



Gene actions and combining ability effects on grain yield and its constituent traits in inbred lines of quality protein maize

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ABSTRACT

In the present study twenty-eight hybrid combinations resulting from the half-diallel mating of eight quality protein maize (QPM) inbred lines were chosen in order to examine the potential to combine and gene activity for ten yield and component attributes. As part of the All India Coordinated Research Project (AICRP) on maize during the kharif-2020 season, the experiment was done at the research farm of college of Agriculture, Odisha University of Agriculture & Technology (OUAT) Bhubaneswar, using a randomized complete block design replicated thrice. Every observation recorded was subjected to statistical evaluation and it was revealed that the mean squares derived from the general combining ability (gca) and specific combining ability (sca) were highly significant ($p \geq 0.01$). Estimates of sca effects were greater than that of gca effects for all of the variables used in the study, suggesting to the predominance of dominant gene action. The inbred lines Q4-DQL 2221-1-1(833.792), Q2-DQL 2099 (517.658) and Q3- DQL 2159 (350.325) shows high gca effects for yield and its attributing traits due to more additive gene action thus identified as good general combiners for yield. Twelve of the twenty-eight crosses showed significant ($p \geq 0.01$ and 0.05) positive sca effect on grain yield. The best experimental crosses for grain yield based on per se performance and sca effects were Q2 x Q8 (2106.748), Q1 x Q6 (2053.048), Q3 x Q7 (2027.082), and Q3 x Q6 (1719.884).

Introduction

The most robust and adaptable food crop, maize (*Zea mays* L.; $2n = 20$; Poaceae), is grown across the world in different agro-ecological zones. It is India's third most popular cereal, behind rice and wheat (Poehlman, 2006). Maize is a miracle crop, popularly known as the "Queen of Cereals" due to its very high yield potential (Shinde *et al.*, 2021). The protein content in maize is crucial for the country's food and dietary wellbeing since more than 85 per cent of it is used directly as food and feed. On the other hand, Normal maize has a high zein proportion that is deficient in tryptophan and lysine

content (Das *et al.*, 2021). In 1964, scientists at Purdue University identified the opaque-2 (o-2) gene mutation, which provided endless potential for enhancing the protein content of maize kernels and eventually led to the creation of Quality Protein Maize (QPM). QPM protein has a biological value of 80%, which is comparable to milk protein (90%) and nearly double that of ordinary maize protein (50%) (Agarwal *et al.*, 2018). The diallel approach is used to evaluate both general and specific combining abilities as well as supplementary hereditary characteristics. A hybrid's performance is

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directly associated with the GCA and SCA of the inbred lines used in the crossing, therefore estimates of combining ability are very helpful in figuring out how useful a pair of parents will be in a hybrid combination and in selecting better parents for the generation of hybrids (Bahari *et al.*, 2012). The SCA is predominantly a result of dominance genetic variance, whereas the GCA is mostly a consequence of additive genetic variance and additive x additive epistasis (Sprague and Tatum, 1942). By examining the variance components of GCA and SCA, it is possible to determine the prevalence of additive or dominant gene activity. Standard selection procedures can fix the additive fraction of genetic variation, but the non-additive fraction cannot, and its presence for controlling characteristics needs the employment of hybrid vigour in heterosis breeding. The study of gene function concerning several morphological criteria might aid in developing a breeding strategy for high-yielding, high-quality protein maize varieties. Plant breeders may find this information useful when planning hybridization programs. As a result, the current investigation was carried out to learn more about the gene action and combining ability for grain yield and other features that contribute to yield.

Material and Methods

The study was carried out by utilizing eight parent QPM inbred lines *viz.*, Q1 (DQL 2261), Q2 (DQL 2099), Q3 (DQL 2159), Q4 (DQL 2221-1-1), Q5 (DQL 70160), Q6 (DQL 71266), Q7 (DQL 72154), and Q8 (DQL-72242), to produce 28 F₁ hybrids using an 8 x 8 half diallel mating system. The eight parents and their 28 crosses were grown in randomized complete block designs, replicated thrice during *kharif* 2020 at research farm, AICRP on Maize, OUAT, Bhubaneswar. The plants are grown in two rows measuring 4 metres in length, with a 60 cm by 20 cm space between them. For each replication, observations on yield and its contributing traits were made. *viz.*, grain yield (GY) (kg/ha), number of kernel rows per cob (NKRPC), number of grains per row (NGPR), plant height (PH) (cm), Cob diameter (CD) (cm), Cob length (CL) (cm), ear height (EH) (cm), days to 50% pollen shedding (50%PS), days to 50% silk emergence (50%SE), and days to 75% dry husk (75% DH). The

mean squares for GCA and SCA were compared to the corresponding error variances obtained from an ANOVA that had been averaged down. The mean data were submitted to combining ability analysis using Griffing's Model I's Method II (1956) using R-software.

Results and Discussion

The analysis of variance (Table 1) revealed that parents and crosses were significantly different from each other for all the traits under study. The table showed that the mean sums of squares due to GCA and SCA for all characters under study were highly significant ($p \geq 0.01$) indicating the prevalence of both additive and dominant gene action. The influence of both type of gene action also reported by Hemlatha *et al.* (2014), Patel *et al.* (2016), Ali *et al.* (2020) and Scaria *et al.* (2020). Kamal *et al.* (2023) reported non-significant mean squares for yield and component traits. Table 2 represents combining ability variance of GCA, SCA and their ratio. It was found that for all of the traits evaluated, SCA variances (σ_{sca}^2) were higher than that of GCA variances (σ_{gca}^2) and the SCA to GCA variance ratios were more than one for all characters undertaken. This finding pointed out that dominant or non-additive types of gene activity predominate in these genotypes. This result is in contrast with Tilahun *et al.* (2017) and Karim *et al.* (2018) who reported prevalence of additive gene action for all the traits except days to silking. Dominant or non-additive gene action was also reported by Yerva *et al.* (2016), Kumar *et al.* (2017), Hassan *et al.* (2019) and Arunkumar *et al.* (2022). The gca effects were presented in the Table 3 for each of the ten yield and component traits. The significant negative gca effects for early maturity traits, such as 50%PS, 50%SE, and 75%DH were observed in three parents Q2, Q3, and Q4 out of the eight parents. The highest significant gca effects for 50%PS (-1.50), 50%SE (-1.62), and 75%DH (-1.30) were reported in parent Q4. These parents (Q2, Q3, and Q4) are good combiners for transfer of early maturity traits. Krupakar *et al.* (2013), E1-Shamarka *et al.* (2015) and Patel *et al.* (2016) also reported significant negative gca effects for these traits. When it comes to PH and EH, significant negative gca effects were

Table 1: Analysis of variance for yield and component traits in QPM inbred lines

Sl. No.	Source of variation	d.f.	50%PS	50%SE	75%DH	PH	EH	CL	CD	NKRPC	NGPR	GY
1	Genotypes	35	17.855**	17.101**	17.431**	1453.762**	853.165**	13.009**	9.633**	10.304**	117.646**	6160725.997**
2	Parents	7	3.238**	3.405**	4.423**	362.280**	475.119**	11.174**	10.050**	13.466**	100.964**	219755.804**
3	Hybrids	27	11.828**	10.873**	16.728**	367.898**	393.680**	5.407**	4.350**	2.046**	44.342**	4049471.480**
4	Parents vs. Hybrids	1	282.881**	281.153**	127.461**	38412.461**	15905.567**	231.084**	149.352**	211.131**	2213.641**	104751389.303**
5	GCA	7	23.179**	24.264**	18.743**	3074.455**	1729.436**	28.193**	21.480**	29.818**	250.613**	11052372.788**
6	SCA	28	16.524**	15.311**	17.103**	1048.588**	634.097**	9.213**	6.671**	5.426**	84.405**	4937814.299**
7	Error	70	1.369	1.014	1.311	89.628	52.008	0.474	0.223	0.379	2.533	283410.323

Table 2: GCA, SCA variance and their ratio for yield and component traits in QPM inbred lines

Characters	σ_{gca}^2	σ_{sca}^2	$\frac{\sigma_{gca}^2}{\sigma_{sca}^2}$
50%PS	2.181	15.155	0.143913
50%SE	2.325	14.297	0.162622
75%DH	1.7432	15.792	0.110385
PH	298.4827	958.96	0.311257
EH	167.7428	582.089	0.288174
CL	2.7719	8.739	0.317187
CD	2.1257	6.448	0.329668
NKRPC	2.9439	5.047	0.583297
NGPR	24.808	81.872	0.30301
GY	1076896	4654404	0.231371

Table 3: gca effects of 8 parental lines for yield and component traits in QPM inbred lines

S. No.	Parents	50%PS	50%SE	75%DH	PH	EH	CL	CD	NKRPC	NGPR	GY
1	Q1	0.758**	0.608**	0.800**	12.058**	1.958	0.448**	0.403**	0.355**	1.543**	28.158
2	Q2	-0.575**	-0.658**	-0.700**	5.425**	1.925	1.508**	1.083**	1.188**	3.993**	517.658**
3	Q3	-0.675**	-0.592**	-0.500*	8.058**	7.925**	-0.082	0.223**	0.835**	1.600**	350.325**
4	Q4	-1.508**	-1.625**	-1.300**	7.992**	11.825**	0.848**	0.350**	0.648**	1.800**	833.792**
5	Q5	-0.142	-0.025	0.333	1.358	0.225	0.348**	0.670**	0.222*	0.367	234.225*
6	Q6	0.458*	0.642**	-0.067	-10.542**	-8.042**	-1.265**	-1.430**	-1.778**	-4.583**	-368.142**
7	Q7	1.092**	1.042**	1.000**	-10.708**	-6.575**	-0.798**	-0.363**	-0.665**	-3.377**	-679.342**
8	Q8	0.592**	0.608**	0.433*	-13.642**	-9.242**	-1.008**	-0.937**	-0.805**	-1.343**	-916.675**
SE G(I)		0.200	0.172	0.196	1.617	1.232	0.118	0.081	0.105	0.272	90.918

* Significant at 5% level of probability ($p \geq 0.05$)** Significant at 1% level of probability ($p \geq 0.01$)

* SE G(I)

Standard error for gca effects

observed in parents Q6, Q7, and Q8. The highest significant negative gca effects for PH (Q8 - 13.642) and EH (-9.242) were reported in the parent Q8. Yerva *et al.* (2016) and Scaria *et al.* (2020) also reported significant negative gca effects for plant and ear height. Karim *et al.* (2018) found non-significant gca effect for plant height. The parents (Q6, Q7, and Q8) showed good combining ability for lowered plant and ear height characters and can be utilized for development of short stem-type plants. The significant positive gca effects for yield and its attributing traits viz., CL, CD, NKRPC, and NGPR were observed in parents Q2, and Q4. Similarly, parent Q3 also showed significant positive gca effects for all the traits except CL while parent Q5 showed significance for all the traits except NGPR. The highest positive significant gca effects for GY was reported in the parent Q4 (833.79) followed by Q2 (517.65) and Q3 (350.32) and the highest significant positive gca effects were for yield attributing traits viz., CL (1.50), CD (1.08), NKRPC (1.18), and NGPR (3.99) were observed in the parent Q2. Singh *et al.* (2014) and E1-Shamarka *et al.* (2015), Basser *et al.* (2021) and Kamal *et al.* (2023) also reported positive gca effects for yield component traits. Parents Q2 and Q4 were best general combiners for yield and its attributing traits. These parents can be utilized as donor parents for accumulation of favorable genes. For each of the ten yield and component characters, specific combining ability effects have been computed and are presented in Table 4. Eight, ten and eleven crosses showed significant negative sca effects for early maturity

traits viz., 50%PS, 50%SE, and 75%DH respectively. Cross Q3 \times Q8 (-4.22) recorded highest significant negative sca effects for 50%PS followed by the crosses Q1 \times Q6 (-4.18), and Q5 \times Q6 (-3.59). Cross Q1 \times Q7 (-4.04) recorded highest significant negative sca effects for 50%SE followed by the crosses Q3 \times Q8 (-3.74), and Q5 \times Q6 (-3.68). Cross Q5 \times Q6 (-4.52) recorded highest significant negative sca effects for 75%DH followed by the crosses Q3 \times Q8 (-4.19), and Q1 \times Q6 (-2.99). The parents involved in these crosses also showed good general combining ability effects and performed substantially better in specific crosses. E1-Shamarka *et al.* (2015), Basser *et al.* (2021) and Arunkumar *et al.* (2022) also reported desirable significant negative sca effects for earliness in their experiment while Karim *et al.* (2018) reported non-significant sca effect for days to 50% silking. Most of these crosses have at least one parent with low gca effects. Significant negative sca effects for PH were observed in five crosses, namely Q5 \times Q7 (-39.47), Q5 \times Q8 (-23.20), Q6 \times Q7 (-13.57), Q1 \times Q3 (-12.94) and Q3 \times Q4 (-10.54), and for EH four crosses, namely Q6 \times Q7 (-29.50), Q5 \times Q7 (-26.43), Q5 \times Q8 (-18.77) and Q2 \times Q4 (-8.87) showed significant negative sca effects. Low EH and shorter plants are correlated to lodging resistance (Arunkumar *et al.*, 2022). These crosses showed best specific combining ability for shorter plant and ear height traits. The number of crosses showing significant positive sca effects for GY and other yield attributing traits viz., CL, CD, NKRPC, and NGPR were twelve, eleven, fourteen, eleven, and fifteen respectively. For CL,

Table 4: sca effects of 28 F1 crosses for yield and component traits in Quality Protein Maize

Sl. No.	Crosses	50%PS	50%SE	75%DH	PH	EH	CL	CD	NKRPC	NGPR	GY
1	Q1 x Q2	2.511**	2.985**	1.641**	-7.974	2.996	-1.547**	-2.353**	-1.801**	-7.944**	-1101.751**
2	Q1 x Q3	-1.722**	-1.748**	1.107*	-12.941**	-3.337	-0.357	-1.093**	-0.047	0.816	-576.419*
3	Q1 x Q4	1.111	1.285**	-1.426**	5.126	-2.570	-0.654*	0.880**	0.806**	2.349**	928.448**
4	Q1 x Q5	1.411**	1.352**	0.274	13.426**	25.030**	1.646**	1.193**	-0.101	2.116**	1495.349**
5	Q1 x Q6	-4.189**	-3.648**	-2.993**	16.993**	6.963*	3.259**	4.060**	1.833**	7.399**	2053.048**
6	Q1 x Q7	-3.489**	-4.048**	-1.393**	15.826**	-0.837	0.526	-0.407	-0.614*	2.226**	1059.915**
7	Q1 x Q8	-0.656	-0.948*	1.174*	17.426**	1.163	1.369**	0.467*	-0.141	3.559**	-411.419
8	Q2 x Q3	1.278*	1.185*	-2.393**	15.026**	9.030**	0.749*	0.793**	-0.747**	2.199**	556.748*
9	Q2 x Q4	-0.222	-0.115	2.741**	-0.907	-8.870**	-0.014	-0.967**	-0.427	-4.434**	-238.052
10	Q2 x Q5	-0.256	-0.381	-0.226	6.393	-1.270	-0.581	0.413	-0.534	0.666	1026.182**
11	Q2 x Q6	-1.189*	-1.381**	-1.826**	10.626*	-2.337	0.366	-0.387	0.999**	4.583**	259.882
12	Q2 x Q7	-0.156	-0.448	1.107*	6.793	1.530	0.066	-0.353	1.686**	-6.057**	-1235.251**
13	Q2 x Q8	0.344	0.319	2.674**	29.393**	23.530**	1.109**	1.187**	0.759**	3.243**	2106.748**
14	Q3 x Q4	2.878**	2.485**	4.207**	-10.541*	-6.537	-0.257	-0.507*	0.259	-4.241**	-839.051**
15	Q3 x Q5	-0.156	0.552	0.907	-1.241	-5.604	-0.491	-1.793**	0.153	-5.241**	-2633.818**
16	Q3 x Q6	-1.756**	-1.115*	-2.026**	22.326**	18.663**	2.556**	1.940**	2.219**	7.709**	1719.881**
17	Q3 x Q7	-1.056	-1.181*	-1.093*	14.159**	22.196**	1.556**	0.807**	0.773**	4.536**	2027.082**
18	Q3 x Q8	-4.222**	-3.748**	-4.193**	-0.907	-3.804	-2.101**	0.680**	0.713*	-1.497*	-79.919
19	Q4 x Q5	0.011	-0.081	-2.959**	11.826**	16.163**	1.179**	0.613**	0.006	3.426**	625.048
20	Q4 x Q6	0.078	0.252	1.441**	0.059	5.430	2.426**	-0.387	0.206	-0.891	510.415*
21	Q4 x Q7	0.111	0.852	0.374	19.559**	19.630**	1.693**	1.380**	0.759**	6.736**	659.615**
22	Q4 x Q8	-2.722**	-3.048**	-2.393**	17.826**	-1.704	-0.197	0.987**	0.566*	2.536**	520.615*
23	Q5 x Q6	-3.956**	-3.681**	-4.526**	9.359*	6.030	1.326**	1.993**	2.366**	5.309**	-176.352
24	Q5 x Q7	3.078**	2.585**	1.407**	-39.474**	-26.437**	-1.774**	-0.207	0.253	-5.931**	-1243.485**
25	Q5 x Q8	2.578**	2.352**	2.307**	-23.207**	-18.770**	-1.264**	-1.267**	-1.941**	-7.797**	-1253.485**
26	Q6 x Q7	1.811**	1.585**	2.141**	-13.574**	-29.504**	-3.961**	-2.240**	-3.681**	-7.947**	-932.785**
27	Q6 x Q8	2.311**	2.685**	2.707**	-2.974	3.496	-0.317	-1.833**	-1.074**	-5.414**	-775.452**
28	Q7 x Q8	-0.656	0.000	-0.693	5.526	10.696**	-0.117	0.767**	0.413	6.479**	300.082
SE S(I,J)		0.533	0.459	0.521	4.312	3.284	0.314	0.215	0.280	0.725	242.449

* Significant at 5% level of probability (p ≥0.05)
Standard Error for sca effects

** Significant at 1% level of probability (p ≥0.01) * SE S (I, J)

the cross Q1 X Q6 (3.25) performed best followed by the crosses Q3 X Q6 (2.55) and Q4 X Q6 (2.42). For CD also best performance was reported in the cross Q1 X Q6 (4.06) followed by Q5 X Q6 (1.99) and Q3 X Q6 (1.94). Three best crosses for NKRPC were Q5 X Q6 (2.36), Q3 X Q6 (2.219) and Q1 X

Q6 (1.833) while for NGPR three best performance were found in the crosses Q3 X Q6 (7.70), Q1 X Q6 (7.39) and Q4 X Q7 (6.73). For GY the cross Q2 X Q8 (2106.748) showed highest significant positive sca effects followed by Q1 X Q6 (2053.04) and Q3 X Q7 (2027.08). Netravati et al. (2014), E1-

Shamarka *et al.* (2015), Patel *et al.* (2016), Sandesh *et al.* (2018), Arunkumar *et al.*, (2022) and Kamal *et al.* (2023) also found significant positive sca effects for grain yield and its component traits. Karim *et al.* (2018) observed non-significant sca effect for yield. Crosses showing high sca effects for grain yield have at least one parent with low gca effects. These crosses have potential to produce hybrids with high yielding capability.

Conclusion

It may be concluded that superior inbred lines which showed significant positive gca effects for grain yield and yield-attributing traits can be used as parents in breeding for improvement in yield and its attributing traits. They can also be utilized as a component line for development of synthetic and composite variety of maize. The superior crosses

resulted from the crosses can be directly use as hybrid or can be improved further for other important agronomic traits. These crosses reflected that there is high amount of non-additive gene action present in the crosses so there is scope of exploitation of heterosis and biparental mating for improvement of yield and other important traits.

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Conflict of interest

The authors declare that they have no conflicts of interest.

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