



# Combining Ability and Heterosis Studies for Yield and Quality Traits in Quality Protein Maize

GR LAHANE, RM CHAUHAN AND JM PATEL\*<sup>1</sup>

CP College of Agriculture, SD Agricultural University, Sardarkrushinagar, Gujarat (India)

## ABSTRACT

A field study was conducted using eight parents and 28  $F_1$  cross combinations of quality protein maize during *rabi* 2012-13 with objective to identify the best parental genotypes and cross combinations. None of the tested parents were found good for general combiner with respect to yield attributing traits and yield. Inbred lines I-07-6-4-4( $P_2$ ), I-07-65-18-3 ( $P_5$ ) and I-07-65-13-1( $P_6$ ) were found good general combiners for direct yield attributing traits whereas inbreds I-07-13-1-3( $P_1$ ), I-07-65-13-1( $P_6$ ) and I-07-59-5 ( $P_7$ ) contributed maximum genes for protein and its related traits. Among the hybrids,  $P_7 \times P_8$ ,  $P_2 \times P_3$  and  $P_6 \times P_8$  exhibited positive and significant specific combining ability effects for ear weight. High standard heterosis values were observed for lysine content whereas low values of heterosis were observed for tryptophan in protein over standard check hqpm1.

**Keywords:** Combining ability, Heterosis, Maize, QPM

## ARTICLE INFO

Received on	: 28.06.2014
Revised received on	: 27.07.2014
Accepted on	: 06.08.2014
Published online	: 07.09.2014

## INTRODUCTION

Maize (*Zea mays* L.) plays a significant role in human and livestock nutrition worldwide. Quality protein maize (QPM) contains high quality amino acids lysine and tryptophan, which are two times higher in QPM than normal maize. Mutant alleles, *opaque-2* (*o2*) and *floury-2* (*fl2*) discovered by Purdue University researchers were found to alter the amino acid profile and composition of maize endosperm protein and result in two fold increase in the levels of lysine and tryptophan compared to what is met in normal maize genotypes. The mutants derive their name from soft, floury opaque endosperm, respectively. With its high nutritional quality QPM can offer an easy and in expensive source of high quality protein to the millions of poor. Development and adoption of QPM would increase the nutritional quality of food and feed as well. Information on heterotic patterns and combining ability among maize germplasm is essential in maximizing the effectiveness of hybrid development. 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. It also helps to know the genetic architecture of various helps to know the genetic architecture of various breeding plan. The study involving of quality protein maize focused on to assess the gene action for quantitative and qualitative traits and to explore heterotic hybrid combinations.

## MATERIALS AND METHODS

Eight parents *viz.*; I-07-13-1-3 ( $P_1$ ), I-07-6-4-4 ( $P_2$ ), I-07-9-3-1( $P_3$ ), I-07-11-3-3 ( $P_4$ ), I-07-65-18-3 ( $P_5$ ), I-07-65-13-1( $P_6$ ), I-07-59-5 ( $P_7$ ), and I-07-7-1-1( $P_8$ ) were obtained from Maize Research Station, Godhra, Anand Agriculture University, Gujarat. For crossing programme each parental line was sown in two rows each of 5 meters length during *kharif* 2012 at Maize Research Station, Bhiloda (Gujarat). Hybrids were built up through

<sup>1</sup>Maize Research Station, SD Agricultural University, Bhiloda, Gujarat (India)

\*Corresponding author E-mail: dr.jmpatel.63@gmail.com

diallel crossing pattern (excluding reciprocal using eight parents. A set of 37 genotypes comprising of 8 parents and their 28 F<sub>1</sub> hybrids along with standard check hqpm 1 were sown in randomized block design (RBD) with three replications during *rabi* 2012-13. Each genotype was sown in one row maintaining 70 cm distance row to row and 20 cm distance plant to plant. The recommended agronomical practices and plant protection measures were adopted for raising a good crop. Standard heterosis was estimated and tested according to (Meredith and Bridge, 1972). Combining ability analysis was carried out following Model I Method 2 described by Griffing (1956). Protein content of the grinded sample was estimated by NIR (Instant analyses) made by Dikey-john, USA. Lysine content in protein of seeds of plants was estimated by using colorimetric method given by Tsai et al. (1972) and optical density was measured at 390 nm whereas, tryptophan content in protein of seeds plants was estimated by using colorimetric method given by Hernandez and Bates

(1969) and optical density was measured at 545nm. The mean squares for (General Combining Ability) GCA and (Specific Combining Ability) SCA were tested against their respective error variances derived from ANOVA reduced to mean level.

## RESULTS AND DISCUSSION

The analysis of variance showed that genotypes were differed significantly for all the characters (Table 1). The analysis of variance for combining ability showed that mean square due to GCA were found highly significant for all characters whereas, mean square due to SCA were found highly significant for all the characters indicated that non-additive gene action was important for the characters studied.

### General Combining Ability (GCA) Effects

Perusal of GCA effects (Table 2) revealed that no line was observed to be good general combiner for all the traits.

**Table 1:** Analysis of variance (mean square) for combining ability, estimation of components of variance and their ratio for various characters in quality protein maize

Sources of Variation	d.f.	Ear weight (g)	Shelling (%)	100- Grain weight (g)	Protein Content (%)	Lysine in protein (%)	Tryptophan in protein (%)
Replication	2	0.161	25.92	0.11	0.03	96.44	0.083
Treatments	35	628.33**	45.29**	42.93**	1.27**	14458.28**	485.79**
GCA	7	275.6**	23.936**	7.885**	0.93**	1570.57**	130.87**
SCA	28	192.88**	12.88**	15.917**	0.294**	5631.63**	169.69**
Error	70	5.775	3.289	0.341	0.010	29.17	0.342
$\sigma^2$ GCA	-	26.991	2.064	0.754	0.092	154.13	13.05
$\sigma^2$ SCA	-	187.10	9.598	15.575	0.284	5602.46	169.35
$\sigma^2$ GCA/ $\sigma^2$ SCA	-	0.144	0.215	0.048	0.326	0.027	0.077

\*, \*\* Significant at 5 per cent and 1 per cent levels of significance, respectively

**Table 2:** Estimates of general combining ability (GCA) effects of parents for thirteen characters in Quality protein maize

Parents	Ear weight (g)	Shelling (%)	100-Grain weight (g)	Protein content (%)	Lysine in protein (%)	Tryptophan in protein (%)
P <sub>1</sub>	-7.726**	-0.577	-1.1**	0.318**	27.617**	3.075**
P <sub>2</sub>	2.013**	0.351	0.3	-0.265**	-0.05	-1.125**
P <sub>3</sub>	-6.973**	-3.365**	1.1**	-0.009	-7.217**	-3.325**
P <sub>4</sub>	7.39**	-0.285	-1.1**	-0.044*	-11.983**	6.175**
P <sub>5</sub>	4.663**	1.295*	1.3**	0.122**	-9.35**	-4.925**
P <sub>6</sub>	1.859*	1.528**	-0.1	0.447**	1.117	1.575**
P <sub>7</sub>	-0.767	0.125	-0.1	-0.052	5.05**	0.675**
P <sub>8</sub>	-0.460	0.929	-0.3	-0.516**	-5.183**	-2.125**
S.Em Gi ±	0.71	0.53	0.17	0.029	1.59	0.173

\*, \*\* Significant at 5 per cent and 1 per cent levels of significance, respectively

However, the parents  $P_4$  (7.39),  $P_5$  (4.663),  $P_2$  (2.013), and  $P_6$  (1.859) were found good general combiner for ear weight. The parents  $P_5$  (1.295) and  $P_6$  (1.258) could be consider as good general combiner for Shelling (%). Amongst the parent two parent  $P_5$  (1.3) and  $P_3$  (1.1) had significant positive general combining ability effect and thus these parent were good general combiner for augmenting higher seed weight. In respect of protein content the parents  $P_6$  (0.447),  $P_1$  (0.318) and  $P_5$  (0.122) found to be good general combiners as they showed significant positive general combining ability effect. For lysine content the parents  $P_1$  (27.617) and  $P_7$  (5.05) contributed maximum genes. In respect of tryptophan content the parents  $P_4$  (6.175),  $P_1$  (3.075) found to be

good general combiners as they showed significant positive general combining ability effect. Results are in confirmation with that of [Hemavath and Balaji \(2008\)](#), [Laude and Salazar \(2008\)](#), [Abdel-Moneam \*et al.\* \(2009\)](#), [Jampatong \*et al.\* \(2010\)](#) and [Zare \*et al.\* \(2011\)](#).

### Specific Combining Ability (SCA) Effects

A critical evaluation of the results with respect to specific combining ability effects showed that none of the hybrids exhibited desirable significant SCA effects for all the characters (Table 3). However, hybrids  $P_4 \times P_8$  (0.944),  $P_2 \times P_5$  (0.596) and  $P_4 \times P_6$  (0.481) manifested desirable SCA effects for protein content, whereas cross

**Table 3:** Estimates of SCA effects and per cent standard Heterosis for different characters in Quality protein maize

Sr. No.	Crosses	Ear weight (g)	Het-erosis (%)	Shelling (%)	Het-erosis (%)	100-Grain weight (g)	Hetero-sis (%)	Protein content (%)	Het-erosis (%)	Lysine in protein (%)	Het-erosis (%)	Try-ptophan (%)	Het-erosis (%)
1	$P_1 \times P_2$	-18.442**	-18.89**	-3.988	-5.05	-3.756**	-14.30*	0.057	7.37**	11.044	7.93**	9.244**	-5.55**
2	$P_1 \times P_3$	0.547	-20.48**	-2.031	-7.38*	1.444**	17.30**	-0.612**	1.94	52.211**	19.65**	8.444**	-8.88**
3	$P_1 \times P_4$	-5.953**	-4.16	0.548	0.10	-0.356	-3.58	-0.7**	0.38	-27.356**	-9.65**	9.944**	3.33
4	$P_1 \times P_5$	-5.926**	-6.25*	0.164	1.69	3.244**	28.54**	0.303**	15.52**	37.344**	13.79**	-4.956**	-25.55**
5	$P_1 \times P_6$	5.911**	1.275	8.225**	12.65**	-5.356**	-25.01**	0.358**	20.43**	19.878**	11.37**	-1.456**	-14.44**
6	$P_1 \times P_7$	-3.496	-10.5**	-5.682**	-7.59*	-1.356*	-3.58	0.118	10.86**	89.944**	36.89**	9.444**	-3.33
7	$P_1 \times P_8$	11.764**	4.22	-2.405	-2.19	2.844**	17.82**	0.321**	7.50**	56.178**	14.82**	11.244**	-4.44*
8	$P_2 \times P_3$	14.971**	9.58**	-0.444	-4.047	2.044**	28.54**	-0.542**	-4.65*	64.878**	14.48**	2.644**	-20.00**
9	$P_2 \times P_4$	5.608*	13.75**	-4.307**	-5.09	8.244**	49.97**	0.446**	7.63**	47.644**	6.89**	7.144**	-4.44*
10	$P_2 \times P_5$	-16.032**	-6.55*	-2.271	-0.30	-2.156**	7.12	0.596**	11.77**	58.011**	11.37**	-1.756**	-26.66**
11	$P_2 \times P_6$	14.799**	16.8**	0.206	3.28	-4.756**	-14.30**	0.111	9.70**	31.544**	5.86*	13.744**	-2.22
12	$P_2 \times P_7$	19.332**	18.39**	5.143**	7.94	1.244*	17.83**	-0.479**	-4.39*	50.611**	13.79**	9.644**	-7.77**
13	$P_2 \times P_8$	-2.208	0.69	1.976	4.82	-2.556**	-3.58	0.324**	0.00	10.844*	-3.44*	-11.55**	-34.44**
14	$P_3 \times P_4$	-3.739	-1.525	-0.1	-4.44	-6.556**	-25.01**	-0.463**	-0.77	4.811	-10.34**	-14.65**	-31.11**
15	$P_3 \times P_5$	-0.913	-1.44	3.356*	2.22	1.044	28.54**	0.444**	13.06**	5.178	-9.31**	1.444**	-25.55**
16	$P_3 \times P_6$	10.125**	5.41*	-6.807**	-11.04**	-1.556*	7.12	0.266**	15.00**	8.711	-4.48*	1.944**	-17.77**
17	$P_3 \times P_7$	-8.249**	-12.08**	-0.87	-4.92	-5.556**	-14.30*	-0.395**	0.00	-12.222*	-10.34**	9.844**	-10.00**
18	$P_3 \times P_8$	-3.656	-8.00*	-0.737	-3.67	6.644**	49.97**	-0.221*	-3.75	71.011**	14.82**	14.644**	-7.77**
19	$P_4 \times P_5$	11.958**	21.16**	-1.065	0.44	-0.756	7.12*	-0.044	6.33**	63.944**	9.31**	21.944**	7.77**
20	$P_4 \times P_6$	-27.605**	-14.05**	1.733	4.45	0.644	7.12*	0.481**	17.33**	73.478**	16.20**	-9.556**	-20.00**
21	$P_4 \times P_7$	12.388**	17.08**	-3.594*	-4.44	2.644**	17.83**	-0.46	-1.29	12.544**	-3.44*	-7.656**	-18.88**
22	$P_4 \times P_8$	-2.919	4.58	-0.548	0.64	4.844**	28.54**	0.944**	10.86**	19.778**	-4.48*	-8.856**	-23.33**
23	$P_5 \times P_6$	2.055	8.39*	-4.648**	-1.89	-1.756**	7.12*	-0.336**	8.92**	-6.156	-10.34**	10.544**	-10.00**
24	$P_5 \times P_7$	3.114	7.08*	-1.878	-0.079	2.244**	28.54**	-0.02	6.59**	71.911**	17.93**	-0.556	-23.33**
25	$P_5 \times P_8$	-4.292	1.16	0.432	4.03	-3.556**	-3.58	-0.123	-0.77	7.144	-7.93**	19.244**	-4.44*
26	$P_6 \times P_7$	1.252	3.19	4.856**	9.12**	3.644**	28.54**	-0.301**	7.11**	29.444**	6.89**	11.944**	-2.22
27	$P_6 \times P_8$	18.212**	17.58**	-0.207	3.49	1.844**	17.83**	-1.418**	-13.32**	56.344**	12.41**	2.744**	-15.55**
28	$P_7 \times P_8$	25.238**	21.25**	2.332	4.86	-6.156**	-25.01**	0.002	-1.42	-7.256	-7.93**	-4.356**	-24.44**
	<b>S.Em</b>	<b>2.17</b>	<b>3.39</b>	<b>1.64</b>	<b>2.56</b>	<b>0.53</b>	<b>0.82</b>	<b>0.091</b>	<b>0.14</b>	<b>4.89</b>	<b>7.63</b>	<b>0.53</b>	<b>0.82</b>
	<b>Sij ±.</b>												

\*, \*\* Significant at 5 per cent and 1 per cent levels of significance, respectively

combinations *viz.*,  $P_1 \times P_6$  (8.22),  $P_2 \times P_7$  (5.143),  $P_6 \times P_7$  (4.856)  $P_3 \times P_8$  (3.497),  $P_4 \times P_7$  (3.152), and  $P_4 \times P_5$  (3.111) showed desirable significant SCA effects for shelling (%). Crosses  $P_1 \times P_7$  (89.944),  $P_4 \times P_6$  (73.478) and  $P_5 \times P_7$  (71.911) exhibited desirable significant positive SCA effect for lysine content. Significant and positive SCA effects for tryptophan content was recorded by crosses  $P_4 \times P_5$  (21.944),  $P_5 \times P_8$  (19.244), and  $P_3 \times P_8$  (14.644). These results are supported by Lukose and Godawat (2007), Hemavathy and Balaji (2008), Alam et al. (2008), Laude and Salazar (2008), Abdel-Moneam et al. (2009), Jampatong et al. (2010), Gichuru et al. (2011), Zare et al. (2011), and Amiruzzaman et al. (2011).

### Heterosis

Percent standard heterosis expressed by the F1 hybrids over the check hybrid, hqpm-1 for yield and other traits are presented in Table 3. The degree of heterosis varied from cross to cross and from character to character. Heterosis ranged from -20.48 to 21.25%; -11.04 to 12.65%; -25.01 to 49.97%; -13.32 to 15.52%; -9.65 to 36.89% and -34.44 to 7.77%, for ear weight, Shelling (%), 100-grain weight, protein content, lysine in protein and tryptophan in protein respectively. Positive heterosis is desirable for ear weight, shelling (%) and 100-grain weight, protein content, lysine in protein and tryptophan in protein of hybrid. For ear weight, 11 crosses exhibited significant positive heterosis over standard check. Only four crosses manifested significant positive heterosis for bold grain over check hybrid hqpm 1. None of the cross combinations expressed desirable heterosis for tryptophan whereas 18 hybrids showed positive and significant results for protein content. Results are in conformity with earlier findings of Hemavathy and Balaji (2008), Vieira et al. (2009), Mutimaamba et al. (2010), Sundararajun and Shenthil (2011) and Premlatha (2011).

### CONCLUSION

Based on foregone results and discussion, it can be concluded that parents having good general combining ability for ear weight ( $P_4$  and  $P_5$ ) and bold grains ( $P_6$ ) could be utilized as donor parents for obtaining high grain yield and desirable traits. For quality protein traits parent  $P_1$  and  $P_6$  was found as good general combiner. The cross combinations  $P_2 \times P_3$ ,  $P_2 \times P_7$  and  $P_6 \times P_8$  had maintained high SCA coupled with high and desirable heterosis for most of the traits could effectively be exploited in hybrid breeding programme.

**Correct Citation:** Lahane GR, Chauhan RM and Patel JM. 2014. Combining ability and heterosis studies for yield and quality traits in quality protein maize. *Journal of AgriSearch* 1(3):135-138.

### REFERENCES

- Abdel-Moneam MA, Attia A N, Emery MI and Fayed EA. 2009. Combining ability and heterosis for some agronomic traits in crosses of maize. *Pak. J. of Biol. Sci.* **12** (5): 433-438.
- Griffing B. 1956. Concepts of general and specific combining ability in relation to diallel crossing systems. *Aus. J. Bio. Sci.* **9**: 463-493.
- Hemavathy AT and Balaji K. 2008. Analysis of combining ability and heterosis groups of white grain quality protein maize (QPM) inbreds. *Crop Res.* **36** (1/3):224-234.
- Hernandez HH and Bates LS. 1969. A modified method for rapid tryptophan analysis of maize. *Res. Bul.* **13** CIMMIYT, Mexico.
- Jampatong S, Ngean MT, Balla C, Boonrumpun P, Mekarun A, Jompuk C and Kaveeta R. 2010. Evaluation of improved maize populations and their diallel crosses for yield. *Kasetsart J. Nat. Sci.* **44** (4): 523 – 528.
- Laude TP and Salazar AM. 2008. Combining ability and heterotic relationship in yellow quality protein maize varieties. *Philippine J. crop sci.* **33** (2): 25-26.
- Lukose S and Godavat SL. 2007. Combining ability for grain yield and drought related morphological trait in maize (*Zea mays* L.) under late sown condition. *Indian J. Genet.* **67** (1): 79-80.
- Meredith WR and Bridge RR. 1972. Heterosis and gene action in cotton (*Gossipium hirsutum* L.). *Crop Sci.* **12**: 304-310.
- Mutimaamba C, Lungu D and MacRobert J. 2010. Combining ability analysis of quality protein maize (QPM) and non-QPM inbred lines for kernel quality and some agronomic characteristics. Second Ruforum Biennial Meeting Entebbe, Uganda, 20-24.
- Premlatha M, Kalamani A and Nirmalakumari A. 2011. Heterosis and combining ability studies for grain yield and quality in maize. *Adv. Environ. Biol.* **5** (6): 1264-1266.
- Sundararajun R and Shenthil KP. 2011. Studies on heterosis in maize (*Zea mays* L.). *Plant Archives* **11** (1): 55-57.
- Tsai CY, Fiensel LW and Nelson OE. 1972. A calorimetric method for screening maize seeds for lysine content. *Cereal chem.* **49**: 572-579.
- Vieira RA, Souzaneto IL, Bignotto LS, Cruz CD, Amral AT and Scapim CA. 2009. Heterotic parametrization for economically important traits in popcorn. *Acta Sci. Agron.* **31** (3): 411-419.
- Zare M, Choukan R, Heravan EM, Mohammad RB and Kouros O. 2011. Gene action of some agronomic traits in corn (*Zea mays* L.) using diallel cross analysis. *African J. Agril. Res.* **6** (3): 693-703.