International Journal of Sustainable Agriculture 3 (3): 76-81, 2011
ISSN 2079-2107


# Heterosis and Combining Ability of CIMMYT's Tropical × Subtropical Quality Protein Maize Germplasm

*[1]M. Amiruzzaman, [2]M.A. Islam, [3]K.V. Pixley and [1]M.M. Rohman*

[1]Plant Breeding Division, Bangladesh Agricultural Research Institute, Gazipur, Bangladesh
[2]Department of Genetics and Plant Breeding, Bangladesh Agricultural University, Mymensingh
[3]Ex-Associate Director, CIMMYT, Mexico

**Abstract:** Combining ability and heterosis was studied in 7 × 7 diallel cross in quality protein maize for kernel yield plant$^{-1}$, number of kernels ear$^{-1}$, 1000-kernel weight, lysine and tryptophan. Variance due to GCA and SCA were highly significant, indicating both additive and non-additive types of gene action are important for controlling the traits. Predominance of non-additive gene action was observed for all the quantitative and qualitative traits. Standard heterosis ranged from -14.26 to 6.35% for kernel yield and other two yield components from -26.77 to 7.21% and -16.71 to 1.53% for kernel number and weight, respectively. Fot quality traits, heterosis varied from -7.34 to 15.60% and -8.77 to 14.47% for lysine and tryptophan content. Average heterosis for yield and other two components were negative value, but it showed positive values for both the quality traits. In general kernel yield decreased when quality of the crosses increases and vice versa.. Parent $P_1$ was the best combiner for kernel yield coupled with both the yield component kernel number and weight. For quality traits, $P_5$ was the best combiner showing significant positive gca effect both for lysine and tryptophan. The parent $P_2$ was also a good combiner for kernel yield and quality trait lysine. Additive × additive, additive × dominance and dominance × dominance gene interactions were involved in deriving good specific crosses for different traits. The cross combinations $P_2 \times P_4$ and $P_3 \times P_5$ simultaneously possessed significant desirable sca effects and high heterosis both for kernel yield, yield components and quality traits might be used for obtaining high yielding quality hybrids.

**Key words:** General combining ability % Hybrid vigor % Maize breeding % Yield

## INTRODUCTION

Maize (*Zea mays* L.) plays a significant role in human and livestock nutrition worldwide [1]. Quality protein maize (QPM) contains high quality amino acids lysine and tryptophan, which are two times higher in QPM than normal maize. With its high nutritional quality QPM can offer an easy and inexpensive source of high quality protein to the millions of poor [2]. Development and adoption of QPM would increase the nutritional quality of food and feed as well [3].

Information on heterotic patterns and combining ability among maize germplasm is essential in maximizing the effectiveness of hybrid development [4]. Development of commercial maize hybrid usually requires a good knowledge of combining ability of the breeding materials to be used. Selection of parents based on combining ability has been used as an important breeding approach in crop improvement. Combining ability analysis is of special importance in cross-pollinated crops like maize as it helps in identifying potential inbred parents that can be used for producing hybrids and synthetics [5]. It also helps to know the genetic architecture of various characters that enables the breeder to design effective breeding plan. The study involving of quality protein maize focused on to asses the gene action for quantitative and qualitative traits and to explore heterotic hybrid combinations.

## MATERIALS AND METHODS

Seven CIMMYT's tropical and subtropical quality protein maize (QPM) inbreds viz. CML 161, CML 171, CML 172, CML 192, CML 193, CML 170 and CML 165

**Corresponding Author:** Dr. Md. Motiar Rohman, Plant Breeding Division,
Bangladesh Agricultural Research Institute, Gazipur, Bangladesh.

originated from different source populations (Table 1) designated as $P_1$, $P_2$, $P_3$, $P_4$, $P_5$, $P_6$ and $P_7$ were crossed in a diallel fashion (excluding reciprocals) in the kharif (rainy) season of 2006 at the research farm of Bangladesh Agricultural Research Institute, Gazipur. In the following rabi (winter) season of 2007 all the hybrids, their respective parents along with a commercial QPM check BARI hybrid maize 5 (BHM 5) were grown in the same farm following alpha lattice design [6] with three replications. Each plot comprised two rows of 5 m long. Row to row and plant to plant spacing was 75 cm and 20 cm, respectively. One healthy seedling per hill was kept after proper thinning at two weeks after germination. Fertilizers were applied @ 250, 120, 120, 40 and 5 kg/ha of N, $P_2O_5$, $K_2O$, S and Zn, respectively. Two border rows were used at each end of the replications to minimize border effect. Ten randomly selected competitive plants (5 from each row in a plot of each genotype in each replication) excluding any plant surrounding by a missing hill and border plants were used for recording observation on kernel yield plant$^{-1}$, number of kernels ear$^{-1}$ and 1000-kernel weight (g). Quality parameters lysine and tryptophan were estimated from $F_2$ kernels taken from middle of the selfed ears of each hybrid and check variety. Standard heterosis was estimated (against check variety) and tested according to Singh and singh [7]. Combining ability analysis was carried out following Model I Method 2 described by Griffing [8] using CropStat [9] software programme. Tryptophan and lysine was estimated following AOAC [10] and Joslyn [11].

## RESULTS AND DISCUSSION

The analysis of variance for genotypes and combining ability (gca and sca) are presented in Table 2. Genotypes differed significantly for all the quantitative and qualitative traits, indicating sufficient genetic variability present among them.

Analysis of variance for combining ability revealed that estimates of mean squares due to gca and sca were highly significant for all the quantitative and qualitative characters, indicating these traits are governed by both additive and non-additive gene action. The result agreed with those of Debnath and Sarker [12] in normal maize and Verma and Narayan [13] in QPM maize.

In the present study, the magnitude of sca variance was higher than gca for all the studied parameters, indicating the importance of non-additive gene action (dominance and epistasis) in the inheritance of the traits. The result is in close agreement with Bhatnagar *et al*. [3], who reported the importance of both additive and non-additive genetic variances in QPM maize and found greater magnitude of sca variance than gca in their study. The predominance of non-additive gene action for yield-related and quality characters was also reported by Hossain and Prasanna [14] in QPM maize. In a study Hallauer and Miranda Filho [15] reported that non-additive gene effects seem to be small, but they may be important for specific combinations.

In case of quality amino acids lysine and tryptophan, the gca and sca variances are of almost equal magnitude indicating additive and non-additive genes equally important in the expression of these traits (Table 2).

**General Combining Ability (GCA) Effects:** The estimates of gca effects of the parents for different characters are presented in Table 3. A wide range of variability for gca effects was observed among the parents for different characters. The gca effects are important indicators of the value of inbreds in hybrid combinations.

It was observed from the gca effects that, none of the parents individually showed good general combiner for all the characters. Among the parents, $P_1$ and $P_2$ had desirable significant gca effects for yield; $P_1$ for both of kernel number and weight; $P_2$, $P_5$ and $P_6$ for lysine and only $P_5$ for tryptophan content (Table 3).

Table 1: Origin and important features of CIMMYTs seven tropical and subtropical QPM inbred lines.

| Parent lines/ Inbreds | Origin | Source germplasm | Kernel colour | Kernel texture | Adaptation & maturity |
|---|---|---|---|---|---|
| $P_1$ (CML 161) | CIMMYT, Mexico | G25Q | Yellow | Flint | Tropical lowland, late |
| $P_2$ (CML 171) | CIMMYT, Mexico | G25Q | Yellow | Flint | Tropical lowland, late |
| $P_3$ (CML 172) | CIMMYT, Mexico | G25Q | Yellow | Flint | Tropical lowland, late |
| $P_4$ (CML 192) | CIMMYT, Mexico | G34Q | Yellow | Dent | Subtropical, late |
| $P_5$ (CML 193) | CIMMYT, Mexico | South Africa CYO162 | Yellow | Dent | Subtropical, late |
| $P_6$ (CML 170) | CIMMYT, Mexico | G26Q | Yellow | Dent | Tropical lowland, late |
| $P_7$ (CML 165) | CIMMYT, Mexico | P66 | Yellow | Dent | Tropical lowland, late |

Table 2: Analysis of variance for genotypic difference and combining ability for yield and quality traits in 7×7 diallel cross of quality protein maize

| | | Mean of squares | | | | |
|---|---|---|---|---|---|---|
| Source | df | Kernel yield plant$^{-1}$ (g) | No. of kernels ear$^{-1}$ | 1000-kernel weight (g) | Lysine (%) | Tryptophan (%) |
| Genotypes | 20 | 257.48** | 5132.58** | 388.83** | 0.0018** | 0.00007** |
| GCA | 6 | 81.47** | 1876.58** | 263.45** | 0.0016** | 0.00005** |
| SCA | 14 | 332.92** | 6528.02** | 442.57** | 0.0019** | 0.00008** |
| Error | 40 | 55.64 | 624.53 | 54.22 | 0.0002 | 0.00001 |
| Variance components: | | | | | | |
| $\sigma^2$gca/$\sigma^2$sca | - | 0.18 | 0.16 | 0.09 | 0.03 | 0.09 |
| $\sigma^2$A | - | 44.70 | 826.92 | 31.84 | 0.00064 | 0.000006 |
| $\sigma^2$D | - | 164.31 | 3498.36 | 230.13 | 0.00105 | 0.000041 |

**significant at p=0.01

Table 3: Estimates of general combining ability (gca) effects of the parents for yield and quality traits in quality protein maize.

| Parents | Kernel yield plant$^{-1}$ (g) | No. of kernels ear$^{-1}$ | 1000-kernel weight (g) | Lysine (%) | Tryptophan (%) |
|---|---|---|---|---|---|
| $P_1$ | 4.51* | 14.81* | 8.11** | -0.0001 | -0.0007 |
| $P_2$ | 4.38* | 0.34 | 0.33 | 0.0059* | 0.0003 |
| $P_3$ | -1.35 | -15.06* | 0.25 | -0.0147** | -0.0023* |
| $P_4$ | -2.49 | -10.45 | -5.48* | -0.0007 | -0.0015 |
| $P_5$ | 0.05 | 13.48 | -0.45 | 0.0139** | 0.0025* |
| $P_6$ | -1.98 | -5.52 | -3.01 | 0.0072* | 0.0009 |
| $P_7$ | -0.02 | 3.41 | 0.25 | -0.0114** | -0.0022* |
| $SE_{(gi)}$ | 1.78 | 5.98 | 1.76 | 0.0029 | 0.0009 |
| $SE_{(gi-gj)}$ | 2.72 | 9.13 | 2.69 | 0.0045 | 0.0013 |
| $LSD_{(5\%)}$ | 4.35 | 14.60 | 4.30 | 0.0048 | 0.0022 |

* significant at p=0.05, **significant at p=0.01

The significant gca effect for kernel yield was observed highest (4.51) in $P_1$ (CML 161) followed by (4.38) in $P_2$ (CML 171). In a study Xingming *et al*. [16] also found CML 161 and CML 171 as good combiner in their study with QPM.

In case of quality parameters, $P_2$, $P_5$ and $P_6$ was good general combiner for lysine content and only $P_5$ was good combiner for tryptophan content showing significant positive gca effects. The parent $P_5$ had the best combination for quality traits showing high gca effects for both the quality amino acids lysine and tryptophan. Parent $P_3$ and $P_7$ were the poorest combiner for both the quality traits.

The gca effect suggested that QPM parents $P_1$ was the best combiner for kernel yield along with the two major yield components. On the other hand, $P_5$ was the best combiner for quality traits showing significant gca effects both for lysine and tryptophan. The parent $P_2$ was good combiner both for yield and quality. These parents could be used in hybridization to improve yield as well as quality with desirable traits as donor parents for the accumulation of favorable genes.

**Specific Combining Ability (SCA) Effects:** The estimates of sca effects of the QPM crosses are presented in Table 4. For number of kernels ear$^{-1}$ and kernel weight in six and three crosses identified as good specific combinations for these two yield components.

In case of kernel yield, four crosses viz. $P_1 \times P_2$, $P_1 \times P_7$, $P_2 \times P_4$ and $P_3 \times P_5$ showed significant positive sca effects for this character. Among these crosses, the first two with high sca effect for yield was $P_1 \times P_2$ and $P_1 \times P_7$ (Table 4), one or both of their parents were related to good combiner ($P_1$ and $P_2$) for yield (Table 2) indicate gca of the parental lines plays a key role for high yield. This is supported by Xingming *et al*. [16], who reported involvement of good gca parents in high yielding crosses. The above four significantly high yielding crosses involved high × high, high × low and low × low general combining parents. This result is partially supported by Roy *et al*. [17], who obtained significant positive sca effects for kernel yield in high × low and low × low combiners and Ivy and Hawlader [18] obtained high sca effect of yield in low × low general combining parents.

For quality parameters, eight and five crosses were found as superior combinations for lysine and tryptophan showing significant positive sca effects for these two traits. Five crosses viz. $P_1 \times P_6$, $P_2 \times P_4$, $P_3 \times P_5$, $P_4 \times P_7$ and $P_5 \times P_6$ possessed significant positive sca effect both for lysine and tryptophan (Table 4).

Table 4: Estimates of specific combining ability (sca) effects for yield and quality traits in 7×7 diallel crosses of quality protein maize

| Crosses | Kernel yield plant$^{-1}$ (g) | No. of kernels ear$^{-1}$ | 1000-kernel weight (g) | Lysine (%) | Tryptophan (%) |
|---|---|---|---|---|---|
| $P_1 \times P_2$ | 8.50* | 25.27* | -2.73 | -0.034** | -0.0056** |
| $P_1 \times P_3$ | -12.50** | -45.68** | -9.22* | 0.007 | 0.0013 |
| $P_1 \times P_4$ | 2.18 | 13.04 | 6.41 | 0.019** | -0.0009 |
| $P_1 \times P_5$ | -10.93** | -46.22** | -1.82 | 0.004 | -0.0009 |
| $P_1 \times P_6$ | -0.39 | -2.56 | -4.38 | 0.021** | 0.0045* |
| $P_1 \times P_7$ | 13.15** | 57.18** | 9.17* | -0.004 | 0.0010 |
| $P_2 \times P_3$ | -18.56** | -86.88** | -12.50** | 0.014* | -0.0006 |
| $P_2 \times P_4$ | 9.64* | 55.84** | 7.67* | 0.023** | 0.0045* |
| $P_2 \times P_5$ | 0.86 | 15.91 | -0.67 | -0.005 | 0.0015 |
| $P_2 \times P_6$ | 0.31 | -11.08 | 4.16 | 0.008 | 0.0012 |
| $P_2 \times P_7$ | -0.75 | 1.98 | 1.10 | -0.006 | -0.0011 |
| $P_3 \times P_4$ | 7.49 | 17.24 | 7.17 | -0.016** | -0.0019 |
| $P_3 \times P_5$ | 11.26** | 38.98** | 2.24 | 0.029** | 0.0065** |
| $P_3 \times P_6$ | 6.83 | 54.31** | 7.14 | -0.031** | -0.0069** |
| $P_3 \times P_7$ | 3.38 | 22.04 | 3.41 | 0.011* | 0.0015 |
| $P_4 \times P_5$ | -9.53* | -36.62** | -22.65** | -0.048** | -0.0091** |
| $P_4 \times P_6$ | -2.62 | -12.29 | 2.60 | -0.002 | 0.0003 |
| $P_4 \times P_7$ | -9.27* | 37.22** | -4.18 | 0.024** | 0.0070** |
| $P_5 \times P_6$ | 5.37 | 21.78 | 7.44 | 0.024** | 0.0059** |
| $P_5 \times P_7$ | 2.98 | 6.18 | 8.05* | -0.004 | -0.0040* |
| $P_6 \times P_7$ | -9.48* | -50.16** | -23.12** | -0.021** | -0.0050* |
| $SE_{(ij)}$ | 3.51 | 11.78 | 3.47 | 0.006 | 0.0017 |
| $LSD_{(5\%)}$ | 7.52 | 25.26 | 7.44 | 0.011 | 0.0036 |
| $LSD_{(1\%)}$ | 10.44 | 35.06 | 10.33 | 0.015 | 0.0051 |

* significant at p=0.05, **significant at p=0.01

Table 5: Percent standard heterosis (%) for yield and quality traits in 7×7 diallel crosses of quality protein maize

| Crosses | Kernel yield plant$^{-1}$ (g) | No. of kernels ear$^{-1}$ | 1000-kernel weight (g) | Lysine (%) | Tryptophan (%) |
|---|---|---|---|---|---|
| $P_1 \times P_2$ | 6.10** | 0.26 | -5.76** | -4.59** | -5.70** |
| $P_1 \times P_3$ | -12.02** | -16.22** | -7.86** | -2.75 | 0.00 |
| $P_1 \times P_4$ | -2.81 | -3.99* | -4.70** | 8.26** | 2.19 |
| $P_1 \times P_5$ | -10.00** | -10.81** | -5.72** | 8.26** | 3.51* |
| $P_1 \times P_6$ | -4.22** | -6.05** | -7.36** | 11.01** | 8.33** |
| $P_1 \times P_7$ | 6.35** | 7.21** | 1.17 | -0.92 | 0.44 |
| $P_2 \times P_3$ | -14.26** | -26.77** | -11.39** | 4.59** | -1.32 |
| $P_2 \times P_4$ | 4.15** | 3.67* | 1.33 | 11.01** | 10.53** |
| $P_2 \times P_5$ | -0.09 | -1.42 | -7.84** | 7.34** | 7.89** |
| $P_2 \times P_6$ | -1.86 | -10.30** | -7.12** | 9.17** | 5.26** |
| $P_2 \times P_7$ | -1.22 | -6.05** | -7.05** | 0.00 | -1.75 |
| $P_3 \times P_4$ | 0.29 | -8.75** | -6.97** | -5.50** | -1.32 |
| $P_3 \times P_5$ | 3.15* | 0.06 | 1.53 | 11.01** | 10.96** |
| $P_3 \times P_6$ | -1.25 | -0.64 | -5.63** | -7.34** | -8.77** |
| $P_3 \times P_7$ | -2.24 | -5.15** | -6.34** | -0.92 | -1.75 |
| $P_4 \times P_5$ | -11.77** | -13.64** | -16.71** | -6.42** | -4.39** |
| $P_4 \times P_6$ | -8.46** | -12.61** | -9.47** | 4.59** | 5.70** |
| $P_4 \times P_7$ | -11.63** | -15.70** | -10.59** | 6.42** | 10.53** |
| $P_5 \times P_6$ | -1.29 | -1.42 | -4.91** | 15.60** | 14.47** |
| $P_5 \times P_7$ | -1.56 | -2.70 | 1.19 | 2.75 | -2.63 |
| $P_6 \times P_7$ | -11.43** | -17.25** | -15.85** | -3.67* | -6.14** |
| Mean of heterosis | -3.62 | -7.16 | -7.59 | 3.23 | 2.19 |
| $CD_{(0.05)}$ | 2.87 | 3.63 | 1.65 | 3.09 | 2.95 |

* significant at p=0.05, **significant at p=0.01

The results showed that, generally gca effects of the parents did not reflected in their sca effect for all the traits which is reported by Ivy and Howlader [18]. Moreover, Amiruzzaman *et al*., [19] also pointed out that the sca is a result of the interaction of gca effects of the parents and that it can improve or deteriorate the hybrid expression compared to the expected effect based on gca only. The sca effects of the crosses did not show any specific trends in cross combinations between parents possessing high, medium and low gca. In most of the cases, the crosses those showed high sca effects involved at least one good combiner. Aguiar *et al*. [20] also pointed out similar opoinon that in the diallel analyses, one must select hybrids of highest specific combining ability in which one of the parental lines presents highest general combining ability.

**Heterosis:** The percent standard heterosis expressed by $F_1$'s for different characters is presented in Table 5. The level of heterois varied widely among the crosses. Heterosis for number of kernels ear$^{-1}$ and kernel weight were not as high as other traits. Most of the crosses showed negative or significantly negative heterosis for these two important yield components. However, two crosses ($P_1 \times P_7$ and $P_2 \times P_4$) exhibited significant positive heterosis for kernels number and none had shown significant positive heterosis for kernel weight. Generally this might be due to the smaller kernel size and low kernel weight of QPM inberds than normal maize lines. Heterosis for these two traits ranged from -26.77 to 7.21% for kernel number and from -16.71 to 1.53% for kernel weight (Table 5). The maximum heterosis 7.21% and 1.53% was expressed by the crosses $P_1 \times P_7$ and $P_3 \times P_5$ for kernel number and kernel weight, respectively. Mean of heterosis were negative values (-7.16% and -7.59%) for both of these two traits.

For kernel yield, out of 21 $F_1$'s only four ($P_1 \times P_2$, $P_1 \times P_7$, $P_2 \times P_4$ and $P_3 \times P_5$) exhibited significant positive heterosis over the QPM check BHM 5 (Table 5). In normal maize, Akhter and Singh [21] and Debnath [22] obtained high heterosis for kernel yield in most of their studied crosses, while Bhatnagar *et al*. [3] and Hellin *et al*. [23] reported low performance of QPM hybrids compare to commercial checks, which supported the present result. Heterosis for yield ranged from -14.26 to 6.35% with an average negative value (-3.36%). In this study the highest heterosis reached only up to 6.35% over the commercial check. The lowest heterosis (-14.26%) was observed in $P_2 \times P_3$. Lowest heterosis of this cross might be due to both of the parents $P_2$ (CML 171) and $P_3$ (CML 172) originated from the same source population G25Q (Table 1). The result is in confirmity with that of Saxena *et al*. [24] who opined that hybrids produced from inbred lines having different origins tended to have greater consistent yield levels than hybrids of parental lines originating from the same source population. They also suggested that hybrids should include inbred lines that have different origins as in the highest heterotic cross $P_1 \times P_7$ ($P_1$ and $P_7$ originated from different source population G25Q and P66) (Table 1). In general it is observed from the heterotic results that, when quality of the QPM crosses increased side by side yield decreases ($P_1$ x $P_2$ and $P_1$x$P_7$) and vice versa as in the crosses $P_4$ x $P_6$ and $P_4$ x $P_7$.

In case of quality traits, the range of heterosis varied from -7.34 to 15.60% for lysine and from -8.77 to 14.47% for tryptophan content. Significant positive heterosis over the check was exhibited by eleven and nine crosses for lysine and tryptophan, respectively. Among the 21 $F_1$s, significant positive heterosis for both the quality traits was shown by nine crosses. The highest heterosis 15.60% and 14.47% was expressed by the same cross $P_5 \times P_6$ for both the quality traits lysine and tryptophan. The mean of heterosis value was positive (3.23% and 2.19%) for both the quality trait lysine and tryptophan.

Based on the results, it is observed that only two cross $P_2 \times P_4$ and $P_3 \times P_5$ simultaneously possessed high yield with high quality. The parental lines $P_2$ and $P_4$ of the cross $P_2 \times P_4$ and $P_3$ and $P_5$ of the cross $P_3 \times P_5$ were originated from different source population (Table 1). This is corroborated with the result of Nigussie and Zelleke [25], who reported that crossing of maize genotypes those obtained from different sources, could result in better utilization of hybrid vigour. The mean of heterosis for yield and yield components showed negative values whereas, possitive values were observed for both the quality traits. As depicted from the gca effects, parent $P_1$ and $P_2$ were good general combiner for kernel yield and $P_5$ for both the quality traits.

It can be concluded from the present results that the parental lines $P_1$, $P_2$ and $P_5$ would be the ideal lines as donor to obtain high yield as well as good quality. The two QPM cross $P_2 \times P_4$ and $P_3 \times P_5$ simultaneously possessing high sca effects and high heterosis for yield along with high quality could be used for commercial variety after verifying the performances.

## REFERENCES


1. Bantte, K. and B.M. Prasanna, 2004. Endosperm protein quality and kernel modification in the quality protein maize inbred lines. J. Plant Biochemistry and Biotechnology, 13: 57-60.
2. Singh, S.B., J. Kaul, R. Singh and O.P. Sharma. 2008. Development of early maturing single cross QPM hybrids for Indian conditions. Book of Abstracts. The 10th Asian Reg. Maize Workshop. Makassar, Indonesia, October 20-23, 61 p.
3. Bhatnagar, S., E.J. Bertran and L.W. Rooney. 2004. Combining abilities of quality protein maize inbreds. Crop Sci., 44: 1997-2005.
4. Beck, D.L., S.K. Vasal and J. Carossa, 1990. Heterosis and combining ability of CIMMYT's tropical early and intermediate maturity maize (*Zea mays* L.) germplasm. Maydica, 35: 279-285.
5. Vasal, S.K., 1998. Hybrid maize technology: Challenges and expanding possibilities for research in the next century. *In:* Vasal, S.K., C.F. Gonzalez and F. Xingming (ed). Proc. 7th Asian Reg. Maize Workshop. Los Banos, Philippines, February, 23-27, pp: 58-62.
6. Patterson, H.D., E.R. Williams and E.A. Hunter, 1978. Block design for variety trials. J. Agric. Sci., (Cambridge), 90: 395-400.
7. Singh, R.K. and P.K. Singh, 1994. A Manual on Genetics and Plant Breeding Experimental Techniques. Kalyani Publs., Ludiana, New Delhi, pp: 99-107.
8. Griffing, B., 1956. Concept of general and specific combining ability in relation to diallel crossing systems. Aust. J. Biol. Sci., 9: 463-493.
9. CropStat, 2007. Crop Research Informatics Laboratory. International Rice Research Institute. Los Banos, The Philippines.
10. AOAC (Association of Official Analytical Chemists). 1975. 7th edition, Washington, USA.
11. Joslyn, M.A., 1976. Methods in food analysis. Academic Press, New York, 2nd edn. Chapter XVI: pp: 475-509.
12. Debnath, S.C. and K.R. Sarker, 1990. Combining ability analysis of grain yield and some of its attributes in maize (*Zea mays* L.). Indian J. Genet., 50: 57-61.
13. Verma, S.S. and A. Narayan, 2008. Heterosis, combining ability and phenotypic stability for yield and other characters in high quality protein maize (*Zea mays* L.). Book of Abstracts. The 10th Asian Reg. Maize Workshop. Makassar, Indonesia, pp: 89.
14. Hossain, F. and B.M. Prasanna, 2008. Genetic and biochemical analysis of quality protein maize (QPM) lines in India. Book of Abstracts. The 10th Asian Reg. Maize Workshop. Makassar, Indonesia, pp: 7.
15. Hallauer, A.R. and J.B. Miranda Filho, 1988. Quantitative genetic in maize breeding, 2nd edn. Iowa State Univerity Press, Ames, USA.
16. Xingming, F., J. Tan, Z. Chen and J. Yang, 2002. Combining ability and heterotic grouping of ten temperate, tropical and subtropical quality protein maize. *In:* Srinivasan, G., P.H. Zaidi, B.N. Prasanna, F.C. Gonzalez and K. Lesnick (ed). Proc. 8th Asian Reg. Maize Workshop. Bangkok, Thailand,
17. Roy, N.C., S.U. Ahmed. S.A. Hussain and M.M. Hoque. 1998. Heterosis and combining ability analysis in maize (*Zea mays* L.). Bangladesh J. Pl. Breed. Genet., 11: 35-41.
18. Ivy, N.A. and M.S. Howlader, 2000. Combining ability in maize. Bangladesh J. Agril. Res., 25: 385-392.
19. Amiruzzaman M., M.A. Islam, L. Hasan, M. Kadir and M.M. Rohman, 2011. Heterosis and combining ability in a diallel among elite inbred lines of maize (*Zea maize* L.). Emir. J. Agric., 23: 204-208.
20. Aguir, C.G., L.A. Carlini-Garcia, A.R. Silva, M.F. Da Santos, A.A.F. Garcia and C.L. DeSouja Jr, 2003. Combining ability of inbred lines of maize and stability of their respective single crosses. Scientia Agricola., 60: 83-89.
21. Akhtar, S.A. and T.P. Singh, 1981. Heterosis in intervarietal crosses of maize. Madras. Agric. J., 68: 47-51.
22. Debnath, S.C., 1992. Analysis of heterosis in a 10 × 10 diallel cross of maize. Bangladesh J. Agril. Sci., 19: 161-164.
23. Hellin, J., O. Erenstein and K. Pixley, 2008. Maize-poultry value chains and quality protein maize in India: Implications for research and development. Book of Abstracts. The 10th Asian Reg. Maize Workshop. Makassar, Indonesia, pp: 26.
24. Saxena, V.K., N.S. Mathi, N.N. Singh and S.K. Vasal, 1998. Heterosis in maize: Grouping and patterns. *In:* Vasal, S.K., F.C. Gonzalez and F. Xingming (ed). Proc. 7th Asian Reg. Maize Workshop. Los Banos, Philippines. February, pp: 124-133.
25. Nigussie, M. and H. Zelleke, 2001. Heterosis and combining ability in a diallel among eight elite maize populations. African Crop Sci. J., 9: 471-479. pp: 10-18.