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Gene action studies in quality protein maize

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Abstract
The study involved quality protein maize (QPM) inbreds in a line × tester programme comprising twenty-four hybrids produced by crossing eight QPM lines with three testers. Eight inbred lines (KDQPM-13, KDQPM-14, KDQPM-20, KDQPM-21, KDQPM-49, KDQPM-50, KDQPM-58 and KDQPM-60) were crossed with three testers (VQL1, VQL2 and VQL17) to produce twenty four F_1 hybrids during *Kharief* 2015. Twenty four F_1 hybrids were evaluated in a randomized complete block design with two replications during *Kharief* 2016 and 2017 at Dryland (*Karewa*) Agricultural Research Station. Significant genetic differences were observed for mean squares of treatments for all traits under study. KDQPM-60 was identified as a good general combiner for grain yield plant^{-1} followed by KDQPM-21 and KDQPM-50. Also, KDQPM-60 was accompanied with significant and desirable GCA effects for days to 50 percent tasseling, days to 50 percent silking, number of kernels row^{-1}, 100 grain weight, and protein content and hence can be selected for the development of QPM hybrids. Among the crosses, KDQPM-50 × VQL-1, KDQPM-60 × VQL-17 and KDQPM-13 × VQL-17 exhibited highly significant and desirable SCA effects for grain yield plant^{-1}.

Keywords: gene action, general combining ability, specific combining ability, QPM

Introduction

Maize belongs to family Poaceae, tribe Maydeae. It is of high significance due to its demand for food, feed and industrial utilization and is also important for human and animal nutrition. 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. (Vassal, 2000) [8]. 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) [5]. 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) [2]. The protein quality of opaque2 maize is 43 percent higher than that of common maize and 95 percent of the value of casein (Mertz 1992) [4]. 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) [1]. 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) [9]. 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) [9]. Krivanek *et al*. (2007) [3] 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. Combining ability analysis is one of the most powerful tools in identifying the best combiners that may be used in crosses either to accumulate productive genes or to exploit heterosis. 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.

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Materials and Methods

The experiment was conducted by generating twenty four single cross hybrids by line x tester mating design during *Kharief* 2015 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. The resulting twenty-four crosses were evaluated in a randomized block design with two replications during *Kharief* 2016 and *Kharief* 2017 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, grain yield plant[-1] 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) [11] 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 combing ability revealed significant mean squares of GCA and SCA for all the traits in individual as well as pooled analysis. It was fund that the non-additive gene action played a major role in expression 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). 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.

Table 1: Analysis of variance for different characters in maize (*Zea mays* L.)

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 maize (*Zea mays* L.)

Components of variance	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
σ^2 lines	2.5999	2.3701	228.0381	113.4308	0.5319	8.9496	4.7427	424.6606	0.0967
σ^2 lines × 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 × environments	0.0296	0.0013	-0.1510	-0.1181	0.0004	-0.0163	0.0087	0.3739	-0.0009
σ^2gca	2.7814	2.8635**	76.1057**	60.5380*	0.1489	2.9506	1.8470	120.0007	0.0326
σ^2gca × environments	0.0365	0.0279	1.6210	1.0067	0.0004	0.0405	0.0285	3.4930	0.0010
σ^2sca (lines × testers)	5.3021	4.3469**	205.6946**	97.1078**	2.0178**	23.8147**	9.6819**	1041.1598**	0.1708**
σ^2sca × environments (L× T ×E)	0.0133	-0.1167	8.9562	18.7641	-0.0023	0.3769	0.1948	-0.6645	0.0134
σ^2E	0.2142	0.3405	2.1446	1.2625	0.0186	0.1952	0.0622	2.4568	0.0077
σ^2A	5.5629	5.7271	152.2114	121.0760	0.2978	5.9013	3.6941	240.0014	0.0652
σ^2D	5.3021	4.3469	205.6946	97.1078	2.0178	23.8147	9.6819	1041.1598	0.1708
σ^2A/σ^2D	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

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 percent tasseling, days to 50 percent 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) [7] 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 hybrids

Table 3: General combining ability effects of lines and testers for different characters in maize (*Zea mays* L.)

Parents	Days to 50% tasselling	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
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: Contd: General combining ability effects of lines and testers for different characters in maize (*Zea mays* L.)

Parents	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
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$_i$ (lines)	0.2867	0.3895	0.5108	0.3971	0.0918	0.2851	0.2108	0.9326	0.0493
S.E.gi(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 maize (*Zea mays* L.)

Crosses	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
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: Contd: Specific combining ability effects (pooled) of lines and testers for different characters in maize (*Zea mays* L.)

Crosses	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
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

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) [6]. 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) [10] 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] can be used directly or exploited for future hybrid breeding programmes.

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