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Identification and genetic estimation of nutritional parameters of QPM hybrids suitable for animal feed purpose

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Abstract

Maize plays a significant role in human as food and livestock nutrition as feed. Quality protein maize (QPM) contains, in general, 55% more tryptophan and 30% more lysine in protein than that of normal maize. The QPM hybrids are rich in nutrition with higher biological value (80%) and have more balanced amino acid composition than normal maize, and if, fed to animal that improves health and milk production. In the present experiment, attempt were made to develop QPM hybrids using eight QPM inbreds lines, 56 single cross hybrids including reciprocals were developed using Griffing (1956) full diallel to estimate the genetic components and heterosis for quality parameters of grain used for feed purpose. General combining ability and specific combining ability effect were significant for all the quality traits. The parents VQL-1 and BQPM-4 were found to be good general combiner for quality traits. The variance due to dominance effects were found to be much higher compared to the variance due to additive effects, signifying the utility of heterosis breeding in the QPM genotypes. In case of reciprocal crosses it is governed by dominance effect. The hybrids identified as good performers were VQL-1 x VQL-2 and CML-161 x VQL-5 for protein content; BQPM-4 x VQL-1 for tryptophan content; BQPM-2 x VQL-2 for starch content; BQPM-4 x VQL-5, HKI-163-1-2 x VQL-2 and VQL-1 x VQL-2 for sugar content. These hybrids may be utilized for production of grain, which is used for feeding livestock and monogastric animals.

Keywords: Diallel, GCA, Heterosis, QPM, SCA

Abbreviations: ANOVA: Analysis of variance; **CD:** Critical difference; **ck1:** First check; **ck2:** Second check; **df:** Degree of freedom; **F_1s:** First filial generation hybrids; **GCA:** General combining ability; **p:** Probability; **q/ha:** Quintal/ hectare; **QPM:** Quality protein maize; **RCA:** Reciprocal combining ability; **SCA:** Specific combining ability; **SE:** Standard error

Introduction

Maize is known as the king of feed ingredients. It plays a significant role in human as food and livestock nutrition as feed (Bantte and Prasanna, 2004; Singh *et al.*, 2013). The grain can contribute about 30 percent protein, 60 percent energy and 90 percent starch in an animal's diet (Dado, 1999). Out of the total maize grain produced, about 70-80 percent used as a feed in the world. In India, out of total grain production, about 12% is used as animal feed, 49% as poultry feed, 25% as food and remaining used as starch, brewery and seed (Kaul *et al.,* 2009; Singh *et al.*, 2013; Katoch and Kumar, 2014; Kumar *et al.*, 2014a). The normal maize grain contains 8 to 9%t protein, low in essential amino acids (lysine and tryptophan) i.e., below nutritional requirements for monogastric animals (FAO/ WHO/UNO, 1985) and low biological value between 40-57% (Bressani, 1992). Therefore, utilizing QPM grain as feed may be the solution to provide better nutrition to livestock and monogastric animals. Mutant maize germplasm has opaque-2 gene which changed the amino acid composition of the endosperm protein enhancing lysine and tryptophan and ultimately its nutritional value (Mertz *et al.*, 1964). The studies indicated that QPM protein contains, in general, 55% more tryptophan and 30% more lysine than that of normal maize. The QPM lines/hybrids are rich in nutrition with higher biological value (80%) and more balanced amino acid composition than normal maize (Mertz *et al.,* 1964), and if, fed to animals that improves health and milk production (Kumar *et al.*, 2014b). One of the major difficulties in more widespread planting of QPM is lack of information on nutrition and the utilization of QPM grain in animal diets. Keeping this view in mind the present experiment was conducted to identify QPM hybrids with rich in amino acids, starch and sugar in grain to be used as feed purpose for livestock and monogastric animals.

Materials and Methods

The experimental materials consisted of 8 QPM inbred lines (BQPM 2, BQPM 4, CML-161, HKI 163-1-2, VQL 1, VQL 2, VQL 5, VQL 17), 56 F_1s and 2 checks (Shaktiman 4 and Vivek QPM-9). The seeds of the 8 QPM inbred lines obtained from Maize Research Scheme, BAU, Ranchi were crossed in full diallel fashion (Griffing, 1956) to develop 28 F_1 hybrids, 28 F_1 reciprocal hybrids. The seeds were sown (July 2010) in RBD with 3 replications during *kharif* 2010. The genetic materials were sown in 75 x 25 cm spacing with recommended agronomic practices. From each entry five random plants were selfed for quality analysis and yield (q/ha) was calculated from grain yield/plot.

The selfed ears were hand shelled and grain samples from each ear were collected by the quartering method. The kernel protein was determined by Micro Kjeldahl method (Nelson and Sommers, 1973), kernel tryptophan content by standard papain hydrolysis method, lysine content by Calorimeter method, starch content by Anthrone reagent method and kernel sugar content by Nelson Somogyi method. The average of F_1 values over replications were used for the estimation of heterosis and expressed as standard commercial heterosis. The ANOVA for combining ability and estimation for other genetic components for parents and crosses were obtained following Griffing (1956), by using INDOSTAT 7.5 software.

Results and Discussion

Variance component and per se performance: The results of combining ability analysis showed significant GCA, SCA and RCA (Table 1). This suggests significant difference among the GCA effects of 8 parents, SCA effect of 28 crosses and RCA effect of 28 reciprocal crosses. The result also indicated role of additive genetic and non - additive genetic component in the inheritance of characters in QPM maize. The presence of marked additive and non-additive gene effects indicated the need for exploiting both fixable and non-fixable components of genetic variance for increasing productivity in maize (Amiruzzaman *et al.,* 2010). The variance due to dominance effects were found to be much higher compared to the variance due to additive effects, signifying the utility of heterosis breeding in the QPM genotypes for the characters under study except lysine content where higher magnitude of additive variance suggested the predominance of additive gene action for this trait. But in case of reciprocal crosses it is governed by dominance effect *i.e.* the choice of female parent also playing the role on estimation of gene action for lysine content (Table 2). The superiority of SCA may be due to complementary type of gene action or involvement of non-allelic interaction of fixable and non-fixable genetic variance. These types of findings are also reported by Muthuramu *et al.* (2010), and Bhatnagar *et al.* (2004). The predominance of non-additive gene action for yield attributes and quality characters was also reported by Hossain *et al.* (2007), in QPM maize. In a study Hallauer and Miranda Filho (1988) reported that non-additive gene effects seem to be small, but they may be important for specific combinations.

Identification of good combining parents: The potentiality of a genotype to be used as a parent in hybridization, or in a cross to be used as a commercial hybrid, may be judged by comparing the *per se* performance of the parents, the F_1 value and the combining ability effects (Venkateshwaralu and Singh, 1982). The partitioning of cross combinations exhibiting significant SCA and RCA effects with desirable *per se* performance for different traits involved parents with good × good, good × poor, poor × good and poor × poor combining abilities (Table 3). Parents with positive signi-

Table 1. ANOVA of combining ability for quality parameters and grain yield

Sources		Mean sum of square					
	df	Protein content (%)	Tryptophan content (%)	Lysine content (%)	Starch content (%)	Sugar content (%)	Grain yield (q/ha)
GCA	2	0.185**	0.0047**	0.062**	4.032**	0.324**	56.02**
SCA	63	0.457**	0.003**	0.032**	6.851**	0.165**	1005.5**
RCA	63	0.213**	0.0024**	0.026**	10.61**	0.152**	110.52**
Error	126	0.0010	0.00004	0.005	0.001	0.00006	2.14
Estimate of variance component							
ó^{2}GCA		0.001	0.0002	0.0036	0.251	0.020	3.37
ó^{2}SCA		0.456	0.0029	0.0027	6.850	0.165	1003.36
ó^{2}RCA		0.212	0.0023	0.0215	10.614	0.152	108.37
ó^{2}GCA/SCA		0.002	0.1000	1.3300	0.036	0.121	0.0033
ó^{2}Error		0.001	0.00004	0.0051	0.001	0.00006	2.149

*, **Significant at pd"0.05 and ≤"0.01, respectively

-ficant value of GCA effect were considered as good combiner (VQL-1 for all the traits, HKI-163-1-2 for protein & sugar content, CML-161 for tryptophan, lysine & starch content, VQL-2 for protein content, VQL-5 for starch content and BQPM-4 for grain yield (q/ha)) while parents exhibiting low value of GCA effect with any sign of GCA but giving high *per se* performance in their crosses were termed as poor (Table 3) combiner.

Maize hybrids with good × good combining parents: These parents are proven to be worthy of exploitation in varietal development programme. The cross combination of the above parents including reciprocal (good ×good) which showed significant SCA effects was VQL-1 x VQL-2 for protein content, whereas none of the cross found to be significant for RCA effect (Table 4). If these hybrids are utilized in pedigree breeding, there is a possibility of isolating high yielding genotypes (Manonmani and Faslullah, 2003) with rich in nutritional quality (Table 4-5). But, good x good parents were not always giving superior performance because GCA effects of the parents did not reflect in their SCA effect for all the traits (Ivy and Howlader, 2000). Moreover Amiruzzaman *et al*. (2010) 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 good and poor GCA crosses.

Maize hybrids with good × poor or poor × good combining parents: The cross combinations (Table 4) using one good and one poor combiners (good × poor or poor × good) showed highly significant SCA effect as well as significant *per se* performance over mean or either of checks were BQPM-2 x HKI-163-1-2, BQPM-2 x VQL-1, BQPM-2 x VQL-2, BQPM-4 x VQL-1, BQPM-4 x VQL-2, CML-161 x HKI-163-1-2, VQL-1 x VQL-17 for protein content; BQPM-4 x VQL-1 for tryptophan content; HKI-163-1-2 x VQL-1 for lysine content; BQPM-2 x CML-161, BQPM-2 x VQL-1, BQPM-4 x CML-161, CML-161 x VQL-2, HKI-163-1-2 x VQL-1, HKI-163-1-2 x VQL-5, VQL-1 x VQL-17, VQL- 2 x VQL-5 for starch content; BQPM-4 x HKI-163-1-2, BQPM-4 x VQL-5, CML-161 x HKI-163-1-2, CML-161 x VQL-1, CML-161 x VQL-5, HKI-163-1-2 x VQL-2, VQL-1 x VQL-2 for sugar content; BQPM-2 x BQPM-4, BQPM-4 x VQL-17, HKI-163-1-2 x VQL-1, VQL-1 x VQL-2, VQL-1 x VQL-5, VQL-1 x VQL-17 for grain yield. Besides, there were several reciprocal crosses (Table 5) found to be

Table 2. *Per se* performance and GCA effects of parents for quality parameters and grain yield

Parents	**Protein content (%)**	**Tryptophan content (%)**	**Lysine content (%)**	**Starch content (%)**	**Sugar content (%)**	**Grain yield (q/ha)**
BQPM-2	8.53(-0.09)**	0.75(0.00)	3.00(0.02)	60.28(-0.57)**	3.55(-0.21)**	31.40(-0.16)
BQPM-4	8.80(-0.04)**	0.76(-0.01)**	3.03(-0.02)	64.50(-0.12)**	3.87(-0.05)**	31.8(1.27)**
CML-161	9.18(-0.10)**	0.85(0.02)**	3.35(0.06)**	66.60(0.44)**	3.74(-0.02)**	31.3 (0.28)
HKI-163-1-2	10.62(0.10)**	0.70(-0.03)**	2.79(-0.09)**	64.50(-0.21)**	3.62(0.27)**	30.5(-1.07)**
VQL-1	10.49(0.21)**	0.83(0.03)**	3.28(0.10)**	65.21(0.86)**	3.84(0.03)**	30.9(1.54)**
VQL-2	10.71(0.04)**	0.79(-0.01)**	3.10(-0.06)**	63.68(-0.57)**	3.94(-0.01)**	30.6(-0.24)
VQL-5	10.31(-0.06)**	0.76(0.00)	3.02(0.00)	66.04(0.31)**	4.01(0.09)**	30.0(-1.11)**
VQL-17	10.53(-0.06)**	0.77(-0.01)**	3.00(-0.02)	63.21(-0.14)**	4.19(-0.09)**	31.4(-0.51)
Mean	9.90	0.77	3.07	64.25	3.85	31.0
CD at 5%	0.13	0.025	0.28	0.13	0.03	5.43
For genetic component comparison						
SE(gi) ±	0.0077	0.0015	0.016	0.0079	0.0019	0.32
SE(gi-gj) ±	0.0011	0.0022	0.025	0.011	0.0028	0.48
CD at 5%	0.013	0.002	0.031	0.015	0.0037	0.63
CD at 1%	0.017	0.003	0.041	0.020	0.0048	0.82

*, **Significant at ≤”0.05 and ≤”0.01, respectively. Figure in parenthesis are GCA effect value.

Table 3. Parent identified as good combiner from GCA effect and per se performance values

Parents	**Protein content (%)**	**Tryptophan content (%)**	**Lysine content (%)**	**Starch content (%)**	**Sugar content (%)**	**Grain yield (q/ha)**
Good combiner	VQL-1, HKI-163-1-2, VQL-2	VQL-1, CML-161	CML-161, VQL-1	CML-161, VQL-1, VQL-5	HKI-163-1-2, VQL-1, VQL-5	VQL-1, BQPM-4

be significant for RCA effect with significantly high *per se* performance over mean or either of checks for different traits; they are CML-161 x BQPM-2, VQL-1 x BQPM-4, VQL-5 x VQL-1 for tryptophan content; VQL-1 x BQPM-4, VQL-1 x HKI-163-1-2 for the lysine content; CML-161 x BQPM2, CML-161 x BQPM-4, VQL-1 x BQPM-4, VQL-17 x CML-161, VQL-1 x HKI-163-1-2, VQL-5 x VQL-1 for starch content; HKI-163-1-2 x CML-161, VQL-1 x CML-161 for sugar content; VQL-17 x BQPM-4, VQL-2 x VQL-1 for grain yield. The significant difference in RCA justified the importance of choice of the female parent during hybridization. These hybrids formed by good × poor or poor × good may throw transgressive segregants in their segregating generations for the respective traits. To obtain desirable early segregants, biparental mating or reciprocal recurrent selection method can be followed.

Maize hybrids with poor x poor combining parents: The crosses of both poor combiners (poor x poor) with highly significant SCA effect as well as significant *per se* performance over grand mean or either of checks were BQPM-2 x BQPM-4, BQPM-2 x VQL-17, BQPM-4 x CML-161, CML-161 x VQL-5, CML-161 x VQL-17, HKI-163-1-2 x VQL-5 for protein content; BQPM-2 x BQPM-4, BQPM-4 x VQL-2 (at per with mean) for tryptophan content; BQPM-2 x HKI-163-1-2 (at per with mean) for lysine content; BQPM-2 x BQPM-4, BQPM-2 x VQL-2, BQPM-2 x VQL-17, BQPM-4 x VQL-17 for starch content BQPM-2 x VQL-2, B

Table 4. *Per se* performance and SCA effect of selected hybrids for quality parameter and grain yield

Parents	Protein content (%)	Tryptophan content (%)	Lysine content (%)	Starch content (%)	Sugar content (%)	Grain yield (q/ha)
BQPM-2 x BQPM-4	10.62(0.46)**	0.73(0.02)**	2.89(0.02)	64.70(1.30)**	3.54(0.06)**	69.1(12.6)**
BQPM-2 x CML-161	10.54(0.03)	0.73(0.01)**	2.89(0.02)	64.71(0.31)**	3.03(0.01)**	56.6(3.75)**
BQPM-2 x HKI-163-1-2	10.94(0.17)**	0.68(0.02)**	2.70(0.11)**	66.25(-1.09)**	3.82(-0.36)**	56.8(-1.51)
BQPM-2 x VQL-1	10.39(0.28)**	0.74(-0.03)**	2.94(-0.10)**	67.60(1.08)**	3.87(-0.23)**	50.9(2.26)**
BQPM-2 x VQL-2	10.60(0.39)**	0.64(-0.04)**	2.56(-0.08)*	69.22(3.35)**	3.98(0.21)**	52.3(-0.44)
BQPM-4 x CML-161	10.12(0.37)**	0.76(-0.08)**	2.83(-0.24)**	67.70(2.37)**	3.55(-0.08)**	62.7(7.80)**
BQPM-4 x HKI-163-1-2	10.53-0.20**	0.68(-0.03)**	2.83(-0.05)	64.71(-0.45)**	3.99(0.30)**	59.3(-2.48)**
BQPM-4 x VQL-1	10.44(0.19)**	0.78(0.02)**	2.92(0.04)	66.93(-1.62)**	3.73(0.06)**	59.6(2.65)**
BQPM-4 x VQL-5	9.82(0.35)**	0.67(-0.05)**	2.73(-0.13)**	60.33(-1.01)**	4.85(0.04)**	53.7(-4.84)**
BQPM-4 x VQL-17	10.29(-0.34)**	0.69(0.04)**	2.73(0.14)**	67.49(1.90)**	4.63(-0.02)**	57.7(7.10)**
CML-161 x HKI-163-1-2	10.93(0.15)**	0.66(-0.04)**	2.69(-0.09)*	68.71(-3.41)**	4.63(0.09)**	57.3(2.88)**
CML-161 x VQL-1	10.54(-0.22)**	0.70(0.02)**	2.74(-0.07)	69.52(-0.87)**	3.97(0.09)**	59.4(0.90)
CML-161 x VQL-2	9.83(0.22)**	0.84(-0.01)**	3.12(-0.07)	67.48(0.96)**	4.01(-0.40)**	58.7(7.72)**
CML-161 x VQL-5	11.50(0.14)**	0.75(0.02)**	3.10(0.06)	70.72(1.29)**	4.00(0.39)**	62.6(2.93)**
HKI-163-1-2 x VQL-1	10.60-0.58**	0.65(0.04)**	2.65(0.08)*	66.71(1.18)**	3.01(0.21)**	60.2(4.07)**
HKI-163-1-2 x VQL-2	9.87(-0.33)**	0.63(-0.03)**	2.54(-0.10)**	60.63(-0.94)**	4.82(0.36)**	55.6(1.69)
HKI-163-1-2 x VQL-5	9.65(0.12)**	0.66(0.02)**	2.55(0.04)	65.78(3.11)**	3.88(0.45)**	61.3(5.20)**
VQL-1 x VQL -2	10.65(0.25)**	0.75(-0.04)**	2.94(-0.05)	69.10(-0.12)**	4.81(0.47)**	57.0(7.33)**
VQL-1 x VQL-5	9.74(0.14)**	0.77(0.00)	3.05(0.07)	65.27(1.25)**	3.32(-0.36)**	54.8(6.41)**
VQL-1 x VQL-17	10.41(0.16)**	0.73(-0.07)**	2.93(-0.19)**	64.22(1.38)**	3.49(-0.13)**	61.0(3.28)**
VQL-2 x VQL-5	9.74(-0.56)**	0.73(0.00)	2.90(-0.02)	67.27(0.14)**	3.49(-0.30)**	61.9(4.74)**
Mean	10.36	0.71	2.83	65.94	3.92	58.3
Shaktiman-4	9.84	1.04	4.13	64.83	4.63	75.7
Vivek QPM-9	9.04	0.74	2.89	61.62	4.12	57.8
CD at 5%	0.13	0.025	0.28	0.13	0.03	5.43
For genetic component comparison						
SE(sij) ±	0.020	0.0045	0.044	0.021	0.0051	0.86
SE(sij-sik) ±	0.030	0.006	0.066	0.031	0.0076	1.28
SE(sij-skl) ±	0.028	0.005	0.062	0.029	0.0070	1.19
CD at 5%	0.039	0.0079	0.08	0.041	0.010	1.70
CD at 1%	0.051	0.010	0.105	0.053	0.013	2.21

*, **Significant at ≤”0.05 and ≤”0.01, respectively. Figure in parenthesis are SCA effect value

QPM-2 x VQL-17, CML-161 x VQL-17 for sugar content; BQPM-2 x CML-161, CML-161 x HKI-163-1-2, CML-161 x VQL-2, CML-161 x VQL-5, HKI-163-1-2 x VQL-5, HKI-163-1-2 x VQL-17, VQL-2 x VQL-5, VQL-5 x VQL-17 (at per with mean) for grain yield. Beside this, there were several reciprocal crosses (Table 5) found to be significant RCA effect with significantly high *per se* performance over mean or either of checks for different traits, they are VQL-17 x CML-161, VQL-5 x HKI-163-1-2 for protein content; HKI-163-1-2 x BQPM-4 for tryptophan content; HKI-163-1-2 x BQPM-2, HKI-163-1-2 x BQPM-4, VQL-5 x HKI-163-1-2, VQL-17 x VQL-2 (at per with mean) for lysine content; BQPM-4 x BQPM-2, VQL-17 x BQPM-2, HKI-163-1-2 x BQPM-4, VQL-2 x BQPM-4 for starch content; BQPM-2, VQL-2 x BQPM-2, VQL-17 x BQPM-2, VQL-17 x CML-161 for sugar content; VQL-17 x VQL-2 for grain yield. Here also, reciprocal differences between the crosses for different traits were observed. For poor x poor combinations, since they involve non-additive gene action, cyclic method of breeding involving selection of desired recombinants and their inter crossing would be more desirable. This type of finding was also reported by Sankarapandian (1986).

Identification of best maize hybrids for different quality traits: High SCA and RCA effects may not be the appropriate choice for heterosis exploitation because hybrid with low mean values may also possess high SCA and RCA effects. Furthermore, heterosis value alone may also mislead the identity of superior hybrids. Exploitation of hybrids for heterosis breeding is best judged by *per se* performance, SCA and RCA effects and magnitude of heterosis. Based on these criteria, the hybrid with significant combining ability effect, high *per se* performance with either of the checks and desirable heterosis were VQL-1 x VQL-2, BQPM-2 x HKI-163-1-2, BQPM-2 x VQL-1, BQPM-2 x VQL-2, CML-161 x VQL-5, BQPM-2 x BQPM-4, BQPM-2 x VQL-17 for protein content, BQPM-4 x VQL-1 for tryptophan content; CML-161 x VQL-5, VQL-1 x VQL-5, BQPM-2 x VQL-1, BQPM-4 x CML-161, CML-161 x VQL-2, HKI-163-1-2 x VQL-5, BQPM-2 x BQPM-4, BQPM-2 x VQL-2, BQPM-2 x VQL-17, BQPM-4 x VQL-17 for starch content; BQPM-4 x VQL-5, CML-161 x HKI-163-1-2, HKI-163-1-2 x VQL-2, VQL-1 x VQL-2 for sugar content; BQPM-2 x BQPM-4, CML-161 x VQL-5, VQL-2 x VQL-5 (at per mean with checks) for grain yield (Table 6). Theses hybrids may be suitable for heterosis breeding since it exhibited desirable mean, SCA effects and standard heterosis. The above said hybrids are highly suitable for commercial exploitation of heterosis. Most of

Table 5. *Per se* performance and RCA effect of selected hybrids for quality parameter and grain yield

Parents	Protein content (%)	Tryptophan content (%)	Lysine content (%)	Starch content (%)	Sugar content (%)	Grain yield (q/ha)
BQPM-4 x BQPM-2	10.16(0.01)	0.74(0.00)	2.96(-0.01)	64.20(1.67)**	3.82(0.17)**	69.1(-3.27)**
CML-161 x BQPM-2	10.85 (-0.02)	0.74(0.01)**	2.93(0.00)	64.75(1.75)**	3.01(-0.14)**	56.6(4.08)**
CML-161 x BQPM-4	10.44(-0.54)**	0.67(-0.04)**	2.79(-0.20)**	67.68(4.61)**	3.53(0.06)	62.7(-0.20)
VQL-1 x BQPM-4	9.93(-0.27)**	0.77(0.07)**	3.04(0.23)**	66.50(0.11)**	3.93(-0.21)**	59.6(1.58)
VQL-17 x BQPM-4	10.33(0.02)	0.69(-0.05)**	2.68(-0.13)**	67.46(-0.35)**	4.27(-0.25)**	57.7(2.90)**
HKI-163-1-2 x CML-161	11.15(-0.23)**	0.68(-0.03)**	2.73(-0.07)	69.15 (-3.42)**	4.13(0.28)**	57.3(0.52)
VQL-1 x CML-161	10.10(-0.70)**	0.72(-0.05)**	2.79(-0.24)**	69.50(-4.79)**	4.00(0.40)**	59.4(0.52)
VQL17 x CML-161	10.33(0.34)**	0.68(-0.01)**	2.77(-0.05)	69.71 (1.30)**	3.98(0.44)**	56.0(-0.07)
VQL-1 x HKI-163-1-2	10.47(-0.48)**	0.68(0.05)**	2.66(0.12)*	66.24(0.26)**	3.93(0.10)	60.2(0.12)
VQL-2 x VQL-1	9.97(-0.11)**	0.77(-0.01)**	2.94(-0.08)	69.23(-0.14)**	4.82(-0.25)**	57.0(3.13)**
VQL-5 x VQL-1	9.80(0.04)	0.76(0.01)**	3.02(-0.03)	65.52(2.27)**	3.50(-0.34)**	54.8(-0.73)
Mean	10.24	0.71	2.84	66.02	3.92	62.9
Shaktiman 4	9.84	1.04	4.13	64.83	4.63	75.7
Vivek QPM-9	9.04	0.74	2.89	61.62	4.12	57.8
CD at 5%	0.13	0.025	0.28	0.13	0.03	5.43
For genetic component comparison						
SE(rij) ±	0.023	0.005	0.050	0.023	0.006	
SE(rij-rkl) ±	0.032	0.006	0.071	0.033	0.008	
CD at 5%	0.045	0.008	0.099	0.040	0.011	
CD at 1%	0.059	0.011	0.128	0.050	0.014	

*, **Significant at ≤”0.05 and ≤”0.01, respectively. Figure in parenthesis are RCA effect value

Table 6. Heterosis (%) over checks for kernel protein, tryptophan, lysine, kernel starch & sugar contents and grain yield for selected hybrids

Crosses	Protein (%)		Tryptophan (%)		Lysine (%)		Starch (%)		Sugar (%)		Grain yield (q/ha)	
	Ck-1	Ck-2	Ck-1	Ck-2	Ck-1	Ck-2	Ck-1	Ck-2	Ck-1	Ck-2	Ck-1	Ck-2
BQPM-2 x BQPM-4	7.89**	17.40**	-30.13**	-1.80	-30.02**	0.00	-0.20*	5.00**	-23.61**	-14.16**	-27.97**	19.64**
BQPM-2 x HKI-163-1-2	11.21**	21.01**	-34.62**	-8.11**	-34.54**	-6.46*	2.20**	7.51**	-17.49**	-7.28**	-20.53**	-1.65
BQPM-2 x VQL-1	5.59**	14.89**	-28.85**	0.00	-28.81**	1.73	4.27**	9.70**	-16.34**	-5.99**	-13.82**	-11.95**
BQPM-2 x VQL-2	7.76**	17.25**	-38.14**	-13.06**	-38.10**	-11.53**	6.78**	12.33**	-14.04**	-3.40**	-32.27**	-9.48**
BQPM-2 x VQL-17	6.78**	16.18**	-39.42**	-14.86**	-33.58**	-5.07	4.44**	9.87**	-13.46**	-2.75**	-16.34**	-13.19**
BQPM-4 x CML-161	2.85**	11.91**	-26.92**	2.70*	-31.56**	-2.19	4.43**	9.86**	-23.33**	-13.83**	0.23	8.52**
BQPM-4 x VQL-1	6.10**	15.44**	-25.32**	4.95**	-29.22**	1.15	3.24**	8.62**	-19.44**	-9.47**	-25.04**	3.16
BQPM-4 x VQL-5	-0.17	8.63**	-35.26**	-9.01**	-33.98**	-5.65*	-6.94**	-2.10**	4.68**	17.64**	-28.18**	-7.14*
BQPM-4 x VQL-17	4.54**	13.75**	-33.65**	-6.76**	-33.82**	-5.42	4.10**	9.52**	0.00	12.38**	-27.87**	-0.14
CML-161 x HKI-163-1-2	11.04**	20.83**	-36.22**	-10.36**	-34.79**	-6.81*	5.98**	11.50**	-0.07	12.30**	-22.10**	-0.82
CML-161 x VQL-2	-0.07	8.74**	-19.55**	13.06**	-24.54**	7.84**	4.09**	9.50**	-13.32**	-2.59**	-19.59**	1.51
CML-161 x VQL-5	16.84**	27.13**	-27.56**	1.80	-24.94**	7.27**	9.09**	14.77**	-13.61**	-2.91**	-9.73**	8.38**
HKI-163-1-2 x VQL-2	0.30	9.14**	-39.10**	-14.41**	-38.42**	-12.00**	-6.48**	-1.62**	4.03**	16.91**	-15.29**	-3.71
HKI-163-1-2 x VQL-5	-1.96**	6.67**	-36.86**	-11.26**	-38.18**	-11.65**	1.47**	6.75**	-16.13**	-5.74**	-30.28**	6.18*
VQL-1 x VQL-2	7.96**	17.47**	-27.56**	1.80	-28.73**	1.85	6.59**	12.14**	3.89**	16.75**	-23.15**	-1.37
VQL-2 x VQL-5	-0.98*	7.74**	-29.49**	-0.90	-29.86**	0.23	3.76**	9.16**	-24.62**	-15.29**	-28.08**	7.14*
VQL-2 x VQL-17	8.06**	17.58**	-39.10**	-14.41**	-37.45**	-10.61**	2.61**	7.95**	-21.89**	-12.22**	-18.01**	24.18**
CD at 5%	0.08	0.08	0.02	0.02	0.16	0.16	0.08	0.08	0.02	0.02	3.21	3.21
CD at 1%	0.10	0.10	0.03	0.03	0.21	0.21	0.10	0.10	0.03	0.03	4.16	4.16

*, **Significant at ≤”0.05 and ≤”0.01, respectively. Ck 1 =Shaktiman-4, Ck 2 =Vivek QPM- 9

the good hybrids were usually generated from the crosses between parents with good and poor GCA. Generally, highest heterosis was observed in crosses in which one of the two parents had poor general combining ability. This indicated the role of both additive and non-additive gene action in producing heterosis. There were also a few hybrids with high heterosis values from the crosses between two parents with good general combining abilities. In many cases, however, the crosses of good x good GCA led to inferior hybrids for many studied traits, indicating epistatic gene actions in controlling these traits. Remaining crosses involving poor combiners suggesting the epistatic gene action, which could be mainly due to genetic diversity in the form of heterozygous loci (Ram *et al*., 1998).

Conclusion

The experimental finding indicated that VQL-1 was the best among eight QPM inbred for quality breeding in maize in relation to protein, tryptophan, lysine, starch and sugar content, while BQPM-4 was the best for grain yield. These inbreds are highly valuable genetic material that could be successfully used for crossing and generation of desirable segregants form improvement of QPM. Out of all the 56 hybrids, the suitable hybrids for grain quality parameters were VQL-1 x VQL-2 and CML-161 x VQL-5 for protein content; BQPM-4 x VQL-1 for tryptophan content; BQPM-2 x VQL-2 for starch content; BQPM-4 x VQL-5, HKI-163-1-2 x VQL-2, VQL-1 x VQL-2 for sugar content.

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