged among parents from 65.07 (DMR-N4) to 176.27cm (CM-600). Small and medium stature plant in maize crop is desirable and it can tolerate heavy winds and can be prevented from lodging. The lowest plant height was recorded by hybrids (DMR-N_4 X CM-600 (140.27 cm) followed by CM-138-1 X JP-25-W95 (143.47 cm) and TARUN-83-1-32 X JP-25-W95 (154.13 cm).

Anthesis Silking Interval in maize can provide adequate time for grain formation. Parent (HKI-34 (H2) (1.34 days) and hybrids *viz*., TARUN-83-1-32 X JP-25-W95, LM-13 X CM-600, HKI-34 (H2) X CM-600, TMT-TROP-(QPM) X DMR-N4 and POP-31Q-182Q11 X HKI-193-1 (1.67 days) were found significantly superior among all genotypes.

Cob height among parents ranged from 36.47 (LM-13) to 83.60 cm (CM-600). Low cob placement in maize crop is preferred because it can tolerate heavy winds and can be prevented from lodging. Hybrid TMT-TROP-(QPM) X CM-138-1(49.40 cm) were found lowest cob placement among all crosses.

Days to maturity among parents ranged from 88.34 (CM-138-1) to 93.00 days (DMR-N4). Early maturity is preferable in most of the plant species especially in maize because delayed maturity causes yield loss due to rise in temperature. Hybrids *viz*., HKI-34 (H2) X LM-13 84.33 days), POP-31Q-182Q11 X HKI-193-1 (84.33 days), POP-31Q-182Q11 X JP-25-W95 (84.33 days), LM-13 X TARUN-83-1-32 (84.67 days), HKI-34 (H2) X HKI-193-1 (84.67 days) were found significantly superior with minimum days to maturity.

Number of kernels per row among parents ranged from 15.60 (TARUN-83-1-32) to 30.53 (JP-25-W95). Highest number of kernels per row is desirable character in maize. Hence, hybrids *viz*., HKI-34 (H2) X CM-600 (33.86), DMR-N4 X CM-138-1 (32.60), POP-31Q-182Q11 X HKI-193-1 (32.20) and POP-31Q-182Q11 X TARUN-83-1-32 (31.73) were found significantly superior.

Number of kernel rows per cob among parents ranged from 9.73 (CM-138-1) to 13.46 (POP-31Q-182Q11). Highest number of kernel rows per cob is desirable character in maize. Hence, hybrids *viz*., POP-31Q-182Q11 X HKI-193-10 (13.60), HKI-34 (H2) X LM-13 (13.46), TMT-TROP-(QPM) X CM-138-1 (13.46), TMT-TROP-(QPM) X CM-138-1 (13.46) and POP-31Q-182Q11 X TARUN-83-1-32(13.33) were found significantly superior among all genotypes.

Test weight among parents ranged from 18.51 (CM-600) to 26.41g (POP-31Q-182Q11). Highest test weight in Quality Protein Maize is good for good quality seed and highest yield. Hybrid *viz*., TARUN-83-1-32 X DMR-N4 (31.88 g), POP-31Q-182Q11 X TARUN-83-1-32 (31.44g), POP-31Q-182Q11 X HKI-193-1 (30.49 g) and TARUN-83-1-32 X CM-138-1 (31.20 g) were found significantly superior with higher 100 grain weight (or) test weight.

Mid and Better-parent Heterosis

The estimates of mid parent heterosis (MPH) and best parent heterosis (BPH) was evaluated for grain yield and yield related traits that showed significant variations.

The highest significant positive MPH for grain yield per plant was observed by crosses *viz*., POP-31Q-182Q11 X HKI-193-1 (227.14 **), TMT-TROP-(QPM) X TARUN-83-1-32 (214.50 **), and POP-31Q-182Q11 X TARUN-83-1-32 (185.09**). It was positive significant for all crosses except one cross for grain yield per plant.

The highest significant positive BPH for grain yield per plant was observed by crosses *viz*., TMT-TROP-(QPM) X TARUN-83-1-32 (205.67**), POP-31Q-182Q11 X HKI-193-1 (191.91**) and POP-31Q-182Q11 X DMR-N_4 (134.42**). It was positive significant for all crosses except four crosses for grain yield per plant.

The highest significant positive relative heterosis for number of kernel row per cob was observed by crosses *viz*., POP-31Q-182Q11 X JP-25-W95 (37.06**), LM-13 X HKI-193-1 (32.39**) and POP-31Q-182Q11 X HKI-193-1 (31.61**). The highest significant positive BPH for number of kernel row per cob was observed by crosses *viz*., POP-31Q-182Q11 X JP-25-W95 (36.11**), LM-13 X HKI-193-1 (30.56**) and LM-13 X JP-25-W95 (28.38**). Forty two crosses exhibited positive significant MPH number of kernel rows per cob revealed increased number of grain rows in a cob. Similar results were reported earlier by Kumar *et al.* (2008) Dubey *et al.* (2009), Singh *et al.* (2010) [7], Kumar *et al.* (2016) [4] and Darshan and Marker (2019) [1] in maize crop.

The highest significant negative MPH for days to maturity was observed by crosses *viz*., POP-31Q-182Q11 X JP-25-W95 (-8.83**), POP-31Q-182Q11 X HKI-193-1 (-8.17**) and LM-13 X TARUN-83-1-32 (-7.47**). The highest significant negative BPH for days to maturity was observed by crosses *viz*., POP-31Q-182Q11 X JP-25-W95 (-8.99 **), POP-31Q-182Q11 X HKI-193-1 (-8.99 **) and (HKI-34 (H2) X HKI-193-1 (-8.30 **).

Hybrids *viz*., POP-31Q-182Q11 X HKI-193-1, POP-31Q-182Q11 X JP-25-W95, TMT-TROP-(QPM) X TARUN-83-1-32 etc. recorded negative heterosis for traits like days to 50% tasseling, days to 50% silking, plant height and ear height are desirable in breeding for earliness and short stature hybrids that could resist lodging particularly in windy environment like the study areas Ruswandi *et al*. (2015) [5] and El-Gazzar *et al*. (2013) [2].

Table 1: List of lines used in the present investigation

S. No.	Notation	Genotypes	Source
Parents			
1	P_1	HKI-193-1	CIMMYT, Mexico
2	P_2	JP-25-W95	BHU, Varanasi
3	P_3	CM-600	DMR, New Delhi
4	P_4	CM-138-1	DMR, New Delhi
5	P_5	DMR-N_4	DMR, New Delhi
6	P_6	TARUN-83-1-32	BHU, Varanasi
7	P_7	LM-13	BHU, Varanasi
8	P_8	HKI-34 (H2)	CIMMYT, Mexico
9	P_9	POP-31Q-182Q11	BHU, Varanasi
10	P_{10}	TMT-TROP-(QPM)	BHU, Varanasi

Table 2: List of hybrids used in the present investigation

S. No.	Notation	Genotypes	Source
Crosses			
11.	L_{11}	JP-25-W95 X HKI-193-1	SHUATS, Prayagraj
12.	L_{12}	CM-600 X HKI-193-1	SHUATS, Prayagraj
13.	L_{13}	CM-600 X JP-25-W95	SHUATS, Prayagraj
14.	L_{14}	CM-138-1 X HKI-193-1	SHUATS, Prayagraj
15.	L_{15}	CM-138-1 X JP-25-W95	SHUATS, Prayagraj
16.	L_{16}	CM-138-1 X CM-600	SHUATS, Prayagraj
17.	L_{17}	DMR-N_4 X HKI-193-1	SHUATS, Prayagraj
18.	L_{18}	DMR-N_4 X JP-25-W95	SHUATS, Prayagraj
19.	L_{19}	DMR-N_4 X CM-600	SHUATS, Prayagraj

20.	L_{20}	DMR-N_4 X CM-138-1	SHUATS, Prayagraj
21.	L_{21}	TARUN-83-1-32 X HKI-193-1	SHUATS, Prayagraj
22.	L_{22}	TARUN-83-1-32 X JP-25-W95	SHUATS, Prayagraj
23.	L_{23}	TARUN-83-1-32 X CM-600	SHUATS, Prayagraj
24.	L_{24}	TARUN-83-1-32 X CM-138-1	SHUATS, Prayagraj
25.	L_{25}	TARUN-83-1-32 X DMR-N_4	SHUATS, Prayagraj
26.	L_{26}	LM-13 X HKI-193-1	SHUATS, Prayagraj
27.	L_{27}	LM-13 X JP-25-W95	SHUATS, Prayagraj
28.	L_{28}	LM-13 X CM-600	SHUATS, Prayagraj
29.	L_{29}	LM-13 X CM-138-1	SHUATS, Prayagraj
30.	L_{30}	LM-13 X DMR-N_4	SHUATS, Prayagraj
31.	L_{31}	LM-13 X TARUN-83-1-32	SHUATS, Prayagraj
32.	L_{32}	HKI-34 (H2) X HKI-193-1	SHUATS, Prayagraj
33.	L_{33}	HKI-34 (H2) X JP-25-W95	SHUATS, Prayagraj
34.	L_{34}	HKI-34 (H2) X CM-600	SHUATS, Prayagraj
35.	L_{35}	HKI-34 (H2) X CM-138-1	SHUATS, Prayagraj
36.	L_{36}	HKI-34 (H2) X DMR-N_4	SHUATS, Prayagraj
37.	L_{37}	HKI-34 (H2) X TARUN-83-1-32	SHUATS, Prayagraj
38.	L_{38}	HKI-34 (H2) X LM-13	SHUATS, Prayagraj
39.	L_{39}	POP-31Q-182Q11 X HKI-193-1	SHUATS, Prayagraj
40.	L_{40}	POP-31Q-182Q11 X JP-25-W95	SHUATS, Prayagraj
41.	L_{41}	POP-31Q-182Q11 X CM-600	SHUATS, Prayagraj
42.	L_{42}	POP-31Q-182Q11 X CM-138-1	SHUATS, Prayagraj
43.	L_{43}	POP-31Q-182Q11 X DMR-N_4	SHUATS, Prayagraj
44.	L_{44}	POP-31Q-182Q11 X TARUN-83-1-32	SHUATS, Prayagraj
45.	L_{45}	POP-31Q-182Q11 X LM-13	SHUATS, Prayagraj
46.	L_{46}	POP-31Q-182Q11 X HKI-34 (H2)	SHUATS, Prayagraj
47.	L_{47}	TMT-TROP-(QPM) X HKI-193-1	SHUATS, Prayagraj
48.	L_{48}	TMT-TROP-(QPM) X JP-25-W95	SHUATS, Prayagraj
49.	L_{49}	TMT-TROP-(QPM) X CM-600	SHUATS, Prayagraj
50.	L_{50}	TMT-TROP-(QPM) X CM-138-1	SHUATS, Prayagraj
51.	L_{51}	TMT-TROP-(QPM) X DMR-N_4	SHUATS, Prayagraj
52.	L_{52}	TMT-TROP-(QPM) X TARUN-83-1-32	SHUATS, Prayagraj
53.	L_{53}	TMT-TROP-(QPM) X LM-13	SHUATS, Prayagraj
54.	L_{54}	TMT-TROP-(QPM) X HKI-34 (H2)	SHUATS, Prayagraj
55.	L_{55}	TMT-TROP-(QPM) X POP-31Q-182Q11	SHUATS, Prayagraj

Table 3: Analysis of Variance for different quantitative parameters in QPM parents and hybrids

S. No	Characters	Mean Sum of Squares						
		Replications (df)	Treatments (df)	Parents (df)	Hybrids (df)	Parent Vs. Hybrids (df)	Error (df)	Total
		2	54	9	44	1	108	164
1.	Days to 50% tasseling	3.67*	17.13**	3.46**	12.96**	323.36**	0.85	6.25
2.	Days to 50% silking	3.07*	19.53**	5.11**	15.78**	314.19**	0.89	7.05
3.	Anthesis Silking Interval	0.95	1.49*	1.54	1.48*	0.53	0.93	1.11
4.	Plant height (cm)	3.38	3785.96**	3124.99**	2319.21**	74272.07**	61.86	1287.38
5.	Cob height (cm)	6.37	1037.77**	687.06**	841.14**	12846.08**	28.56	360.59
6.	Days to maturity	0.15	15.80**	5.63**	16.20**	89.99**	1.63	6.28
7.	Cob girth (cm)	0.10	3.30**	3.78**	1.32**	86.15**	0.24	1.24
8.	Cob length (cm)	0.63	8.33**	11.58**	6.00**	81.48**	2.11	4.14
9.	Number of kernel per row	1.31	50.46**	48.75**	44.79**	315.10**	2.98	18.59
10.	Number of kernels row per cob	1.41**	3.60**	4.07**	2.17**	62.19**	0.25	1.37
11.	100 grain weight (g)	3.42	42.75**	2.33	39.12**	566.25**	2.32	15.64
12.	Grain yield per plant (g)	120.87	1655.88**	410.55**	1435.47**	22561.93**	40.13	573.13

Table 4: Parents Per se performance and Mean Performance of QPM hybrids for different quantitative parameters

S.N.	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 grain weigh (g)	Grain yield per plant (g/plant)
1	P_1	53.67	56.67	3.00	166.13	64.07	90.67	10.80	11.38	22.86	12.00	18.98	53.32
2	P_2	54.67	56.67	2.00	172.34	77.07	91.34	12.27	15.35	30.53	11.60	18.62	68.23
3	P_3	55.67	55.67	2.00	176.27	83.60	92.34	11.30	12.82	25.13	12.26	18.51	57.20
4	P_4	55.34	55.34	3.00	126.13	50.00	88.34	9.66	10.77	18.93	9.73	21.05	36.33
5	P_5	55.00	57.67	2.67	65.07	53.27	93.00	8.19	11.95	15.60	9.86	19.42	32.53
6	P_6	54.00	58.34	2.67	153.80	51.94	90.67	11.04	11.41	18.27	10.93	22.79	46.08
7	P_7	56.34	57.67	2.67	124.27	36.47	92.34	9.20	9.13	19.67	9.60	19.32	45.35
8	P_8	56.00	56.67	1.34	124.27	57.13	91.00	10.38	10.19	22.73	11.20	18.63	46.00

9	P_9	57.00	59.00	2.67	147.00	50.20	92.67	12.18	13.74	27.53	13.46	26.41	96.67
10	P_{10}	56.34	57.34	4.00	133.73	38.27	92.00	10.38	10.1	22.73	11.20	18.63	46.00
11.	L_{11}	52.34	59.67	2.34	159.53	63.47	92.67	11.58	13.13	28.53	13.07	20.03	69.63
12.	L_{12}	52.67	60.34	3.34	194.67	79.94	92.34	12.47	13.14	25.67	12.67	20.63	69.17
13.	L_{13}	51.34	55.00	3.00	190.87	86.87	91.34	12.09	13.47	30.26	11.33	21.10	70.65
14.	L_{14}	51.00	54.00	2.00	182.07	77.53	91.33	12.32	12.70	22.73	13.06	24.05	71.48
15.	L_{15}	52.34	55.34	3.34	143.47	54.20	90.33	12.03	11.04	21.33	12.80	19.83	52.62
16.	L_{16}	51.34	53.34	2.67	176.73	69.13	91.67	11.87	16.38	27.13	12.13	22.19	69.26
17.	L_{17}	51.67	54.67	2.34	157.00	69.00	92.67	11.96	14.72	25.33	11.73	21.82	66.45
18.	L_{18}	51.34	53.67	2.00	169.07	68.20	91.33	12.10	13.80	25.53	13.20	21.00	70.02
19.	L_{19}	52.67	55.00	3.00	140.27	59.87	91.33	11.58	13.25	22.66	12.13	24.67	68.39
20.	L_{20}	53.67	56.00	2.67	162.53	78.40	90.67	12.99	13.28	32.60	12.66	21.82	87.40
21.	L_{21}	52.34	54.67	2.67	168.20	87.07	92.00	11.04	11.41	18.26	10.93	22.79	46.08
22.	L_{22}	52.34	54.67	1.67	154.13	67.20	91.67	10.81	13.92	20.60	11.60	20.74	53.31
23.	L_{23}	52.67	55.34	3.67	191.93	82.07	90.00	11.21	13.76	23.00	11.33	26.43	66.37
24.	L_{24}	51.34	53.34	3.00	201.40	93.07	89.00	12.52	14.98	31.60	13.03	31.20	128.42
25.	L_{25}	52.34	55.34	3.00	198.53	81.73	90.33	12.38	10.50	18.86	10.93	31.88	67.18
26.	L_{26}	51.34	54.00	3.34	191.27	88.54	91.33	12.23	12.21	22.00	12.53	23.57	63.56
27.	L_{27}	52.34	55.67	3.34	210.00	81.73	90.00	11.82	14.06	29.13	12.66	19.76	68.04
28.	L_{28}	54.00	57.00	1.67	189.93	77.93	88.67	11.48	11.59	21.86	12.53	21.90	56.85
29.	L_{29}	52.67	56.34	4.00	206.27	88.13	88.67	12.94	13.25	29.60	13.20	23.75	92.48
30.	L_{30}	53.00	54.67	2.00	201.07	83.07	86.00	11.69	10.78	23.13	12.00	24.38	64.29
31.	L_{31}	46.67	50.00	4.34	207.27	95.80	84.67	12.66	13.88	29.47	11.86	24.90	89.08
32.	L_{32}	47.34	49.67	4.00	231.67	94.13	84.67	12.21	14.12	29.26	12.40	21.44	73.00
33.	L_{33}	53.00	58.00	2.67	222.73	101.00	90.33	11.91	14.76	25.00	11.73	21.94	62.83
34.	L_{34}	54.00	57.00	1.67	241.67	127.60	91.67	11.92	15.00	33.86	11.60	24.37	95.26
35.	L_{35}	51.34	53.67	3.34	241.07	110.13	88.00	12.11	13.87	26.80	11.33	19.87	56.27
36.	L_{36}	51.34	53.67	2.67	244.00	111.33	89.33	13.03	15.98	31.33	13.20	28.97	119.75
37.	L_{37}	51.00	53.67	2.34	243.53	103.27	87.67	11.54	13.18	27.73	12.27	26.20	88.37
38.	L_{38}	46.67	49.67	3.00	238.40	92.80	84.33	12.18	13.74	27.53	13.46	26.41	96.67
39.	L_{39}	46.67	48.67	1.67	218.07	76.27	84.33	13.08	15.25	32.20	13.60	30.49	134.28
40.	L_{40}	47.67	49.67	3.34	220.80	81.60	84.33	12.55	14.75	23.87	13.07	22.47	68.51
41.	L_{41}	51.67	54.00	2.67	219.47	74.00	90.00	12.40	11.49	20.60	11.60	28.57	66.89
42.	L_{42}	48.67	51.67	4.00	214.27	99.47	88.67	10.61	12.05	26.53	11.46	24.18	71.29
43.	L_{43}	52.00	54.33	2.34	221.53	78.40	90.67	11.52	13.20	27.26	11.33	26.59	85.16
44.	L_{44}	52.67	57.00	3.34	207.67	78.07	91.33	12.76	15.95	31.73	13.33	31.44	132.98
45.	L_{45}	51.67	54.00	3.34	186.67	58.13	90.67	11.78	12.40	23.67	13.33	24.51	74.54
46.	L_{46}	55.34	58.66	2.34	220.73	54.67	92.00	10.91	12.48	21.73	11.87	23.95	62.74
47.	L_{47}	56.00	59.66	3.34	170.07	73.47	89.34	11.02	12.87	25.40	12.40	20.51	61.97
48.	L_{48}	52.00	54.00	2.67	160.20	53.13	90.67	12.48	13.15	26.67	11.60	23.53	76.14
49.	L_{49}	52.67	55.33	3.00	207.87	61.33	89.33	11.74	13.78	26.73	12.27	19.16	58.22
50.	L_{50}	51.67	54.33	2.33	179.07	49.40	88.67	11.24	12.22	24.06	13.46	19.03	63.03
51.	L_{51}	53.34	56.00	1.67	182.40	67.60	89.67	12.13	12.95	24.27	12.13	24.61	74.74
52.	L_{52}	52.67	54.67	2.00	191.27	67.00	90.33	13.51	11.28	28.13	13.13	30.03	111.05
53.	L_{53}	52.34	54.67	2.00	162.93	79.73	87.67	11.90	11.08	21.47	12.67	23.32	64.23
54.	L_{54}	52.67	54.67	2.00	188.87	67.87	88.33	12.98	13.20	22.33	9.73	20.30	44.34
55.	L_{55}	54.00	56.34	2.67	185.53	65.13	88.33	12.82	14.34	24.20	11.20	17.38	44.35
	Check (HQPM-5)	62.67	65.00	2.33	174.46	65.46	103.00	11.44	13.99	26.91	12.67	28.86	98.31
	Mean	52.61	55.25	2.71	185.28	74.74	90.10	11.70	12.98	25.19	11.98	22.96	70.05
	Range	46.67 - 62.67	48.67 - 65.0	1.33 - 4.33	65.07 - 244.0	36.46 - 127.6	84.33 - 103.0	8.19 - 13.51	9.13 - 16.38	15.60 - 33.86	9.33 - 13.60	17.38 - 31.88	32.53 - 134.28
	C.V.	1.90	1.80	35.78	4.39	7.22	1.55	4.25	11.28	6.79	4.24	6.59	8.97
	F ratio	22.24	24.56	1.54	56.12	35.11	12.65	13.14	3.83	16.93	13.80	19.12	42.25
	S.E.	0.57	0.57	0.56	4.70	3.11	0.80	0.28	0.84	0.98	0.29	0.87	3.62
	C.D. 5%	1.62	1.61	1.57	13.18	8.73	2.26	0.80	2.37	2.77	0.82	2.45	10.17
	C.D. 1%	2.14	2.13	2.07	17.43	11.55	2.99	1.06	3.13	3.66	1.08	3.24	13.45

Table 5(a): Mid and Better-parent Heterosis

S.N.	Genotypes	Days to 50% tasseling		Days to 50% silking		Anthesis Silking Interval		Plant height (cm)		Cob height (cm)	
		Ha	Hb	Ha	Hb	Ha	Hb	Ha	Hb	Ha	Hb
1	L_1	-3.38**	-4.27**	-2.94*	-2.94 *	-6.67	-22.22	-5.73	-7.43	-10.06	-17.65**
2	L_2	-4.53**	-5.39**	-4.37**	-5.20 **	66.67	66.67	11.68 **	10.44**	-0.50	-4.39
3	L_3	-6.10**	-7.78**	-6.71**	-7.51 **	20.00	0.00	11.49 **	8.28*	17.65 **	3.91
4	L_4	-8.11**	-8.38**	-6.90**	-7.43 **	-20.00	-33.33	20.41 **	3.29	16.07 **	-7.26
5	L_5	-4.85**	-5.42**	-3.77**	-5.14 **	33.33	11.11	-3.86	-16.75**	-14.69 *	-29.67**

6	L_{6}	-5.81**	-7.23**	-7.25**	-8.57 **	-11.11	-11.11	20.94**	6.38	21.22 **	7.91
7	L_{7}	-6.34**	-6.63**	-5.75**	-6.29 **	-17.65	-22.22	64.23**	24.47**	33.63 **	29.54**
8	L_{8}	-7.23**	-7.78**	-6.94**	-6.94 **	-14.29	-25.00	40.11**	-4.08	-0.34	-18.42**
9	L_{9}	-3.95**	-4.24**	-3.79**	-4.62 **	28.57	12.50	18.17**	-18.61**	-8.13	-22.32**
10	L_{10}	-1.23	-2.42	-2.04	-2.89 *	-5.88	-11.11	40.60**	-2.17	33.64 **	22.37**
11.	L_{11}	-3.98**	-4.85**	-4.37**	-5.20**	0.00	0.00	53.70**	9.36*	65.53 **	63.45**
12.	L_{12}	-4.27**	-5.42**	-4.93**	-6.29**	-41.18	-44.44	10.12*	0.22	31.85 **	29.40**
13.	L_{13}	-3.95**	-5.39**	-3.21**	-4.05**	57.14	37.50	16.30**	8.89*	21.10 **	-1.83
14.	L_{14}	-5.52**	-6.10**	-5.88**	-5.88**	28.57	12.50	23.51**	16.87**	44.29 **	20.76**
15.	L_{15}	-2.79*	-3.09*	-2.35	-2.35	5.88	0.00	24.11**	19.50**	40.92 **	27.58**
16.	L_{16}	-6.95**	-8.88**	-6.63**	-8.47**	25.00	25.00	37.57**	24.36**	100.30**	70.47**
17.	L_{17}	-5.99**	-7.1**	-4.57**	-5.65**	25.00	25.00	121.83**	68.99**	82.17**	53.44**
18.	L_{18}	-3.28**	-4.14**	-2.84*	-3.39*	-41.18	-44.44	51.70**	50.58**	80.26**	55.87**
19.	L_{19}	-5.95**	-6.51**	-3.43**	-4.52**	71.43*	50.00	37.27**	17.02**	46.81**	5.42
20.	L_{20}	-4.50**	-5.92**	-5.48 *	-7.34**	-14.29	-25.00	35.58**	16.67**	46.33**	7.79
21.	L_{21}	-15.15**	-17.16**	-13.54**	-15.25**	52.94*	44.44	42.75**	24.76**	90.58**	49.53**
22.	L_{22}	-15.73**	-15.98**	-14.61 **	-15.82**	100.00**	50.00	75.33**	65.48**	101.14**	64.76**
23.	L_{23}	-3.64**	-5.36**	1.75	1.16	33.33	0.00	51.62**	44.82**	85.21**	76.78 **
24.	L_{24}	-2.70*	-3.57**	-0.87	-1.16	-16.67	-37.50	135.70**	72.62**	131.16**	123.34**
25.	L_{25}	-7.78**	-8.33**	-7.20 **	-8.00**	53.85	11.11	81.16**	72.19**	105.60**	92.77**
26.	L_{26}	-8.06**	-8.33**	-6.67 **	-6.94**	60.00	33.33	54.30**	38.43**	58.22**	33.17 **
27.	L_{27}	-7.83**	-8.93**	-5.85 **	-6.40**	40.00	16.67	55.94**	41.32**	53.90**	34.00**
28.	L_{28}	-14.89**	-16.67**	-12.87**	-13.37**	38.46	0.00	55.75**	43.50**	53.14**	44.85**
29.	L_{29}	-17.40**	-18.13**	-16.81 **	-18.44**	-16.67	-37.50	51.96 **	48.34**	42.11**	33.49**
30.	L_{30}	-15.88**	-16.37**	-16.29 **	-16.76**	25.00	25.00	62.79 **	50.20**	88.31**	62.55**
31.	L_{31}	-6.91**	-9.36**	-7.16 **	-9.50**	0.00	0.00	45.92**	42.70**	44.91**	42.49**
32.	L_{32}	-13.10**	-14.62**	-11.93 **	-13.41**	50.00	50.00	102.07**	45.76**	92.27**	86.73**
33.	L_{33}	-7.42**	-8.77**	-7.91 **	-8.94**	-17.65	-22.22	62.22**	50.70**	56.49**	56.18**
34.	L_{34}	-6.51**	-7.60**	-2.84*	-4.47**	42.86	25.00	28.48**	17.81**	16.69**	-6.62
35.	L_{35}	-7.46**	-9.36**	-7.16**	-9.50**	42.86	25.00	16.91**	8.32 *	-8.64	-24.57**
36.	L_{36}	0.00	-2.92*	0.86	-1.68	-17.65	-22.22	40.98**	32.87**	-4.32	-14.67 *
37.	L_{37}	-1.18	-1.75	-0.56	-1.10	0.00	-16.67	21.16**	15.69**	66.09**	46.35**
38.	L_{38}	-7.42**	-7.69**	-8.22**	-10.50**	0.00	-33.33	17.05**	14.43**	11.39	-7.00
39.	L_{39}	-6.51**	-6.51**	-7.26**	-8.29**	-10.00	-25.00	61.14**	55.43**	64.14**	60.28**
40.	L_{40}	-6.34**	-8.28**	-7.12**	-9.94**	-30.00	-41.67*	24.55**	16.43**	9.53	-4.88
41.	L_{41}	-4.19**	-5.33**	-5.08**	-7.18**	-50.00*	-58.33**	83.50**	36.39**	47.71**	26.91**
42.	L_{42}	-5.67**	-6.51**	-7.87**	-9.39**	-42.86*	-50.00*	47.20**	43.02**	51.81**	34.00**
43.	L_{43}	-6.55**	-7.10**	-7.34**	-9.39**	-33.33	-50.00*	5.12	-7.56*	30.85**	-4.63
44.	L_{44}	-5.11**	-6.51**	-6.55**	-9.39**	-33.33	-50.00*	23.42**	9.59*	17.69**	-11.94*
45.	L_{45}	-1.82	-4.14**	-3.70**	-6.63**	-23.81	-33.33	23.74**	11.68**	27.30**	1.66

Table 5(b): Mid and Better-parent Heterosis

S.N.	Genotypes	Cob girth (cm)		Cob Length (cm)		Number of kernel per row		Number of kernel row per cob		100 grain weight (g)		Grain yield per plant (g/plant)	
		Ha	Hb	Ha	Hb	Ha	Hb	Ha	Hb	Ha	Hb	Ha	Hb
1	L_{1}	0.40	-5.60	-1.75	-14.42	6.87	-6.55	10.73**	8.89*	6.56	5.57	14.58	2.06
2	L_{2}	5.86	1.68	-6.65	-14.34	-7.78	-15.94**	6.15*	3.26	11.12	10.77	10.29	1.38
3	L_{3}	9.44**	7.02	11.32	5.10	26.11**	20.42**	-6.59*	-7.61*	12.56*	11.17	27.86**	23.53*
4	L_{4}	17.56**	9.03*	7.69	-0.94	3.18	-9.55	18.79**	6.52	21.60**	14.27*	52.86**	24.97**
5	L_{5}	9.76**	-1.90	-15.45	-28.06**	-13.75**	-30.13**	20.00**	10.34**	-0.06	-5.81	0.65	-22.88**
6	L_{6}	16.06**	9.94**	47.88**	43.85**	29.82 **	18.66**	11.66**	1.11	10.88*	5.43	54.52**	29.90**
7	L_{7}	33.98**	23.8**	29.58**	23.15*	46.72 **	33.80**	13.89**	10.81*	7.82	3.66	92.98**	82.91**
8	L_{8}	24.15**	7.08	11.41	7.64	25.37 **	1.59	21.68**	19.18**	10.71	8.10	56.06**	22.42*
9	L_{9}	13.20**	-5.60	-2.81	-13.55	-1.73	-25.76**	4.94	-7.61*	29.68**	27.01**	35.74**	0.23
10	L_{10}	36.82**	20.3**	13.85	11.15	69.50**	42.57**	24.52**	12.36**	13.63*	12.32	103.61**	63.93**
11.	L_{11}	21.39**	10.39*	5.03	-4.52	0.55	-11.90	2.50	-8.89*	20.10**	17.33**	30.64*	21.23
12.	L_{12}	9.97**	8.06	35.50**	29.29**	3.87	-0.64	21.68**	19.18**	4.82	-1.46	43.43**	40.26**
13.	L_{13}	5.26	-0.77	21.77*	7.33	0.29	-8.49	4.94	-7.61*	42.73**	42.65**	39.42**	16.03
14.	L_{14}	12.42**	2.07	19.24*	-2.39	23.28 **	3.49	24.52**	12.36**	67.97**	67.54**	141.76**	88.22**
15.	L_{15}	19.06**	14.69**	-0.79	-7.79	-13.46 *	-17.49**	2.50	-8.89*	70.02**	68.00**	47.13**	26.01**
16.	L_{16}	27.39**	22.25**	29.15**	24.88*	8.91	6.11	32.39**	30.56**	24.54**	22.00**	52.49**	40.14**
17.	L_{17}	35.99**	28.55**	33.42**	17.68	65.22 **	48.14**	30.14**	28.38**	2.01	1.73	74.71**	50.02**
18.	L_{18}	21.74**	18.84**	16.52	7.68	13.30 *	11.19	29.66**	28.77**	8.50	4.04	39.21**	25.36*
19.	L_{19}	26.31**	14.57**	20.86*	3.48	32.14 **	17.77**	20.73**	7.61*	25.58**	22.95**	80.35**	61.68**
20.	L_{20}	8.94**	-4.67	-11.87	-29.71**	-7.84	-24.24**	13.21**	3.45	28.50**	26.19**	13.21	-5.77
21.	L_{21}	26.60**	17.22**	35.28**	21.90*	38.56**	28.86**	9.88**	-1.11	30.03**	28.88**	80.56**	67.07**

22.	L_{22}	24.71**	17.59**	46.12**	38.52**	38.05**	28.74**	19.23**	10.71**	13.00*	10.97	59.82**	58.70 **
23.	L_{23}	16.84**	14.70**	47.86**	44.87**	15.03**	9.97	14.29**	4.76	18.09**	17.79**	49.58**	36.59 **
24.	L_{24}	28.31**	14.76**	35.52**	25.54*	76.70**	48.97**	10.13**	3.57	28.10**	25.46**	142.60**	107.10**
25.	L_{25}	20.85**	16.62**	32.38**	28.85*	28.64**	17.89**	8.28*	1.19	0.18	-5.59	36.70**	22.33
26.	L_{26}	20.23**	15.37**	38.93**	24.70**	30.92**	24.67**	12.50**	7.61*	56.04**	55.55**	132.08**	109.36**
27.	L_{27}	1.94	-5.87	3.21	-14.12	4.13	-9.17	7.60*	5.75	40.66**	40.66**	54.72**	29.52**
28.	L_{28}	14.98 **	12.78**	27.40**	20.73	20.76**	20.41**	16.09**	12.22**	40.49**	39.18**	94.66**	81.30**
29.	L_{29}	27.86**	25.93**	52.53**	49.64**	44.61**	41.64**	31.61**	21.43**	64.68**	63.73**	227.14**	191.91**
30.	L_{30}	30.27**	24.62**	55.79**	50.44**	15.11*	9.48	37.06**	36.11**	19.14**	16.34*	68.24**	51.07**
31.	L_{31}	23.57**	23.16**	17.36	17.20	-3.13	-5.50	23.40**	22.54**	54.70**	54.20**	80.54**	75.99**
32.	L_{32}	16.20**	5.36	10.78	0.84	41.89**	21.71**	18.62**	16.22**	27.81**	24.47**	107.77**	97.53**
33.	L_{33}	16.76**	14.36**	28.32**	22.60*	33.88**	25.08**	18.06**	16.44**	34.79**	26.33**	135.18**	134.42**
34.	L_{34}	19.40**	12.92**	41.01**	24.44**	35.23**	26.26**	22.70**	8.70*	70.33**	69.87**	185.09**	132.49**
35.	L_{35}	5.52	-3.91	-1.40	-19.20*	-9.55*	-22.49**	26.58**	14.94**	32.39**	31.62**	42.90**	9.25
36.	L_{36}	4.57	1.05	17.77	9.60	-2.69	-4.96	10.56**	-1.11	28.13**	26.20**	40.35**	17.68
37.	L_{37}	10.56**	9.46*	9.52	-5.69	10.12	4.38	17.72**	6.90	13.35*	11.42	76.11**	71.71**
38.	L_{38}	23.26**	20.22**	10.66	-3.14	13.31*	9.59	1.75	0.00	29.25**	26.32**	89.67**	65.53**
39.	L_{39}	23.10**	18.91**	21.40*	1.52	21.52**	9.86	15.72**	5.75	3.28	-0.83	46.20**	28.37*
40.	L_{40}	13.08**	12.33**	4.68	-9.97	6.80	-1.10	28.66**	16.09**	4.85	2.73	74.37**	65.83**
41.	L_{41}	34.32**	22.89**	1.46	-4.61	21.54**	-0.27	13.04**	4.60	32.28**	26.68**	123.69**	117.97**
42.	L_{42}	38.36**	36.87**	-7.34	-16.94	30.05**	15.62**	23.13**	13.22**	54.66**	42.66**	214.50**	205.67**
43.	L_{43}	12.41**	5.31	-16.01*	-18.36*	-13.21**	-14.59*	6.15*	3.26	28.51**	25.99**	40.41**	12.29
44.	L_{44}	17.31**	5.87	-8.69	-13.94	-18.59**	-26.86**	-16.09**	-16.09**	11.54	9.02	-13.52	-35.03**
45.	L_{45}	24.02**	18.70**	14.93	5.65	2.54	-0.55	-5.08	-6.67	-5.45	-8.43	1.26	-16.81

Conclusion

In the state of Uttar Pradesh, area under Quality Protein Maize hybrids/composites is very less due to lack of awareness and understanding among farmers and non availability of superior QPM hybrids and composites for different agro-ecological regions, diseases and insect pests, moisture stress, poor cultural practices, excessive plant height, drought and low soil fertility. Therefore an attempt was made in the present investigation to find out superior lines on the basis of their *per se* performance and hybrids in different maturity groups of QPM suited for growing under Vindhyan agro-climatic conditions. On the basis of *per se* performance for grain yield per plant, best high yielding hybrids *viz*., POP-31Q-182Q11 X HKI-193-1 (134.28 g/plant), POP-31Q-182Q11 X TARUN-83-1-32 (132.98 g/plant) and TARUN-83-1-32 X CM-138-1 (128.42g/plant) were found to be significantly superior with higher yield per plant. Estimates of MPH for grain yield per plant recorded highest positive significant by the crosses *viz*., POP-31Q-182Q11 X HKI-193-1 (227.14**), TMT-TROP-(QPM) X TARUN-83-1-32 (214.50**), POP-31Q-182Q11 X TARUN-83-1-32 (185.0**), HKI-34 (H2) X CM-600 (142.60**) and TARUN-83-1-32 X CM-138-1(141.76**). BPH (Hb) for grain yield per plant recorded highest positive significant by the crosses *viz*., TMT-TROP-(QPM) X TARUN-83-1-32 (205.67**), POP-31Q-182Q11 X HKI-193-1 (191.91**), POP-31Q-182Q11 X DMR-N_4 (134.42**), POP-31Q-182Q11 X TARUN-83-1-32(132.49**) and TMT-TROP-(QPM) X DMR-N_4 (117.97**).

Acknowledgements

Present investigation was done as a part of M.Sc. thesis. The authors are thankful to the Department of Agriculture, Agriculture Educational Research and Government of Uttar Pradesh for providing financial assistance to this project

References

1. Darshan SS, Marker S. Heterosis and combining ability for grain yield and its component characters in quality protein maize (*Zea mays* L.) hybrids. Electronic Journal of Plant Breeding. 2019;10(1):111-118.
2. El-Gazzar IAI, EL-Ghonemy MA, Mousa S. Evaluation of new inbred lines of white maize via line x tester analysis over three locations. Journal Plant Prod. Mansoura University. 2013;4(6):897-906.
3. Malik SI, Malik HN, Minhas NM, Munir M. General and Specific combining ability studies in maize diallel crosses. International Journal of Agriculture & Biology. 2004;(5):856-859.
4. Kumar M, Verma SS, Uniyal M, Barh A, Singh NK. Exploitation of combining ability and heterosis for development of maize hybrids for tarai region of Uttarakhand. Journal of Applied and Natural Science. 2016;8(3):1570-1575.
5. Ruswandi D, Supriatna J, Makkulawu AT, Waluyo B, Marta H, Suryadi E, *et al*. Determination of Combining Ability and Heterosis of Grain Yield Components for Maize Mutants Based on Line x Tester Analysis. Asian Journal of Crop Science. 2015;7(1):19-33.
6. Shah L, Rahman H, Ali A, Shah KA, Si H, Xing WS, *et al*. Early generation testing for specific combining ability and heterotic effects in maize variety Sarhad white. ARPN Journal of Agricultural Biological and Science. 2016;11(1):42-48.
7. Singh SB, Gupta BB, Anjani KS. Heterotic expression and combining ability for yield and its components in maize (*Zea mays* L.). Progressive Agriculture. 2010;10:275-281.
8. Tulu D, Azmach G, Tesso B. Perse Performance and Heterosis of Quality Protein Maize (*Zea mays* L.) Inbred Lines Adapted to Mid-Altitude Sub-Humid Agro-Ecology of Ethiopia. International Journal of Research Studies in Science, Engineering and Technology. 2018;5(8):14-26.