

ESTIMATION OF COMBINING ABILITY INVOLVING QUALITY PROTEIN MAIZE (QPM) INBREDS UNDER TEMPERATE CONDITIONS

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ABSTRACT

Twenty-four quality protein maize (QPM) hybrids were generated by crossing eight QPM lines with three testers to estimate combining ability effects for yield and yield attributing traits. ANOVA for combining ability revealed significant mean squares of GCA and SCA for all the traits in individual and pooled analysis. Non additive gene action played a major role in expression of traits viz., plant height, number of kernel rows cob⁻¹ and number of kernels row⁻¹, 100-grain weight, grain yield plant⁻¹ and protein content. Additive gene action also played a role in expression of traits like days to 50% silking, days to 50% tasseling and ear height. QPM line KDQPM-60 was identified as a good general combiner for grain yield plant⁻¹ followed by KDQPM-21 and KDQPM-50. KDQPM-60 was accompanied with significant and desirable GCA effects for other traits also. Crosses which exhibited highly significant and desirable SCA effects included KDQPM-14×VQL-1, KDQPM-60×VQL-17 and KDQPM-21×VQL-2 for kernel rows cob⁻¹ and KDQPM-50×VQL-1, KDQPM-60×VQL-17 and KDQPM-13×VQL-17 for grain yield plant⁻¹. It can be concluded that the crosses having high SCA effects for grain yield plant⁻¹ and their parents with high GCA can be used directly as donors and exploited for future hybrid breeding programmes.

INTRODUCTION

Maize is the third most important cereal crop after rice and wheat. It belongs to family Poaceae, tribe Maydeae. It is of high significance to both human and animal nutrition due to its demand for food, feed and industrial utilization. However, the normal maize protein is of poor nutritional quality due to a deficiency in two essential amino acids viz., lysine and tryptophan and high leucine-isoleucine ratio. High proportion of zein (seed storage protein of maize) fraction which is completely devoid of lysine and tryptophan is the primary cause of poor protein quality in maize. A reduction in the zein fraction thus results in a proportional elevation of other fractions which are rich in lysine and an elevation of these two amino acids in protein (Vassal, 2000). Therefore, for populations that depend heavily on maize as food source, maize cultivars with an improved amino acid profile are required to be developed. A breakthrough came in the 1960s, with the discovery of the enhanced nutritional quality of the maize mutant opaque2 (Mertz *et al.*, 1964). The opaque2 (o2) gene significantly reduces the level of 22-kD alpha-zeins while increasing the content of non zein proteins particularly, EF-1 alpha, which is positively correlated with lysine content in the endosperm (Habben *et al.*, 1995). The protein quality

of opaque2 maize is 43 per cent higher than that of common maize and 95 per cent of the value of casein (Mertz, 1992).

Globally plant breeders made vigorous efforts to incorporate opaque2 into high yielding commercial cultivars but the numerous agronomic and processing problems associated with opaque2 prevented its acceptance (Glover and Mertz, 1987). It expressed negative pleiotropic effects on the grain quality such as reduced grain yield, soft endosperm, chalky and dull kernel appearance and susceptibility to ear rots and stored grain pests and diseases (Vassal, 2001). The International Maize and Wheat Research Centre (CIMMYT) has developed quality protein maize (QPM) that improves kernel quality characteristics over o2o2 soft genotypes, by introducing modifier genes and selecting for a hard, vitreous endosperm in o2o2 germplasm (Vassal, 2001). Also, the single cross QPM hybrids have become popular among Indian farmers due to their high yield potential and excellent uniformity (Singh *et al.*, 2012). Combining ability is a powerful tool for identifying the best combiners that may be used in crosses either to accumulate productive genes or to exploit heterosis especially, when a large number of advance inbred lines are available and most promising ones are to be selected on the basis of their ability to give superior quality protein maize hybrids (Singh *et al.*, 2012). Krivanek *et al.* (2007)

declared that combining ability is a prerequisite for developing a good economically viable hybrid maize variety. Information on combining ability among maize germplasm is essential in maximizing the effectiveness of hybrid development. General and specific combining ability are due to genes which are largely additive and dominance or epistatic effects respectively (Sprague and Tatum, 1942). Hybrid breeding is imperative to select the cross combinations with high degree of SCA as well as parents with high GCA. The success in commercial production of hybrid QPM maize depends upon the availability of productive diverse QPM inbred lines and clear knowledge of gene action for specific traits. The objectives of the present investigation were to estimate general combining ability (GCA) for eight parents and specific combining ability (SCA) effects for twenty four single cross hybrids and to identify superior quality protein maize hybrids with good yield potential.

MATERIALS AND METHODS

The experiment was conducted by generating twenty four single cross hybrids by line x tester mating design during Kharief 2012 by crossing eight QPM lines with three testers. The QPM lines (KDQPM-13, KDQPM-14, KDQPM-20, KDQPM-21, KDQPM-49, KDQPM-50, KDQPM-58 and KDQPM-60) were crossed with three QPM tester lines viz., VQL1, VQL2 and VQL17 during Kharief 2012. The resulting twenty-four crosses were evaluated in a randomized block design (RBD) with two replications during Kharief 2013 and Kharief 2014 at Dryland (Karewa) Agricultural Research Station. Standard package of agronomic practices were adopted to ensure good crop stand. Observations were recorded on traits viz., days to 50% tasseling, days to 50% of silking, plant height (cm), ear height (cm), number of kernel rows cob⁻¹, number of kernels row⁻¹, 100 grain weight (g), grain yield plant⁻¹(g) and protein content (%). Observational data on days to 50% tasseling and days to 50% silking were recorded on plot basis while data related to other characters were recorded on five randomly selected plants of each row. The mean of five plants was used for all statistical analysis and the recorded data was subjected for analysis of general and specific combining ability analysis as per the procedure of Kempthorne (1957) using statistical software package of Windostat version 9.1.

RESULTS AND DISCUSSION

Analysis of variance (Table 1) revealed significant mean squares for all the traits viz., days to 50% silking, days to 50% tasseling, plant height (cm), ear height (cm), number of kernel row cob⁻¹, number of kernels row⁻¹, 100-grain weight, grain yield plant⁻¹ and protein content (%) over the environments indicating the possibility of carrying out genetic analysis. Significant differences among lines, crosses and lines x testers were observed for all the traits indicating diverse nature of the material. Variation due to interaction effects of lines and testers were also significant for all the traits under study. Analysis of variance for combining ability revealed significant mean squares of GCA and SCA for all the traits in individual as well as pooled analysis. Similar results were observed by Kumar *et al.*, 2013; Krupakar *et al.*, 2013 and Singh *et al.*, 2012. It was found that the non additive gene action played a major role in expression

Table 1: Analysis of variance for different characters in twenty-four QPM cross

Source of variation	d.f.	Days to 50% tasseling	Days to 50% silking	Plant height (cm)	Ear height (cm)	Kernel rows per cob	Kernels per row	100 grain weight (g)	Grain yield per plant (g)	Protein content (%)
		Pooled	Pooled	Pooled	Pooled	Pooled	Pooled	Pooled	Pooled	Pooled
Environments	1	1327.593**	1335.041**	50592.360**	18869.237**	1.181**	149.675**	9.519**	309.350**	0.181**
Replications	1	0.010	0.375	17.543	8.230	0.077	1.023	0.968	26.001	0.021
Replications × environments	1	1.260	1.500	0.339	4.725	0.003	0.974	0.457	3.884	0.0003
Crosses	23	30.640**	28.521**	1368.560**	735.382**	6.911**	92.341**	43.047**	4083.823**	0.789**
Lines	7	91.166*	98.375*	2702.331*	1338.545*	23.501*	190.000*	115.001*	9102.70*	1.966*
Testers	2	31.343	28.690	618.567	1305.800	0.203	23.20	24.679	181.286	0.262
Line × tester	14	21.642**	18.458*	808.817**	352.312**	8.116**	65.000**	38.776**	3169.133**	0.670**
Crosses × environments	23	0.550	0.563	26.901**	32.055**	0.032	1.059**	0.646**	27.945**	0.043
Lines × environments	7	0.712	1.113*	42.697	26.094	0.037	1.426	0.736	77.530**	0.052
Testers × environments	2	0.875	0.541	2.198	0.173	0.040	0.009	0.388	12.649	0.003
Lines × Testers × environments	14	.874*	1.2300*	22.532**	39.589**	0.112**	1.026**	0.638**	19.675**	0.044*
Error Pooled	46	0.396	0.524	4.620	2.061	0.034	0.272	0.248	6.666	0.017

**, * Significant at 5 and 1 percent levels, respectively

Table 2: Estimates of genetic components of variance and degree of dominance for different traits in QPM inbred crosses

Components of variance	Days to 50% tasselling Pooled	Days to 50% silking Pooled	Plant height (cm) Pooled	Ear height (cm) Pooled	Kernel rows per cob Pooled	Kernels per row Pooled	100 grain weight (g) Pooled	Grain yield per plant (g) Pooled	Protein content (%) Pooled
σ^2 lines	2.5999	2.3701	228.0381	113.4308	0.5319	8.9496	4.7427	424.6606	0.0967
σ^2 lines \times environments	0.0522	0.0984	6.3466	4.0057	0.0005	0.1924	0.0812	11.8106	0.0059
σ^2 testers	2.8495	3.0486	19.1311	40.7032*	0.0052	0.7010	0.7619	5.7532	0.0073
σ^2 testers \times environments	0.0296	0.0013	-0.1510	-0.1181	0.0004	-0.0163	0.0087	0.3739	-0.0009
σ^2 gca	2.7814	2.8635**	76.1057**	60.5380*	0.1489	2.9506	1.8470	120.0007	0.0326
σ^2 gca \times environments	0.0365	0.0279	1.6210	1.0067	0.0004	0.0405	0.0285	3.4930	0.0010
σ^2 sca (lines \times testers)	5.3021	4.3469**	205.6946**	97.1078**	2.0178**	23.8147**	9.6819**	1041.1598**	0.1708**
σ^2 sca \times environments (L \times T \times E)	0.0133	-0.1167	8.9562	18.7641	-0.0023	0.3769	0.1948	-0.6645	0.0134
σ^2 E	0.2142	0.3405	2.1446	1.2625	0.0186	0.1952	0.0622	2.4568	0.0077
σ^2 A	5.5629	5.7271	152.2114	121.0760	0.2978	5.9013	3.6941	240.0014	0.0652
σ^2 D	5.3021	4.3469	205.6946	97.1078	2.0178	23.8147	9.6819	1041.1598	0.1708
σ^2 A σ^2 D	1.0498	1.3204	0.7536	0.6853	0.1472	0.2471	0.3811	0.2311	0.3802
Degree of dominance	0.9873	0.8757	1.1545	0.8794	2.6229	2.0128	1.6214	2.0873	1.6292

*** Significant at 5 and 1 percent levels, respectively

Table 3: General combining ability effects of lines and testers for different characters in QPM inbred crosses

Parents	Days to 50% tasselling Pooled	Days to 50% silking Pooled	Plant height (cm) Pooled	Ear height (cm) Pooled	Kernel rows per cob Pooled	Kernels per row Pooled	100 grain weight (g) Pooled	Grain yield per plant (g) Pooled	Protein content (%) Pooled
Lines									
KDQPM-13	-0.146	-0.479	-15.385**	-17.175**	0.328**	-0.228	-1.231**	-4.599**	0.217**
KDQPM-14	-1.146**	-1.313**	-9.802	-4.408**	-0.138	-3.828**	-2.914**	-29.234**	0.067
KDQPM-20	3.521**	3.354**	11.298**	6.842**	-0.688**	0.107	-2.984**	-13.104**	-0.217**
KDQPM-21	0.688*	0.354	0.265	1.125**	0.945**	0.772	2.536**	19.389**	-0.250**
KDQPM-49	0.521	0.854*	-19.462**	-9.975**	0.428**	-2.311**	1.036**	3.896**	-0.500**
KDQPM-50	-2.146**	-1.646**	4.648**	3.458**	-1.188**	1.450**	1.584**	13.471**	0.133*
KDQPM-58	0.188	0.021	15.598**	13.842**	0.445**	-1.436**	-0.197	-17.753**	0.383**
KDQPM-60	-1.479**	-1.146**	12.841	6.292**	-0.132	5.475**	2.169**	27.936**	0.167**

*** Significant at 5 and 1 percent levels, respectively

Table 3: General combining ability effects of lines and testers for different characters in QPM inbred crosses

Parents	Days to 50% tasseling Pooled	Days to 50% silking Pooled	Plant height (cm) Pooled	Ear height (cm) Pooled	Kernel rows per cob Pooled	Kernels per row Pooled	100 grain weight (g) Pooled	Grain yield per plant (g) Pooled	Protein content (%) Pooled
Testers									
VQL-1	1.854**	1.833**	4.958**	3.806**	-0.067	-0.058	0.722**	-0.686	-0.081*
VQL-2	-1.833**	-1.917**	-3.918**	-7.381**	0.020	-0.824**	0.386**	-2.571**	0.094**
VQL-17	-0.021	0.083	-1.040**	3.575**	0.047	0.882**	-1.108**	3.258**	-0.012
S.E.g (lines)	0.2867	0.3895	0.5108	0.3971	0.0918	0.2851	0.2108	0.9326	0.0493
S.E.g(testers)	0.1756	0.2385	0.3128	0.2432	0.0562	0.1746	0.1291	0.5711	0.0302

*,** Significant at 5 and 1 percent levels, respectively

Table 4: Specific combining ability effects (pooled) of lines and testers for different characters in QPM inbred crosses

Crosses	Days to 50% tasseling Pooled	Days to 50% silking Pooled	Plant height (cm) Pooled	Ear height (cm) Pooled	Kernel rows per cob Pooled	Kernels per row Pooled	100 grain weight (g) Pooled	Grain yield per plant (g) Pooled	Protein content (%) Pooled
KDQPM13 × VQL1	2.146**	1.667*	-20.475**	-10.756**	0.684**	-3.526**	-1.706**	-10.539**	-0.285**
KDQPM13 × VQL2	-0.167	0.917	9.302**	-3.469**	-1.653**	2.041**	-0.919*	-15.709**	0.040
KDQPM13 × VQL17	-1.979**	-2.583**	11.173**	14.225**	0.969**	1.485**	2.625**	26.248**	0.246**
KDQPM14 × VQL1	-1.854**	-1.500*	9.392**	3.827**	2.101**	-2.926**	3.878**	3.151	-0.385**
KDQPM14 × VQL2	0.833	0.250	11.368**	10.315**	-1.337**	3.141**	-1.186**	13.861**	0.590**
KDQPM14 × VQL17	1.021	1.250	-20.760**	-14.142**	-0.764**	-0.215	-2.692**	-17.013**	-0.204*
KDQPM20 × VQL1	-1.521**	-1.667*	10.992**	10.227**	-0.249	-0.556	-3.312**	-18.424**	0.648**
KDQPM20 × VQL2	-1.833**	-0.917	-8.232**	-5.285**	1.163**	2.556**	3.284**	27.126**	-0.727**
KDQPM20 × VQL17	3.354**	2.583**	-2.760**	-4.942**	-0.914**	-2.000**	0.028	-8.702**	0.079
KDQPM21 × VQL1	3.313**	2.833**	4.575**	-0.006	0.268	-5.526**	2.028**	-22.027**	-0.169
KDQPM21 × VQL2	-1.500**	-1.917**	-3.898**	-1.919*	1.230**	1.141*	-3.036**	12.123**	-0.144
KDQPM21 × VQL17	-1.813**	-0.917	-0.677	1.925*	-1.498**	4.385**	1.008*	9.904**	0.313**

*,** Significant at 5 and 1 percent levels, respectively

Table 4: Cont....

Crosses	Days to 50% tasseling Pooled	Days to 50% silking Pooled	Plant height (cm) Pooled	Ear height (cm) Pooled	Kernel rows per cob Pooled	Kernels per row Pooled	100 grain weight(g) Pooled	Grain yield per plant (g) Pooled	Protein content (%) Pooled
KDQPM49 × VQL1	1.479**	1.833*	-11.198**	-3.606**	-0.566**	2.408**	-0.222	0.076	0.181*
KDQPM49 × VQL2	1,167*	0.583	9.048**	5.881**	0.097	2.224**	-0.336	14.571**	0.106
KDQPM49 × VQL17	-2.646**	-2.417**	-2.150**	-2.275**	0.469**	-4.632**	0.558	-14.648**	-0.288**
KDQPM50 × VQL1	0.146	0.833	10.692**	1.910*	0.551**	8.796**	3.529**	73.611**	0.048
KDQPM50 × VQL2	-0.167	-0.917	-15.982**	-4.452**	0.563**	-6.788**	1.266**	-25.059**	0.373**
KDQPM50 × VQL17	0.021	0.083	5.290**	2.542**	-1.114**	-2.008**	-4.795**	-48.553**	-0.421**
KDQPM58 × VQL1	-3.188**	-2.833**	-1.708	-2.523**	-1.733**	3.708**	-4.289**	-6.385**	-0.202*
KDQPM58 × VQL2	0.500	0.417	-5.332	0.165	0.430*	-2.001**	2.397**	-5.005**	0.023
KDQPM58 × VQL17	2.688**	2.417**	7.040**	2.358**	1.303**	-1.707**	1.892**	11.391**	0.179*
KDQPM60 × VQL1	-0.521	-1.167	-2.271*	0.927	-1.056**	-2.379**	0.094	-19.464**	0.165
KDQPM60 × VQL2	1.167*	1.583*	3.725**	-1.235	-0.493**	-2.313**	-1.469**	-21.909**	-0.260**
KDQPM60 × VQL17	-0.646	-0.417	-1.454	0.308	1.549**	4.692**	1.375**	41.373**	0.096
S.E.(S _{ij})	0.4966	0.6746	0.8847	0.6878	0.1591	0.4938	0.3651	1.6153	0.0854

*,** Significant at 5 and 1 percent levels, respectively.

of the traits viz., plant height (cm), number of kernel rows cob⁻¹, number of kernels row⁻¹, 100-grain weight and grain yield plant⁻¹ and protein content (%) after comparing the GCA and SCA variances to assess the relative importance of the genetic variance components (Table 2). These results are in agreement with earlier findings of Singh *et al.* (2012) and Pavanet *al.* (2011) for number of kernels row⁻¹, number of kernels ear⁻¹, 100-grain weight and grain yield plant⁻¹. However additive gene

action also played a role in expression of traits like days to 50% silking, days to 50% tasseling and ear height (cm). Average degree of dominance was greater than unity (over dominance range) for most of the traits that included plant height, kernel rows cob⁻¹, 100-grain weight, grain yield plant⁻¹ and protein content (%) revealing that the lines were diverse and contained contrasting alleles in most of the cases in dispersion phase, which increased heterozygosity on crossing indicating

preponderance of dominance variance in controlling these traits.

GCA effect

The GCA effects (Table 3) of eight QPM lines were estimated for determining their genetic worth for production of superior lines. The results revealed that none of the parents showed significant GCA effects in the desired direction for all the traits simultaneously under study. For grain yield plant⁻¹ KDQPM-60 was identified as best combiner followed by KDQPM-21 and KDQPM-50. These QPM lines can be used for developing high yielding single cross QPM hybrids. KDQPM-60 was also accompanied with significant GCA effect in desired direction for days to 50 per cent tasseling, days to 50 per cent silking, 100 grain weight, kernels row⁻¹ and protein content. For flowering traits, KDQPM-14, KDQPM-50, and KDQPM-60 were having highly significant negative GCA effects. Similarly, Sundararajan and Kumar (2011) highlighted the importance of negative GCA effect for days to 50% tasseling and days to 50% silking to develop early maturing varieties. High per se performance for kernels row⁻¹ was exhibited by KDQPM-60 followed by KDQPM-50 and KDQPM-21. For 100 grain weight, KDQPM-21 was found to be best combiner depicted by highly significant positive GCA effects followed by KDQPM-50 and KDQPM-49. Lines showing highly desirable GCA effects for grain yield plant⁻¹ and can be selected for the development of hybrid development as donor parents for the accumulation of favourable genes. These findings are in accordance with Singh *et al.* (2012) and Khalil *et al.* (2010).

SCA effect

The SCA effect is an important criterion to determine the potential and effectiveness of hybrids. The estimates of specific combining ability effects of the twenty-four single cross hybrids for various traits is given in Table 4. It was found that none of the cross combination possessed high SCA effects for all the studied traits. However, crosses which exhibited highly significant and desirable SCA effects included KDQPM-14 × VQL-1, KDQPM-60 × VQL-17 and KDQPM-21 × VQL-2 for kernel rows cob⁻¹; KDQPM-50 × VQL-1, KDQPM-60 × VQL-17 and KDQPM-13 × VQL-17 for grain yield plant⁻¹. The perusal of the SCA effects along with per se performance revealed that some of the crosses showing high desirable SCA effects were also having high per se performance for most of the traits under study (Table 4). Similar results were found by Mosa (2010). There was preponderance of SCA variances showing the greater importance of non-additive genetic component in the inheritance of studied traits. Wali *et al.* (2010) reported that SCA variance was dominance for the inheritance of yield and yield component traits. These crosses having high SCA effects for grain yield plant⁻¹ and their parents with high GCA can be used directly as donors and exploited for future hybrid breeding programmes.

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