

Gene action studies of quantitative and qualitative traits in maize (*Zea mays* L.)

B. B. Patel¹ · P. K. Parmar¹ · M. B. Patel¹ · G. B. Patil² · D. J. Parmar³ · H. S. Vemra¹ · D. N. Rathod¹

Abstract: The present study was undertaken to determine the type of gene action, genetic parameters of yield and other quantitative traits by crossing eight diverse maize inbred lines in half diallel mating fashion. Seed of 28 F₁ population along with their parents and a standard check was planted during *rabi*, 2019-20 in randomized complete block design and replicated thrice at the Main Maize Research Station, Anand Agricultural University, Godhra. The observations were recorded on different quantitative characters and protein content. The results revealed that mean squares due to parents and hybrids were significant for all the characters indicating that parents and hybrids differed significantly in their combining ability effects and importance of both additive as well as non-additive gene effects for their inheritance. The analysis of variance revealed significant differences among genotypes for all the characters. The estimates of components of genetic variation revealed the pre-ponderance of non-additive genetic variance for all the characters under study. The significance of both *gca* and *sca* variance indicated the involvement of both additive and non-additive gene effects for the inheritance of days to 50% tasselling, days to 50% silking, cob weight, number of kernels per row, shelling %, 100 kernels weight, kernel yield per plant and protein content. The predominance of non-additive gene

action resulted in enormous heterotic response in kernel yield and its attributes including quality traits and thus heterosis breeding would be the best approach for yield improvement.

Keywords: Gene action · Diallel · Additive · Dominance · Heterosis

Introduction

Maize is the most important cereal crop in the world after wheat and rice. It has great yield potential and attained the leading position among cereals in term of production as well as productivity. With the introduction of hybrids in maize, the inclinations of acreage and production have been increasing due to its high yield potential. Maize is the most important crop, being grown in over 166 nations throughout the world, in tropical, subtropical and temperate climates and at elevations ranging from sea level to 3000 meters above sea level. Worldwide maize grown on 207.25 million hectare (MH) with total production of 1217.31 million metric tonnes (MMT) and productivity is 5.87 metric tonnes (MT), with a greater range of soil, climate, biodiversity and management approaches, accounting for 37 per cent of global kernel production (Anonymous, 2023). The United States of America (USA) is the world's largest producer of maize, accounting for 30 per cent of global production and maize is recognized as the foundation of the US economy. In the year 2021-2022 in INDIA maize is grown on 10.04 MH with 33.62 MT production and productivity is 3349 kg/ha (Anonymous, 2023). Gujarat contributes approximately 5 per cent of India's total production, with a total production of 6.67 lakh tonnes in the year 2020–

✉ P. K. Parmar: pkp@aau.in, pkparmar7907@gmail.com

¹Main Maize Research Station, Anand Agricultural University, Godhra-389001, Gujarat, India

²Department of Biotechnology, B A College of Agriculture, Anand Agricultural University, Anand, Gujarat, India

³Department of Agriculture Statistics, B A College of Agriculture, Anand Agricultural University, Anand, Gujarat, India

21. The total area under cultivation was 3.88 lakh ha. giving productivity of 1716.32 kg/ha. It is grown primarily in the Panchmahal, Dahod, Chhotaudepur, Mahisagar and Arvalli district of Gujarat (Directorate of Agriculture, 2022).

Planning and execution of a breeding programme requires information on the genetic systems controlling the character of the interest, so that the expected gain can be maximized with the selection process (Viana *et al.*, 1999). A mating design frequently employed by plant breeders to ascertain genetic basis of variation in various attributes is diallel analysis. This approach has been effectively used by Singh and Roy (2007) in maize. Diallel analysis is commonly used for estimation of genetic variances from single crosses. Knowledge of gene action helps in the selection of parents for use in the hybridization programs and also in the choice of appropriate breeding procedure for the genetic improvement of various quantitative characters. The present study was conducted to determine the gene action and genetic variation for kernel yield per plant and other quantitative characters in maize germplasm.

Materials and methods

The study was conducted at Main Maize Research Station, Anand Agricultural University, Godhra. The experimental material comprises of eight parents, their 28 hybrids develop using half diallel mating design and one standard check. Eight inbred lines i.e. HKI 163, GYL-11, CM-500, I-07-57-3-3, I-07-54-3-1, I-07-6-4-5, LM-16 and IL-14-53 were obtained from Godhra station. The crossing program was undertaken using half diallel (excluding reciprocal) method during *rabi* 2019-20. The seeds of all the crosses and parental lines were harvested separately. The experiment was conducted during *rabi* 2020-21 in replicated trial by planting of F_1 hybrid along with the parents at sowing distance of 60 × 20 cm. Each treatment comprised of two rows of four-meter length.

Dose of fertilizer @ 160 kg N and 20 kg P per hectare was applied. Data pertaining to plant height, days to 50% tasseling, days to 50% silking, ear height and kernel yield per plant were recorded. The data was statistically analyzed following Panse and Sukhatme (1978). Genetic analysis was done according to the diallel technique as described by Hayman (1954) and Jinks (1954). Genetic components of variation, D (additive

effects of genes), H1 and H2 (dominance effects of genes) and F were computed from estimates of variances and covariances. The observation on days to 50% tasseling, days to 50% silking and days to maturity were noted on a plot basis. For remaining traits, five competitive plants were randomly selected and tagged at in each plot on which observation was recorded from each genotype at different crop growth stages and the average value calculated.

Results and discussion

Mean sum of squares obtained from analysis of variance indicated significant differences among the parents and derived F_1 hybrids for all the characters (Table 1) and thus allowed to use of Hayman-Jinks model for genetic analysis of these characters.

Gene action

Days to 50% tasseling: The significance of both *gca* and *sca* variance (Table 2) indicated the involvement of both additive and non-additive gene effects for the inheritance of this trait. But the $\sigma^2_{gca}/\sigma^2_{sca}$ ratio less than unity for the character suggested the predominant role of non-additive gene effect. These findings are in agreement with the results of Suneetha *et al.* (2000); Lal *et al.* (2011); Sundararajan and Kumar (2011); Vaghela (2012) and Nanavati (2015) as they reported the significance of both σ^2_{gca} and σ^2_{sca} , while Premalatha and Kalamani (2010) observed preponderance of σ^2_{sca} . Shete *et al.* (2011b) also reported a preponderance of additive gene action for this trait. Kumar *et al.* (2021) also reported effect of environment on stability.

Days to 50% silking: The significance of both *gca* and *sca* variance (Table 2) indicated the involvement of both additive and non-additive gene effects for the inheritance of this trait. But The ($\sigma^2_{gca}/\sigma^2_{sca}$) ratio below unity in present investigation had suggested the predominant role of non-additive gene action. This results are substantiated by Srivastava and Singh (2003); Lal and Kumar (2012); Kumar and Kumar (2014); Aminu *et al.* (2014); Rajesh *et al.* (2018); Gami *et al.* (2018).

Days to maturity: The ratio $\sigma^2_{gca}/\sigma^2_{sca}$ was found to be less than unity (Table 2) indicated the pre-ponderance of

Table 1. Analysis of variances (mean squares) and variance components for various characters

S.No.	Characters ↓	Mean Sum of Square						Error
		Replication	Genotypes	Parents	Hybrids	Parents vs. Hybrids	Check vs. Hybrids	
	df →	2	36	7	27	1	1	72
1.	Days to 50% tasseling	7.31	15.16**	16.23**	11.96**	95.00**	14.18	2.41
2.	Days to 50% silking	5.14	14.22**	17.24**	11.65**	72.90**	3.72	2.55
3.	Days to maturity	2.74	19.33**	36.04**	15.46**	25.15**	0.81	2.74
4.	Plant height	214.71*	723.00**	379.99**	747.73**	3163.34**	15.89	52.52
5.	Ear height	103.17*	305.68**	145.57**	368.71**	2.00	28.42	27.90
6.	Cob length	2.13	11.82**	9.64**	13.01**	5.59	1.27	1.29
7.	Cob weight	396.25*	2412.90**	1054.65**	2829.46**	2003.07**	1083.20**	93.20
8.	Kernel rows per cob	0.13	1.96**	2.64**	1.88**	0.38733	0.90*	0.13
9.	Kernels per row	15.88	60.69**	48.98**	65.72**	50.09*	17.39	7.17
10.	Shelling percentage	13.12	115.94**	46.55	140.18**	61.93	1.30	23.97
11.	100 kernels weight	15.20*	47.10**	80.57**	39.34**	68.15**	1.41	3.10
12.	Kernel yield per plant	3833.31	17430.22**	12967.14**	17753.41**	46212.22**	11163.42*	1975.66
13.	Protein content	0.2768	1.72**	0.82**	1.52**	2.01**	13.29**	0.13

*, ** Significant at P = 0.05 and P = 0.01 probability levels

Table 2. Mean squares due to general and specific combining ability for different characters in maize

Source of variation	d.f.	Days to 50% tasseling	Days to 50% silking	Days to maturity	Plant height	Ear height	Cob length	Cob weight
Replication	2	7.31	5.14	2.74	214.71	103.17	2.13	396.25
GCA	7	15.40**	11.99**	17.02**	406.77**	173.07**	7.03**	1146.38**
SCA	28	2.48**	3.05**	4.02**	207.97**	87.40**	3.29**	734.61**
σ^2_{gca}	-	1.29	0.89	1.30	19.88	8.57	0.37	41.18
σ^2_{sca}	-	1.67	2.20	3.10	190.47	78.11	2.86	703.54
σ^2_A	-	2.58	1.79	2.60	39.76	17.13	0.75	82.35
σ^2_D	-	1.67	2.20	3.11	190.47	78.10	2.86	703.54
$\sigma^2_{gca}/\sigma^2_{sca}$	-	0.77	0.40	0.42	0.10	0.12	0.13	0.10
Error	72	0.80	0.85	0.91	17.51	9.30	0.43	31.07
Average degree of dominance	-	0.81	1.11	1.09	2.19	2.14	1.96	2.92
Predictability ratio	-	0.61	0.45	0.46	0.17	0.18	0.21	0.10

*, ** Significant at P = 0.05 and P = 0.01 levels of probability, respectively. “-” indicate negative estimate

non-additive gene action in expression of this character. These results are in accordance with Lal and Kumar (2012); Kumar and Kumar (2014); Ahmed *et al.* (2016) and Haydar and Paul (2014).

Plant height (cm): A perusal of the data indicated the involvement of both additive and non-additive gene effects for the inheritance of this trait. The ratio $\sigma^2_{gca}/\sigma^2_{sca}$ was found to be less than unity (Table 2) indicated the pre-ponderance of non-additive gene action in the inheritance of the character. The results of present finding

are in agreement with result of Reddy *et al.* (2011); Lal and Kumar (2012); Kumar and Kumar (2014); Haydar and Paul (2014); Gami *et al.* (2018); Rajesh *et al.* (2018) and Akula *et al.* (2018).

Ear height (cm): The estimate of $\sigma^2_{gca}/\sigma^2_{sca}$ (0.14) was found to be less than unity (Table 2) narrated the pre-ponderance of non-additive gene action in the inheritance of the character. These results were in concordance with Reddy *et al.* (2011); Lal and Kumar (2012); Haydar and Paul (2014); Ahmed (2016) and Rajesh *et al.* (2018) reported non-additive gene action.

Cob length (cm): The proportion of additive and non-additive genes estimated by $\sigma^2_{gca}/\sigma^2_{sca}$ was 0.13, (Table 2) which indicated pre-ponderance of non-additive gene action in the inheritance of the character. These results were in similarity with Reddy *et al.* (2011); Kambe *et al.* (2013); Kumar and Kumar (2014); Ahmed *et al.* (2016); Rajesh *et al.* (2018) and Gami *et al.* (2018).

Cob weight (g): The significance of sca variance and gca variance (Table 2) indicated the involvement of both additive and non-additive type of gene effects in the expression cob weight. However, the ratio $\sigma^2_{gca}/\sigma^2_{sca}$ below the unity suggested the pre-ponderance of non-additive gene action in the inheritance of this trait. These results were in accordance with Rajesh *et al.* (2018) and Aminu *et al.* (2014).

Number of kernel rows per cob: The ratio $\sigma^2_{gca}/\sigma^2_{sca}$ was displayed to be less than unity (Table 3) indicated the pre-ponderance of non-additive gene action in the inheritance of the character. The results are in conformity with the finding of Premlatha *et al.* (2011); Kambe *et al.* (2013); Haydar and Paul (2014); Aminu *et al.* (2014); Rajesh *et al.* (2018); Gami *et al.* (2018); Akula *et al.* (2018) and Dar *et al.* (2018) observed non-additive gene action.

Number of kernels per row: The gca and sca variance were significant (Table 3) indicated the involvement of both additive and non-additive gene action in the expression of trait. However, the ratio $\sigma^2_{gca}/\sigma^2_{sca}$ (0.07) was found to be less than unity indicating the pre-

ponderance of non-additive gene action in the inheritance of the character. These results were in concordance with Reddy *et al.* (2011); Kambe *et al.* (2013); Kumar and Kumar (2014) and Rajesh *et al.* (2018).

Shelling percentage (%): The gca and sca variance were significant (Table 3) indicated the involvement of both additive and non-additive gene action in the expression of trait, However the significance of sca variance (Table 3) indicating the pre-ponderance of non-additive gene action in the inheritance of the character. This result was in close agreement with Kumar and Kumar (2014).

100 kernel weight (g): The gca and sca variance were significant (Table 3) indicated the involvement of both additive and non-additive gene action in the expression of trait. Similar gene action was also reported by Reddy *et al.* (2011); Premlatha *et al.* (2011); Kambe *et al.* (2013); Kumar and Kumar (2014); Aminu *et al.* (2014); Rajesh *et al.* (2018) and Gami *et al.* (2018).

Kernel yield per plant (g): The gca and sca variance were significant (Table 3) indicated the involvement of both additive and non-additive gene action in the expression of kernel yield per plant. But the ratio $\sigma^2_{gca}/\sigma^2_{sca}$ (0.08) was found to be less than unity indicated the pre-ponderance of non-additive gene action in the inheritance of the character. This result was in concordance with Reddy *et al.* (2011); Premlatha *et al.* (2011); Lal and Kumar (2012); Kambe *et al.* (2013); Kumar and Kumar (2014); Aminu *et al.* (2014); Kuselan *et al.* (2017) and Rajesh *et al.* (2018).

Table 3. Mean squares due to general and specific combining ability for different characters in maize

Source of variation	d.f.	Kernels row per cob	Numbers of kernals per row	Shelling percentage	100 kernels weight	Kernel yield per plant	Protein content
Replication	2	0.13	15.88	13.12	15.20	3833.31	0.28
GCA	7	1.18**	27.64**	41.82**	19.74**	8917.21**	0.83**
SCA	28	0.53**	18.89**	39.22**	15.23**	5107.89**	0.37**
σ^2_{gca}	-	0.07	0.88	0.26	0.45	380.93	0.05
σ^2_{sca}	-	0.49	16.50	31.23	14.20	4449.34	0.33
$\sigma^2 A$	-	0.13	1.75	0.52	0.90	761.86	0.09
$\sigma^2 D$	-	0.49	16.50	31.23	14.20	4449.34	0.33
$\sigma^2_{gca}/\sigma^2_{sca}$	-	0.14	0.05	0.08	0.03	0.08	0.15
Error	72	0.04	2.39	7.99	1.03	658.55	0.04
Average degree of dominance	-	1.93	3.07	7.76	3.79	2.42	1.88
Predictability ratio	-	0.21	0.10	0.02	0.06	0.15	0.22

*, ** Significant at P = 0.05 and P = 0.01 levels of probability, respectively. ; “-” indicate negative estimate

Protein content (%): The gca and sca variance were significant (Table 3) indicated the involvement of both additive and non-additive gene action in the expression of trait. However, the ratio $\sigma^2_{\text{gca}}/\sigma^2_{\text{sca}}$ was found to be less than unity indicating the pre-ponderance of non-additive gene action in the inheritance of the character. Similar results were reported by Premalatha *et al.* (2011).

Combining ability analysis

The magnitude of GCA and SCA variances revealed that the SCA variances were higher than their respective GCA variances for all the characters except protein content. The GCA and SCA ratio ($\sigma^2_{\text{GCA}}/\sigma^2_{\text{SCA}}$) was less than unity for the traits plant height, cob weight, shelling percentage, kernel yield per plant, 50% tasseling, 50% silking, days to maturity, cob length, kernel rows per cob, kernels per row, 100 kernels weight, protein content indicated that non-additive components play relatively greater role in the inheritance. If GCA and SCA ratio ($\sigma^2_{\text{GCA}}/\sigma^2_{\text{SCA}}$) was more than unity for the traits in which additive components play relatively greater role in the inheritance of these traits. These results are in concordance with Kumar *et al.* (2019) (Table 1).

An overall appraisal of gca effects revealed that among the eight parents, GYL 11, CM 500 and I 07-6-4-5 were found to be good general combiners for kernel yield per plant. The parent is a good combiner for one or more component characters and was thus noted as a source of favourable/desirable genes for accumulating higher yield directly or indirectly through various component characters.

The parents, HKI 193, I 07-54-3-1, I 07-6-4-5 and IL 14-53 were good general combiners for days to 50% silking and tasseling. Whereas, as same parents were good general combiners for days to maturity (Table 4). Therefore, these genotypes were found to be relatively more promising for their utility as donors in breeding program for early flowering and early maturity in maize. Whereas, for plant height and ear height, parents HKI 193, GYL 11, CM 500 and I 07-6-4-5 were good general combiners. For average cob weight HKI 193, CM 500, I 07-57-3-3 and LM 16 these genotypes are more promising for their utility as donor in generating fruit/cob having more weight. The parents HKI 193 and CM 500 were good combiners for 100 kernel weight. Whereas, parent CM 500 and I 07-57-3-3 were good combiners

Table 4. Estimation of GCA effects of parents for various characters in maize

S.No.	Parents	Days to 50% tasseling	Days to 50% silking	Days to maturity	Plant height	Ear height (cm)	Cob length	Cob weight	Kernel rows per cob	Kernels per row	Shelling percentage	100 kernels weight	Kernel yield per plant	Protein content
1.	HKI 193	-1.38**	-1.28**	-2.12**	4.97**	4.32**	0.04	11.52**	-0.57**	-0.2	-4.27**	2.36**	-43.04**	0.09
2.	GYL 11	0.88**	0.65**	-0.52**	4.63**	2.66**	-0.03	-3.69*	0.2**	0.82	-0.17	-0.34	19.23*	0.19**
3.	CM 500	2.42*	1.78*	1.94*	7.30**	1.89*	0.47*	10.73**	0.49**	0.13	-0.4	1.46**	24.46**	0.48**
4.	I 07-57-3-3	-0.18	-0.35	0.18	-5.93**	-0.94	1.43**	5.41**	-0.09	1.24**	-0.03	-0.74*	-11.74	-0.40**
5.	I 07-54-3-1	-0.05**	-0.42*	-0.96**	-10.00**	-2.81**	-0.80**	-3.43*	-0.12*	0.29	2.03*	-0.94**	3.73	-0.37**
6.	I 07-6-4-5	-1.12**	-1.12**	-0.26**	4.37**	5.09**	-0.13	-10.92**	-0.001	1.00*	2.27**	-2.04**	48.96**	0.08
7	LM 16	0.35**	1.18**	1.51**	0.23	-3.54**	0.37	8.12**	0.36**	-3.94**	1.13	0.56	-22.84**	-0.10
8	IL 14-53	-0.92**	-0.45**	0.24**	-5.57**	-6.68**	-1.36**	-17.75**	-0.26**	0.66	-0.57	-0.31	-18.74*	0.02
Range	Max.	2.42	1.78	1.94	7.30	5.09	1.43	11.52	0.49	1.24	2.27	2.36	48.96	0.48
	Min.	-1.38	-1.28	-2.12	-10.00	-6.68	-1.36	-17.75	-0.57	-3.94	-4.27	-2.04	-43.04	-0.40
Significant	Positive	3	3	3	4	4	2	4	3	2	2	2	3	2
	Negative	4	4	4	3	3	2	4	3	1	1	3	3	2
	Total	7	7	7	7	7	4	8	6	3	3	5	6	4
S.E. ±		0.27	0.27	0.28	1.24	0.90	0.19	1.65	0.06	0.46	0.84	0.30	7.59	0.06
C.D. at 5%		0.52	0.53	0.55	2.43	1.77	0.38	3.23	0.12	0.90	1.64	0.59	14.88	0.12

* and **, significant at 5 % and 1 % levels of probability, respectively.

for cob length. The parents GYL 11, CM 500 and LM 16 were good general combiners for number of Kernel rows per cob, while parents like I 07-57-3-3 and I 07-6-4-5 were good general combiner for kernel per row. As these parents possessed high concentration of genes governing more number of kernel yield per plant, they are likely to be produced desirable segregants when used in crossing programme.

Parents showed differences in their general combining ability effects for the same trait e.g., GYL 11, CM 500 and I 07-6-4-5 were good general combiner. Whereas, I 07-57-3-3 and I 07-54-3-1 is average combiner and HKI 193, LM 16 and IL 14-53 were poor combiners for the kernel yield and several yield components (Table 4). Thus, it was evident that each parent has its specific genetic constitution and capacity to transmit its characteristics to the progenies.

Table 5. Estimation of specific combining ability (sca) effects of hybrids for various characters in maize

S.No	Hybrid	Plant height	Ear height	Cob length	Cob weight	Shelling (%)	Kernel yield per plant
1	HKI 193 × GYL 11	9.40*	13.23**	0.72	-16.47**	10.43**	-64.01**
2	HKI 193 × CM 500	0.40	-1.00	-2.31**	52.79**	-3.67	-5.91
3	HKI 193 × I 07-57-3-3	-7.70*	-4.17	2.39**	21.67**	-3.03	-25.71
4	HKI 193 × I 07-54-3-1	1.37	-4.30	-3.64**	-71.79**	5.90*	34.83
5	HKI 193 × I 07-6-5-4	13.33**	5.13	1.39*	5.40	-8.00**	13.59
6	HKI 193 × LM 16	27.80**	8.76**	0.59	27.53**	-2.20	8.39
7	HKI 193 × IL 14-53	17.27**	-0.10	0.22	3.16	-3.17	112.29**
8	GYL 11 × IL 14-53	20.07**	22.66**	4.86**	62.89**	8.23**	97.83**
9	GYL 11 × I 07-57-3-3	-2.03	0.50	-2.90**	0.61	2.87	-3.31
10	GYL 11 × I 07-54-3-1	-8.30*	-3.97	1.14	3.74	4.47	33.89
11	GYL 11 × I 07-6-5-4	24.0**	-12.8**	-1.02*	7.43	-9.43**	-73.34**
12	GYL 11 × LM 16	-10.2**	1.43	-1.20	-13.07**	7.70**	128.46**
13	GYL 11 × CM 500	-9.73*	-11.44**	-0.41**	-12.00*	-14.27**	-102.31**
14	IL 14-53 × I 07-57-3-3	3.97	1.93	-1.90**	-15.14**	-6.23*	-39.21
15	IL 14-53 × I 07-54-3-1	-17.3**	12.80**	2.23	6.26	-3.97	-71.34**
16	IL 14-53 × I 07-6-4-5	4.33	-5.44*	-0.53	-2.91	7.47**	63.09**
17	IL 14-53 × LM 16	6.47	-22.80**	-0.67	-14.82**	0.60	-54.44*
18	IL 14-53 × CM 500	-8.73*	2.33	-1.74**	6.19	-4.03	62.79**
19	I 07-57-3-3 × I 07-54-3-1	14.60**	2.63	-1.39*	8.38	-0.33	36.86
20	I 07-57-3-3 × I 07-6-4-5	5.90	4.06	-1.57**	-9.86	6.10*	-3.37
21	I 07-57-3-3 × LM 16	-9.30*	-7.30**	0.94	-15.93**	1.23	64.43**
22	I 07-57-3-3 × CM 500	18.17**	4.83	2.07	22.94**	1.93	10.99
23	I 07-54-3-1 × I 07-6-4-5	-0.70	-1.07	1.27**	11.47*	6.70**	29.49
24	I 07-54-3-1 × LM 16	3.10	2.90	0.43*	37.37**	1.17	21.29
25	I 07-54-3-1 × CM 500	-9.43*	-10.6**	-1.13	-22.99**	2.87	75.53**
26	I 07-6-4-5 × LM 16	-13.9**	-4.67	-0.57	-2.07	-4.40	20.06**
27	I 07-6-4-5 × CM 500	3.20	5.46*	-0.44	-2.24	3.30	-32.04
28	LM 16 × CM 500	5.00	-0.90	-0.27	-14.04**	3.10	-129.24**
Range	Min.	-17.30	-22.80	-3.64	-71.79	-14.27	-129.24
	Max.	27.80	22.66	4.86	62.89	10.43	128.46
No. of significant crosses	Positive	8	5	5	7	7	8
	Negative	9	6	9	9	4	6
	Total crosses	17	11	14	16	11	14
S. E. ±		3.79	2.77	0.59	5.05	2.56	23.27
C.D. at 5%		7.44	5.42	1.17	9.91	5.02	45.61

*, ** Significant at P = 0.05 and P = 0.01 levels of probability, respectively

The crosses, GYL 11 × IL 14-53 (good × poor) and I 07-6-4-5 × LM 16 (good × poor), has highly significant and sca effect for kernel yield along with heterosis (Table 5). The high sca effects in this cross might be due to additive gene interaction. This indicated good chances of isolating desirable genotypes from this cross in segregating generation because of fixable nature of gene action. This cross also manifested desirable sca effects for component traits viz., plant height, ear height, cob length, cob weight, shelling percentage. This appeared appropriate as yield being a complex character depends on a number of its component traits. The estimates of sca effects (Table 5) revealed that none of the hybrid was consistently significantly superior for all the traits. Out of 28 hybrids evaluated, 8 hybrids had registered significant positive sca effects for kernel yield per plant. The best three hybrid combinations on the basis of significant and positive sca effects for this trait were GYL 11 × LM 16, I 07-6-4-5 × LM 16 and HKI 193 × IL 14-53.

Conclusion

The significance of both gca and sca variance indicated the involvement of both additive and non-additive gene effects for the inheritance of the traits like days to 50% tasselling, days to 50% silking, cob weight, number of kernels per row, shelling %, 100 kernels weight, kernel yield per plant and protein content. Therefore, desirable character improvement could be achieved through the exploitation of heterosis. The parents vs. hybrids comparison was significant for all the characters except ear height, cob length, kernel row per cob, shelling percentage and protein content (%) suggesting that parents and hybrids differed statistically for given traits, which indicates involvement of non-additive gene effect and potential exploitation of heterosis for yield improvement.

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