Combining Ability and Heterosis Studies for Grain Yield and Its Components in Hybrids of Quality Protein Maize (Zea mays L.)

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A B S T R A C T

Combining ability and heterosis for grain yield and its component traits were studied in quality protein maize through line x tester mating design using eight lines and three testers along with two checks, Vivek QPM 9 and HQPM-1. The studies on combining ability in quality protein maize provide information to identify potential parents of hybrids and single cross hybrids (SCH). The results revealed that the existence of non-additive gene action for all the characters studied. The lines DQL685 (Orange) -18-2, DQL596 (U)-2-1-1 and DQL 639 -1-7 and the tester, DMRQPM -03-124 had recorded significant gca for yield and most of the yield component traits studied. The hybrid, DQL599(U)-4-2 x DMRQPM 03-124 recorded negative significant sca values for earliness while considering days to 50 percent flowering and days to maturity. The hybrids DQL599(U)-4-2 × DMRQPM 58, DQL 621-1-1 × DMRQPM 03-102, DQL641-4-2 × DMRQPM 58, DQL 685(Orange)-18-2 × DMRQPM 03-124 with higher per se performance, exhibited significant specific combining ability effects and standard heterosis for grain yield per plant.

Keywords
Hybrid, Protein, Maize, Heterosis, Grain.

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Introduction

Maize is the third most important cereal crop after wheat and rice and is considered one of the most versatile emerging crop having wider adaptability under varied agro-climatic conditions. With its high content of carbohydrates, fats, proteins and some of the important vitamins and minerals, maize acquired a well-deserved reputation as a ‘poor man’s nutricereal (Prasanna et al., 2001). In addition, it is a basic raw material for the production of starch, oil, protein, alcoholic beverages, food sweeteners, fuel and more importantly a model plant exhaustively researched in genetics. Globally, maize is known as “queen of cereals” because it has the highest genetic yield potential among the cereals. During 2015-16, globally maize was cultivated on an area of 178 million ha in about 160 countries with a total production of 1037 million tons (Foreign Agricultural Service, USDA, 2016). In India, the crop was grown on an area of 9.2 million ha with total production of 26.15 million metric tons with an average yield 3340 kg/ha. In Telangana
state, it covers an area of 0.69 million hectares with a production of 2.31 million tonnes and productivity of 3340 kg ha\(^{-1}\) (2014-15) (India Stat, 2015).

Maize is deficient in some essential amino acids such as lysine and tryptophan, provitamin A and in micronutrients such as iron, zinc and calcium whose bioavailability is significantly lowered due to chelators such as phytate which is indigestible by monogastric animals, including humans (Sun et al., 2009). As cereal proteins, however have poor nutritional value because of reduced content of essential amino acids such as lysine, tryptophan. To overcome these problems, decades of efforts by researchers at International Maize and Wheat Improvement Centre (CIMMYT) led to the development of lines with enhanced nutritional values which were designated as “Quality Protein Maize” or QPM lines (Vasal et al., 1980). The conventional breeding procedures helped in releasing several QPM hybrids both in Africa and Latin America. India has imported the Mexican QPM lines and developed several QPM hybrids in recent past. However, it is very much essential to develop the QPM hybrids which can yield on par with normal hybrids. Therefore, the present investigation was carried out to identify superior QPM hybrids.

**Materials and Methods**

Eight inbred lines were crossed with three inbred testers in a line x tester mating design in *summer*, 2015 to generate 24 crosses. All the 24 crosses and two standard checks Vivek QPM-9 and HQPM-1and parents (lines and testers) were evaluated during *kharif*, 2016 at Winter Nursery Center (ARI), Rajendranagar, Hyderabad, Telangana State. Each genotype was grown in three rows of four meters length with 60 x 20 cm\(^2\) spacing in a randomized block design with three replications. The trial was conducted in a sandy loam soils. All the recommended agronomic practices were followed to raise a normal crop. Data were recorded on five randomly selected plants in each treatment for thirteen characters viz., days to 50 per cent tasseling, days to 50 per cent silking, days to maturity, plant height, ear height, ear length, ear diameter, number of kernel rows per ear, number of kernels per row, 100-seed weight, shelling percentage, protein content and grain yield per plant. The data collected were subjected to analysis of variance as suggested by Panse and Sukhatme (1985). The combining ability analysis was done according to Kempthorne (1957) and heterosis by Virmani et al., (1982).

**Results and Discussion**

The analysis of variance for combining ability for grain yield and yield components in quality protein maize are presented in Table 1.

The analysis of variance for combining ability revealed that genotypes exhibited highly significant differences among themselves. Mean sum of squares for combining ability for grain yield and its components in QPM showed that there were significant differences for all the characters except days to 50% tasseling, number of kernel rows per ear and number of kernels per row in hybrids. When the effects of crosses was partitioned into lines, testers and line x tester partitioned into lines, testers and line x tester effects, the means recorded non-significant differences for all the characters except shelling percentage. In testers, the mean sum of squares was positively non-significant for all the characters except days to 50% silking and protein content (%). The interaction effects (lines x testers) were found to be significant for maturity, plant height, ear height, ear length, ear girth, 100-seed weight, shelling percentage, protein content (%) and grain yield per plant. Thus it reveals the presence of
significant variability in the material studied. Components of genetic variation revealed that the estimates of SCA variance were greater than GCA variance for all the characters studied suggesting the predominance of non-additive gene action in expression of various characters. This showed the possibility of exploiting these traits through heterosis breeding. This was further confirmed as $\sigma^2_{gca}/ \sigma^2_{sca}$ ratio is less than unity for all the characters. Similar results were reported by Bupesh Kumar et al., (2015).

Additive component of genetic variance is fixable through normal selection procedures, where as non-additive component is not fixable and its presence for the controlling traits necessitates exploitation of hybrid vigour through heterosis breeding. Ravi and Chikkalingaiah (2012) and Jain and Bharadwaj (2014) also identified good general combiners and superior hybrids in quality protein maize. In the present study, the line, DQL685 (Orange) -18-2 and tester DMRQPM-58 possessed low per se and turned out to be good general combiners for days to flowering and maturity and contributed maximum favourable genes for earliness. Thus, they can be used as potential donors for inducing earliness. Similar results were reported by Bhavana et al., (2011) and Haydar et al., (2014) who reported additive gene action for days to 50 per cent flowering.

Grain yield is a complex character and is influenced by number of component traits. DQL 685 (Orange)-18-2 registered high mean grain yield and was also a good combiner as evidenced by its significant gca effects suggesting that for improving grain yield, this parent would play a key role. Such good combiner could also be intercrossed among the genotypes so as to develop high yielding composites (Table 2). The parents with high gca could produce superior segregates in the $F_2$ as well as in later generations. Jebaraj et al., (2010) emphasized that the selection of parents with good gca was a prime requisite for any successful breeding programme especially for heterosis breeding.

The sca effects are the manifestation of non-additive components of genetic variation and are highly valuable for discrimination of crosses for their genetic worth as breeding material. The significance of sca effects elucidates the presence of genetic diversity among the breeding material tested and illustrated the contribution of dominance and epistatic effects which is non fixable in nature and is a chief cause of heterosis. Earliness is a desirable character as these hybrids mature early and mostly suited for rainfed and low rainfall areas and also intercropping. In the present investigation also, the crosses, DQL 621-1-1 x DMRQPM 58 and DQL641-4-2 x DMRQPM-58 exhibited significant negative sca for earliness and is resultant of non-additive gene action which could be improved through suitable population improvement programme in addition to utilizing them in heterosis breeding. Similar results were in conformity with of Praveen Kumar et al., (2014), Rajitha et al., (2014) and Bupesh Kumar et al., (2015) who reported non-additive gene action for days to maturity. The cross, DQL599(U)-4-2 x DMRQPM 03-124 recorded negative significant sca effects for days to 50% tasseling and days to 50% silking.
Table 1 Analysis of variance for combining ability for grain yield and its component characters in quality protein maize

| Source of variation | d.f | Days to 50% tasseling | Days to 50% silking | Days to maturity | Plant height (cm) | Ear height (cm) | Ear length (cm) | Ear girth (cm) | Kernel rows per ear | Kernels per row | 100 seed weight (g) | Shelling percentage | Protein content | Yield per plant (g) |
|---------------------|-----|-----------------------|---------------------|------------------|------------------|-----------------|-----------------|---------------|----------------------|----------------|---------------------|-------------------|---------------|-------------------|
| Replicates          | 2   | 2.38                  | 4.62                | 3.34             | 8.01             | 44.54           | 1.90            | 0.19          | 1.29                 | 4.26           | 0.43                | 0.51              | 0.072         | 20.81             |
| Genotypes           | 34  | 10.58                 | 10.63               | 36.83            | 1028.68          | 167.12          | 16.37           | 7.78          | 15.37                | 164.46         | 17.06               | 86.27             | 19.59         | 739.79            |
| Parents             | 10  | 13.52                 | 12.02               | 21.35            | 1267.15          | 239.42          | 13.74           | 6.91          | 9.76                 | 67.88          | 6.86                | 35.25             | 3.81          | 272.28            |
| Parent vs crosses   | 1   | 66.43                 | 47.13               | 531.39           | 15015.93         | 113.01          | 328.71          | 194.91        | 356.59               | 4336.55         | 138.30              | 46.23             | 419.46        | 11452.85          |
| crosses             | 23  | 6.883                 | 8.44**               | 22.05*           | 316.86***        | 138.03***       | 3.93***         | 1.33*         | 2.98                 | 25.06          | 16.22***            | 111.29***         | 9.06***       | 477.27***         |
| Lines               | 7   | 6.42                  | 7.68                | 19.73            | 235.92           | 194.27          | 5.96            | 1.78          | 3.71                 | 33.01          | 10.40               | 197.62*           | 4.69          | 480.58            |
| Testers             | 2   | 19.34                 | 24.50*              | 0.09             | 651.93           | 171.16          | 1.76            | 0.40          | 6.54                 | 8.84           | 7.93                | 101.87            | 33.45*        | 465.28            |
| Lines × Testers     | 14  | 5.33                  | 6.53                | 26.35*           | 309.47***        | 105.18***       | 3.23*           | 1.24*         | 2.11                 | 23.40          | 20.32***            | 69.47***          | 7.77***       | 477.33***         |
| Error               | 46  | 4.07                  | 3.63                | 11.28            | 54.55            | 16.68            | 1.33            | 0.62          | 2.32                 | 15.80          | 3.35                | 1.34              | 0.013         | 14.71             |
| σ²gca               |     | 0.003                 | 0.43                | 0.714            | 1.55             | 1.03             | 0.31            | 0.001         | 0.33                 | 0.79           | 0.40                | 0.26              | 0.022         | 0.84              |
| σ²sca               |     | 0.42                  | 0.96                | 5.02             | 84.97            | 29.50            | 0.63            | 0.206         | -0.06                | 2.53           | 5.65                | 22.70             | 0.115         | 154.20            |
| σ²gca/σ²sca         |     | 0.007                 | 0.44                | 0.14             | 0.018            | 0.034            | 0.49            | 0.009         | -5.5                 | 0.31           | 0.07                | 0.011             | 0.191         | 0.005             |

* and ** significant at 5 and 1 per cent level respectively.
### Table 2: Top ranking cross combinations based on Per se performance, SCA, GCA effects and Heterosis

| Characters          | Lines                           | Good general combiners | Per se performance of the best crosses | Good specific combiners | Heterotic combinations |
|---------------------|---------------------------------|------------------------|----------------------------------------|-------------------------|------------------------|
| Days to 50%         | DQL 685 (Orange) -18-2 (1.20)   | DMRQPM-58 (-0.93*)     | DQL05(Orange)-2-1 x DMRQPM 58         | (DQL599 (U))-4-2 x DMRQPM 03-124 (-2.62*) | 1. DQL 599(U)-4-2 x DMRQPM 58 (7.84**) |
| Days to 50%         | DQL 685 (Orange) -18-2 (1.40*)  | DMRQPM-58(1.08)        | DQL05(Orange)-2-1 x DMRQPM 58         | (DQL599 (U)-4-2 x DMRQPM 03-124 (2.94*) | 1. DQL599(U)-4-2 x DMRQPM 03-102(8.50**)  |
| Plant height (cm)   | DQL 685 (Orange) -18-2 (1.97)   | DMRQPM -58(0.05)       | DQL 621-1-1 x DMRQPM-58 (102)         | 1. DQL 621-1-1 x DMRQPM-102(-5.26**) | DQL599(U)-4-2 x DMRQPM 58(11.91**)       |
| Days to maturity    | DQL 685 (Orange) -18-2 (1.97)   | DMRQPM -58(0.05)       | DQL 621-1-1 x DMRQPM-58 (102)         | 1. DQL 621-1-1 x DMRQPM-102(-5.26**) | 2.DQL 641-4-2 x DMRQPM-58(-4.61*)        |
| Plant height (cm)   | 1. DQL596 (U) -2-1-1 (7.91**)   | DMRQPM-03-124(5.77**)  | 1.DQL599(U)-4-2xDMRQPM 03-102 (108.33) | 1.DQL599(U)-4-2 x DMRQPM 03-102(10.23*) | 1.DQL596(U)-2-1-1 x DMRQPM 03-124(11.70**) |
|                    | 2. DQL 639 -1-7(5.47*)          |                        | 2.DQL641-4-2xDMRQPM-03-124(140)       | 2.DQL641-4-2 x DMRQPM 03-124(12***)     | 2.DQL641-4-2 x DMRQPM 03-124(11.70**)    |
|                    |                                 |                        | 3.DQL596(U)-2-1-1 x DMRQPM 03-124(138.33) | 3.DQL596(U)-2-1-1 x DMRQPM 03-124(9.77**) | 2.DQL641-4-2 x DMRQPM 03-124(11.70**)    |
| Ear height (cm)     | DQL596 (U) -2-1-1(8.4***)       | DMRQPM-03-124(2.58**)  | 1.DQL685(Orange)-18-2 x DMRQPM 58(63.33) | 1.DQL596(U)-2-1-1 x DMRQPM 03-124(6.75*) | DQL 621-1-1 x DMRQPM 03-102(2.15)         |
|                    |                                 |                        | 2.DQL 621-1-1 x DMRQPM 58(62.33)      | 2.DQL599(U)-4-2 x DMRQPM 03-124(6.75*) |                          |
|                    |                                 |                        | 3.DQL599(U)-4-2 x DMRQPM 03-102(60.67) | 3.DQL596(U)-2-1-1 x DMRQPM 03-124(9.77**) |                          |
| Ear length (cm)     | DQL596 (U) -2-1-1(1.60***)      | DMRQPM -58(0.26)       | 1.DQL 621-1-1 x DMRQPM 03-102(15.03)  | 1.DQL 639-1-7 x DMRQPM 58(23.59***)     |                          |
|                    |                                 |                        | 2.DQL 685(Orange)-18-2 x DMRQPM 03-124(15.67) | 2.DQL 621-1-1 x DMRQPM 03-124(32.05***) |                          |
| Ear girth (cm)      | 1.DQL505 (Orange) -2-1(0.56)    | DMRQPM-58(0.12)        | 1.DQL 685(Orange)-18-2 x DMRQPM 03-124(12.97) | 3. DQL641-4-2 x DMRQPM 58(63.33)       |                          |
|                    | 2.DQL 639 -1-7(0.40)            |                        | 2.DQL505(Orange)-2-1 x DMRQPM 58(13.33) | 4.DQL599(U)-4-2 x DMRQPM 03-102(5.13**) |                          |
|                    |                                 |                        |                                         | 5.DQL599(U)-4-2 x DMRQPM 03-102(8.97**) |                          |

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**Note:** The table presents various combinations based on per se performance, SCA, GCA effects, and heterosis. The entries include days to mat, silking, characters, and testes results. The table highlights the top-ranking crosses with their performances, including specific and general combiner effects, and heterotic combinations. The data is derived from specific agricultural studies, focusing on plant and ear characteristics such as height, length, and girth.
| Kernel rows per ear | Nil | Nil | 1.DQL 685(Orange)-18-2 x DMRQPM 03-124(15.33) | Nil | 1.DQL505(Orange)-2-1 x DMRQPM 58(4.55**) |
|---------------------|-----|-----|-----------------------------------------------|-----|------------------------------------------|
| Kernels per row     | DQL 639 -1-7(3.50**) | DMRQPM-03-102(0.86*) | 1.DQL 621-1-1 x DMRQPM 03-102(37) | 2.DQL 685(Orange)-18-2 x DMRQPM 03-124(38) | 1.DQL 621-1-1 x DMRQPM 03-102(19.35**) |
|                     |     |     | 2.DQL 599(U)-4-2 x DMRQPM 58(32.33)         | 1.DQL599(U)-4-2 x DMRQPM 58(4.45**) | 2.DQL 621-1-1 x DMRQPM 03-102(19.35**) |
| 100 seed weight (g) | Nil | DMRQPM -03-102(0.91*) | 1.DQL 621-1-1 x DMRQPM 03-102(88.91) | 2.DQL 685(Orange)-18-2 x DMRQPM 03-124(88.99) | 1.DQL685(Orange)-18-2 x DMRQPM 58(6.14**, 2.96, 6.92**, 6.96**) |
| Shelling percentage | DQL 639 -1-7 (3.83**), (DQL 596(U) 2-1-1(2.34**) | Nil | 1.DQL 621-1-1 x DMRQPM 03-102(27.50**) | 2.DQL 685(Orange)-18-2 x DMRQPM 03-124(2.75**, 2.52**) | 1.DQL 621-1-1 x DMRQPM 03-102(19.35**) |
|                     |     |     | 2.DQL 685(Orange)-18-2 x DMRQPM 03-124(88.99) | 1.DQL 621-1-1 x DMRQPM 03-124(13.15) | 2.DQL 685(Orange)-18-2 x DMRQPM 03-124(8.45**) |
| Protein content     | 1.DQL 639 -1-7 (0.46**) | DMRQPM-03-124(1.35**) | 1.DQL599(U)-4-2 x DMRQPM 03-124(13.15) | 2. DQL 639-1-7 x DMRQPM 03-102(13.01) | 1.DQL599(U)-4-2 x DMRQPM 03-124(0.45**) |
|                     | 2.DQL 685 (Orange)-18-2(1.07**) |     | 2.DQL 685(Orange)-18-2 x DMRQPM 03-124(97.17) | 1.DQL 685(Orange)-18-2 x DMRQPM 03-124(0.45**) | 1.DQL 621-1-1 x DMRQPM 03-102(19.49**) |
|                     | 3.DQL 596 (U) -2-1-1(0.31**) |     | 2.DQL 639-1-7 x DMRQPM 03-102(99.27) | 2.DQL 621-1-1 x DMRQPM 03-102(99.27) | 2.DQL 685(Orange)-18-2 x DMRQPM 03-124(0.45**) |
| Yield per plant (g) | 1.DQL685 (Orange)-18-2(8.29**) | DMRQPM -03-124(5.77**) | 1.DQL599(U)-4-2 x DMRQPM 58(97.17) | 2.DQL 621-1-1 x DMRQPM 03-102(99.27) | 2.DQL 685(Orange)-18-2 x DMRQPM 58(99.33) |
|                     |     |     | 1.DQL599(U)-4-2 x DMRQPM 58(97.17) | 2.DQL 621-1-1 x DMRQPM 03-102(99.27) | 3.DQL 641-4-2 x DMRQPM 58(99.33) |
|                     |     |     | 2.DQL 621-1-1 x DMRQPM 03-124(17.66**) | 3.DQL 685(Orange)-18-2 x DMRQPM 03-124(17.66**) | 4. DQL 685(Orange)-18-2 x DMRQPM 03-124(15.20**) |
The crosses DQL 596(U)-2-1-1 x DMRQPM 03-124, DQL599 (U)-4-2 x DMRQPM 03-102 and DQL641-4-2 x DMRQPM 03-124 exhibited significant positive sca effect for plant height, ear height. The crosses, DQL641-4-2 × DMRQPM 58 and DQL 685(Orange)-18-2 × DMRQPM 03-124 recorded significant positive significant sca effects for protein content and grain yield per plant. These hybrids exhibited 15.20 and 19.20 per cent superiority of grain yield over the check hybrid, Vivek QPM 9. Many of the crosses were from either one of the parents with high and significant gca and hence these crosses could be utilized for heterosis breeding. Further, Jebaraj et al., (2010) reported that the expression of high positive sca effects might be due to dominant x recessive interactions. These hybrids were expected to produce desirable segregants in the subsequent generations and could also be improved through recombination breeding.

The commercial hybrid, Vivek QPM 9 was used as a standard check. The hybrids, DQL 599(U)-4-2 x DMRQPM 58 had significant standard heterosis for maturity, DQL596 (U)-2-1-1 × DMRQPM 03-124 for plant height. The crosses DQL641-4-2 × DMRQPM-58, DQL 621-1-1 × DMRQPM 03-102, DQL599 (U)-4-2 × DMRQPM 58 and DQL 685(Orange)-18-2 × DMRQPM 03-124 recorded significant positive standard heterosis of 19.20, 19.12,16.61, and 15.20 respectively for grain yield. The cross, DQL641-4-2 × DMRQPM -58 showed significant standard heterosis for grain yield which was accompanied by significant standard heterosis in ear length, ear girth, number of kernel rows per ear, number of kernels per row, 100 seed weight and shelling percentage. In cross DQL599(U)-4-2 x DMRQPM 58, the significant standard heterosis for grain yield was accompanied by significant standard heterosis in days to 50 per cent tasseling, days to 50 per cent silking, days to maturity, ear length, 100 seed weight and shelling percentage and protein content. Patel et al., (2016), Malik et al., (2004) and Vijay Bhaskar Reddy (2007) recorded positive significant standard heterosis for grain yield per plant in maize.

To develop a commercial hybrid, per se performance, sca effects and the extent of heterosis are chiefly considered (Murali Krishna et al., 2012). In the present study also, the hybrids were evaluated on the basis of the above said three parameters. Among the 24 hybrids, DQL599(U)-4-2 × DMRQPM 58, DQL 621-1-1 × DMRQPM 03-102, DQL641-4-2 × DMRQPM 58, DQL 685(Orange)-18-2 × DMRQPM 03-124 had significant per se performance, sca effects and standard heterosis for grain yield and its contributing characters (Table 2). These hybrids are of considerable practical importance which was proved to be superior over popular commercial hybrid, Vivek QPM 9. These crosses may be advanced for isolation of homozygous inbred lines for use in breeding programmes or may be used as single cross hybrids after evaluation in multi-location trials.

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