Combining ability analysis for yield and quality traits in single cross hybrids of quality protein maize (*Zea mays* L.) using diallel mating design

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Abstract: Forty-five single-cross hybrids developed (in *rabi* 2014) from ten inbred lines of quality protein maize through diallel mating design along with four checks *viz.,* Pratap QPM Hybrid- 1, Vivek QPM- 9, HQPM- 1 and HQPM-5 were evaluated in randomized block design with three replications for yield and quality traits during *kharif*-2014, to estimate the gca (general combining ability) of the parents and sca (specific combining ability) of hybrids considered for the development of high yielding varieties. The analysis of variance for combining ability revealed significant mean sum of squares due to gca and scafor all the traits, except mean sum of square due to gca for number of grain rows per ear. Ratio of σ^2 sca / σ^2 gca was greater than one for all the traits, thereby indicating the preponderance of non-additive gene effects in the expression of these traits. Inbred line P8 and P5 has been found good general combiner with highest magnitude of gca effects 10.46 and 8.89, respectively and high *per se* i.e. 52.33 g and 44.67 g, respectively for grain yield per plant and majority of traits. Hybrids P6xP8, P5xP8, P3xP5, P5xP7 and P1xP8 showed higher significant positive sca effects ranged from 25.66 to 34.59 along with good per se ranged from 98.00 to 107.67 g for grain yield per plant. These hybrids also exhibited significant positive sca effects for most of the yield and quality traits under study, indicating potential and may be used for exploiting hybrid vigour in in QPM hybrid breeding programmes.

Keywords: Quality protein maize, GCA, SCA, Grain yield, Lysine, Tryptophan

INTRODUCTION

Maize (*Zea maize* L.) with 2n=20, is the third most widely distributed crop of the world after Rice and Wheat (Devi *et al.,* 2016)), being grown in diverse seasons and ecologies with highest production and productivity among food cereals. Globally, the crop is growing at an area of 184.8 mha produces 1037.8 mt with the productivity of 5615.7 kg/ha (FAO, 2014) and gained tremendous importance due to rising demand from diversified sectors like human food, animal feed and also serves as a source of basic raw material for a number of industries. Maize oil has high calorific value and is highly suitable especially for heart patients. Maize contains a high percentage of unsaturated fatty acids like oleic acid and linoleic acid 24.1% and61.9%, respectively (Ignjatovic-Micic, 2015) and has a very low content of cholesterol. Normal maize has low protein content i.e 8 to 11 percent of the kernel weight (FAO) with poor protein quality limited by deficiencies in lysine and tryptophan and has an excess of leucine and isoleucine (Mbuya *et al.,* 2011), leading to a poor growth in children and pellagra in adult (Bisen *et al.,* 2017) . Hence genetic manipulation for improved nutritional value, particularly, protein quality was con-

sidered as a noble goal for maize breeding. With the discovery of mutant alleles, opaque-2 efforts were initiated to improve protein quality of normal maize lines. These mutant gene alter the amino acid profile and composition of maize endosperm protein and result in twice increase in the levels of lysine and tryptophan compared to proportion in normal maize genotypes. The discovery of this mutant and subsequently its modifier was considered remarkable and lead to the concept of Breeding for Quality Protein Maize.

Quality protein maize (QPM) is bio fortified maize with increased lysine and tryptophan levels. QPM contains higher amount of lysine and tryptophan in the endosperm ensuring higher biological value (80%) and availability of protein to human and animal so it can help to get rid of human malnourishment (Hussain *et al.,* 2015). To initiate an effective breeding programme, combining ability analysis is an important tool to identify parents with better potential to transmit desirable characteristics to its progenies and to identify the best specific crosses for yield and various quality parameters. Isolation of parental lines having good gca makes the pathway easy and towards the successin crop improvement.. It provides the base to select good

combiners and also to understand the nature of gene action. So far, combining ability effects in maize and heterotic classification of inbred lines has been extensively studied for different sets of new inbred lines developed/introduced and adapted at different times (Hosana *et al.,* 2015). The single cross qpm hybrids have become popular among Indian farmers due to their high yield potential and excellent uniformity (Singh *et al.,* 2012). Moreover, the exploitation of heterosis through conventional two parent's hybrid breeding in maize is primarily dependent on the development of high *per se* performing lines with good general combining ability.

Keeping the above fact in mind, the present study was therefore, undertaken with a view to estimate general and specific combining ability variances and effects to identify superior quality protein maize hybrids with good yield potential.

MATERIALS AND METHODS

Experimental site and design: The experimental material consisted of ten diverse inbred lines (Table 1) of quality protein maize were crossed in all possible combinations using diallel mating design (excluding reciprocals) to obtain 45 single cross hybrids, during *rabi* 2014 under irrigated, normal soil condition at the Instructional farm, Rajasthan College of Agriculture, Maharana Pratap University of Agriculture and Technology, Udaipur, India. These 45 hybrids, 10 parents along with four standard checks were evaluated in randomized block design with three replications, in a single row plot of 4 m length, maintaining crop geometry of 60 x 25 cm in *kharif*- 2014.

Recording of data: The data were recorded from five randomly selected competitive plants on seventeen distinct morphological and quality characters, except

days to 50 per cent tasseling, days to 50 per cent silking and days to 75 per cent brown husk, where it was observed on complete plot basis. The data on plant height, ear height, ear length, ear girth, number of grain rows per ear, 100-grain weight, grain yield per plant, stover yield per plant, Harvest index, grain oil content, starch content, protein content, tryptophan content and lysine content were recorded for statistical analysis.

Biochemical analysis: The total grain oil content was determined by Soxhlet Method using petroleum ether (BP 40-60°C) as a solvent (A.O.A.C., 1965), starch content by Anthrone reagent method (Morris, 1948), protein content by Micro Kjeldahl's Method (Lindner, 1944), tryptophan content by Papain Hydrolysis Method (Hernandez and Bates, 1969) and lysine content by using Colorimetric Method (Villegas and Mertz, 1970).

Statistical analysis: The mean value of the recorded data was subjected to analysis of variance (ANOVA) using the statistical analysis procedures of Panse and Sukhatme, 1985. The combining ability analysis for diallel mating design was performed according to Model-I (fixed effect) Method-II (parents and one set of $F_{1's}$ without reciprocals) proposed by Griffing (1956).

RESULTS AND DISCUSSION

The analysis of variance for combining ability, using diallel (excluding reciprocal) mating design in respect of 45 crosses for all the seventeen characters are presented in Table 3 and combining ability effect of grain yield and its component of quality protein maize are presented in Table 4. The estimate indicated that the mean squares due to genotypes, parents, crosses and parents v/s crosses were significant at p = 0.01 for all

Table 1. List of parental inbred lines and checks.

S. N.	Inbred line Symbol/Code	Pedigree	Source
Details of parents			
1.	EIQ – 105 (P_1)	CATCEYQ-72-5-4-2-2	AICRP on Maize, Udaipur
2.	EIQ – 106 (P_2)	CATCEYQ-72-2-1-1	AICRP on Maize, Udaipur
3.	EIQ – 107 (P_3)	CATCEYQ-72-9-1-2-2	AICRP on Maize, Udaipur
4.	EIQ – 108 (P_4)	CATCEYQ-72-10-3-4-2-1	AICRP on Maize, Udaipur
5.	EIQ – 109 (P_5)	CATCEYQ-72-11-7-1-1-2	AICRP on Maize, Udaipur
6.	EIQ – 110 (P_6)	CATCEYQ-72-9-3-6-1	AICRP on Maize, Udaipur
7.	EIQ – 111 (P_7)	CATCEYQ-72-13-1-1-4	AICRP on Maize, Udaipur
8.	EIQ – 112 (P_8)	CATCEYQ-72-8-2-3-2-2	AICRP on Maize, Udaipur
9.	EIQ – 113 (P_9)	CATCEYQ-72-5-2-3-1	AICRP on Maize, Udaipur
10.	EIQ – 114 (P_{10})	CATCEYQ-72-3	AICRP on Maize, Udaipur
Details of checks			
1.	Pratap QPM Hybrid- 1 (Check-1)		AICRP on Maize, Udaipur
2.	Vivek QPM- 9 (Check-2)		VPKAS. Almora
3.	HQPM- 1 (Check-3)		CCSHAU, Karnal
4.	HQPM- 5 (Check-4)		CCSHAU, Karnal

Where, AICRP- All India Coordinated Research Project; VPKAS- Vivekanand Parvatiya Krishi Anusandhan Shala; CCSHAU-

Table 2. Analysis of variance for seventeen traits in quality protein maize.

Source of variance	Df	Mean Squares																
		Days to 50% tasseling	Days to 50% silking	Days to 75% brown husk	Plant height (cm)	Ear height (cm)	Ear length (cm)	Ear girth (cm)	Number of grain rows per ear	100-grain weight (g)	Grain yield per plant (g)	Stover yield per plant (g)	Harvest index	Oil content (%)	Starch content (%)	Protein content (%)	Tryptophan content (%)	Lysine content (%)
Replication	2	13.82*	6.56*	3.33*	177.19*	290.04**	1.39	1.17	0.17	1.57	15.81	54.89	1.34	0.000 4	1.13*	0.004	1.8	0.001
Genotype	54	25.46*	32.49*	36.06*	1211.56**	275.03**	11.96**	4.17*	2.70*	27.58*	982.0**	934.73**	30.88*	1.55*	21.33*	3.004*	0.03*	1.30**
Parent	9	31.87*	31.90*	36.70*	574.60*	330.60**	11.72**	3.78**	3.70*	8.11**	127.49*	256.08**	18.31*	1.55*	4.02**	2.09**	0.01*	0.18*
Crosses	44	19.55*	29.10*	32.75*	673.23*	192.82	10.05**	2.98*	2.24*	28.08*	853.21*	734.79	27.90*	1.32*	18.70*	2.30**	0.024**	0.99*
Parent vs. Crosses	1	227.50**	186.88**	176.00**	30630.8**	3392.0 1**	97.82**	60.10**	14.30**	180.51**	14341.8 4**	15840. 4**	274.80	11.80**	293.05**	42.39**	0.47*	25.22**
Error	108	0.85	0.80	0.95	56.08	27.30	0.54	0.56	1.13	0.83	10.41	19.09	2.55	0.001	0.323	0.004	4.13	0.000 3

*, **; Significant at 0.05 and 0.01 levels of probability, respectively

the traits under study, except for grain oil content which was found significant at $p = 0.05$ due to parents. Significant mean squares due to parents and crosses suggested that the parental lines selected were diverse and with a different genetic background. Premlatha *et al.,* worked on maize and found the significant difference due to parents as well as crosses for all traits. Similarly, significant mean squares due to parents vs. crosses indicated presence of considerable amount of variability and overall heterosis for all the traits under study. These results were in confirmation with Avinashe *et al.* (2013), Premlatha *et al.* (2011) and Sundararajan and Kumar (2011). Avinashe *et al.* (2013) found significant difference due to parent vs crosses for grain moisture, protein content, lysine in protein and tryptophan in protein, whereas Rajitha *et al.* (2014) for majority of the characters except days to maturity and grain protein content.

Estimates of combining ability variance: The analysis of variance for combining ability revealed that the mean sum of square due to gca was significant for all the characters except for number of grain rows per ear, while sca was significant for all the characters (Table 3). As significant gca and sca, respectively provide relative genetic effects of additive and non-additive gene action. Hence, results suggested the existence of additive and non-additive gene actions for various traits in the materials under study. Highly significant additive gene action for grain yield per plant and other traits indicating that further improvement can be done in these genotypes through recurrent selection method. Elmyhum 2013; Ofori *et al.,* 2015 worked on qpm and found the similar trends of results.

The magnitude of mean sum of square due to gca was higher than sca for most of the characters *viz.,* days to 50 per cent tasseling, days to 50 per cent silking, days to 75 per cent brown husk, ear length, ear girth, 100 grain weight, grain yield per plant, stover yield per plant, harvest index and tryptophan content. This indicates the predominance of additive gene action to control these characters. The role of non-additive gene action for grain yield and other traits have been reported earlier by Premlatha *et al.,* (2011) and Mural *et al.,* 2012.

Similarly, the magnitude of mean sum of square due to sca was higher than that of gca for some of the characters *viz.,* plant height (434.90), ear height (93.22), number of grain rows per ear (0.99), grain oil content (0.54), starch content (7.35), grain protein content (1.08) and lysine content (0.48). Besides this the ratio of σ^2 sca / σ^2 gca was greater than one for all the traits, thereby indicating the preponderance of non-additive gene effects in the expression of these traits. These results were in accordance with the findings of Estakhr and Heidari (2012) and Amiruzzaman *et al.* (2013) in maize for nearly all traits which were studied in the present investigation. Both general and specific

Table 3. Analysis of variance for combining ability for seventeen traits in quality protein maize.

S.N.	Characters	GCA	Source SCA	Error	Var. Model I σ^2 GCA	σ^2 SCA	σ^2 SCA / σ^2 GCA
		[9]	[45]	[108]			
1	Days to 50 % tasselling	22.92**	5.60**	0.28	16.9773	239.182	14.08834
2	Days to 50% silking	25.09**	7.98**	0.27	18.6137	347.035	18.64406
3	Days to 75 % brown husk	24.90**	9.44**	0.31	18.4274	410.859	22.29609
4	Plant height	248.80**	434.90**	18.69	172.572	18727.8	108.5217
5	Ear height	83.93**	93.22**	9.10	56.1202	3785.62	67.45557
6	Ear length	4.70**	3.841**	0.18	3.39501	164.811	48.54507
7	Ear girth	1.60**	1.350**	0.19	1.04853	52.3889	49.96414
8	Number of grain rows per ear	0.47	0.99**	0.38	0.0674	27.4815	407.4212
9	100-grain weight	10.75**	8.89**	0.28	7.85193	387.251	49.31921
10	Grain yield per plant	441.615**	304.50**	3.47	328.609	13546.1	41.22255
11	Stover yield per plant	406.95**	292.50**	6.36	300.439	12876.3	42.85828
12	Harvest index	10.73**	10.20**	0.85	7.41	420.87	56.79757
13	Grain Oil content	0.41**	0.54**	0.0004	0.31	24.22	78.12903
14	Starch content	5.902**	7.35**	0.11	4.346	325.911	74.98654
15	Grain Protein content	0.61**	1.08**	0.001	0.456	48.5203	106.344
16	Tryptophan content	0.0102**	0.0098**	1.38e-005	0.0076	0.44018	57.29116
17	Lysine content	0.198**	0.48**	9.57e-005	0.1483	21.6168	145.7217

*, **; Significant at 0.05 and 0.01 levels of probability, respectively

combining ability were important but the former played an important role in the expression of all the characters.

Estimates of combining ability effects: The combining ability analysis was performed to obtain information on selection of better parents and crosses for their further use in breeding programme. The estimate of gca effects among the parental lines for yield and quality traits to identify the best parent for subsequent hybrid development programme. Estimates of sca effect of the hybrids for different characters are presented in Table 4.

The estimates of gca effects revealed that good general combiner inbred lines for grain yield per plant were P8 (10.46), P5 (8.89) and P2 (3.05). In general, inbred line P8 has been found good general combiner for all the traits under study *viz.,* days to 50 per cent tasseling (-1.51), days to 50 per cent silking (-2.06), days to 75 per cent brown husk (-1.33), ear length (1.17), ear girth (0.75), 100 grain weight (1.17), grain yield per plant (10.46), stover yield per plant (11.58), harvest index (0.87), grain oil content (0.36), starch content (0.87), protein content (0.33), tryptophan content (0.05) and lysine content (0.27) except plant height, ear height and number of grain rows per ear. Inbred line P2 found good general combiner for days to 50 per cent tasseling, days to 50 per cent silking, days to 75 per cent brown husk, plant height, ear height, 100 grain weight, grain yield per plant, harvest index and lysine content and P5 for ear girth, grain yield per plant, stover yield per plant, harvest index, grain oil content, starch content, protein content, tryptophan content and lysine content. negative value of gca effect for flowering character indicating the earliness of the parental lines.

Sundararajan and Kumar (2011), Elmyhum (2013) revealed the importance of negative gca effect for days to 50% tasseling and days to 50% silking to develop early maturing varieties. This result indicates the preponderance of additive and additive x additive gene effects Premlatha *et al.,* (2011) Among the hybrids, P6 x P8 showed highest significant sca effects in positive direction for grain yield per plant followed by (P5 x P8), (P3 x P5), (P5 x P7) and (P1 x P8). In addition to grain yield per plant, hybrid P6 x P8 also exhibited positive significant sca effects for ear length, ear girth, 100-grain weight, stover yield per plant, harvest index, oil content, starch content, grain protein content, tryptophan content and lysine content, and significant negative sca effects for days to 75 per cent brown husk. This was a cross between poor x good gca effect parent for grain yield per plant. Similarly, hybrid P1 x P8 exhibited highest positive significant sca effects for ear girth and P1 x P9 for harvest index along with positive significant sca effects for grain yield per plant. Similar finding for identification of superior inbred lines and hybrids based on gca and sca effects for grain yield and its components in maize were also reported by Amiruzzaman *et al.* (2013), El-Badawy (2013), and Izhar and Chakraborty (2013). Hybrids P5 x P7 and P1 x P8 showed negative significant sca effects for days to 50 per cent tasseling, days to 50 per cent silking, days to 75 per cent brown husk. Hybrid P3 x P5 exhibited negative significant sca effects for days to 50 per cent silking, days to 75 per cent brown husk.

Among the hybrids for quality traits, P3 x P5 showed maximum significant sca effects in positive direction for oil content followed by (P5 x P8), (P3 x P5), (P5 x P7) and (P1 x P8). In addition to above character, hy-

Table 4. GCA and SCA effects for parents, and best hybrids.

S.N	Geno-type	DT	DS	DBH	PH (cm)	EH(cm)	EL (cm)	EG (cm)	GRE	100-GW (g)	GY (g)	SY (g)	HI (%)	GOC (%)	SC (%)	GPC (%)	TC (%)	LC(%)
1	P1	1.13**	1.42**	1.22**	-4.94**	-3.02**	-0.04	-0.56**	-0.18	-0.98**	-2.41**	-2.73**	-0.45	-0.11**	-0.90**	-0.16**	-0.03**	-0.06**
2	P2	-1.62**	-1.50**	-1.22**	-3.25**	-1.83*	-0.09	-0.04	-0.12	0.45**	3.05**	0.55	1.13**	-0.15**	-0.12	-0.34**	-0.03**	0.01*
3	P3	-0.98**	-1.06**	-0.75**	2.14	-1.22	0.38**	-0.03	0.04	0.05	-4.11**	-1.17	-1.42**	-0.30**	0.33**	0.25**	0.01*	-0.12**
4	P4	0.22	0.22	0.08	-1.36	-3.16**	-0.24*	-0.24*	-0.07	-1.80**	-9.97**	-7.87**	-1.62**	0.07*	-0.35**	-0.14**	-0.03**	-0.06**
5	P5	-0.09	-0.11	-0.25	4.56**	1.28	0.19	0.34**	-0.01	0.16	8.89**	8.58**	0.93**	0.15**	1.33**	0.30**	0.03**	0.13**
6	P6	-0.87**	-0.94**	-1.44**	-1.67	-1.13	0.51**	-0.34**	-0.18	-0.09	-1.38**	-0.53	-0.20	-0.02*	0.16	-0.11**	0.02**	-0.12**
7	P7	-0.09	0.64**	0.22	6.61**	4.01**	-0.30*	0.14	-0.18	1.47**	-2.61**	-4.14**	0.19	0.14**	-0.18	0.03**	0.01**	0.02**
8	P8	-1.51**	-2.06**	-1.33**	4.64**	4.01**	1.17**	0.75**	0.21	1.17**	10.46**	11.58**	0.87**	0.36**	0.87**	0.33**	0.05**	0.27**
9	P9	0.88**	0.67**	0.14	0.75	1.84*	-0.38**	0.05	0.04	-0.26	-0.36	-1.98**	0.46	-0.08**	-0.83**	-0.15**	-0.03**	0.07**
10	P10	2.91**	2.72**	3.33**	-7.47**	-0.77	-1.19**	-0.07	0.43*	-0.19	-1.58**	-2.28**	0.11	-0.06**	-0.31**	-0.01	-0.02**	-0.14**
11	P1 x P8	-3.27**	-3.60**	-4.46**	25.34**	10.93**	1.76**	2.25**	0.74	2.59**	25.95**	24.27**	3.39**	1.20**	5.07**	1.64**	0.27**	1.13**
12	P3 x P5	-0.91	-1.41**	-1.58**	11.00**	4.18	3.50**	2.12**	1.41**	4.07**	31.22**	29.38**	4.14**	2.01**	0.24	1.31**	0.16**	0.56**
13	P5 x P7	-1.80**	-1.77**	-2.21**	13.86**	7.29**	0.85*	1.12**	-0.37	-1.01*	28.72**	25.02**	3.62**	0.05**	4.46**	0.94**	-0.01**	0.08**
14	P5 x P8	0.29	-1.08*	-2.33**	9.17*	5.63*	2.54**	1.01*	1.24*	-1.22*	20.65**	15.63**	2.98**	0.65**	2.53**	1.47**	0.20**	1.16**
15	P6 x P8	-0.94	-1.24*	-0.80	25.72**	9.38**	2.56**	2.03**	-0.59	7.86**	34.59**	27.07**	4.54**	1.42**	4.40**	1.83**	0.23**	1.37**

*, **; Significant at 0.05 and 0.01 levels of probability, respectively;DT: Days to 50% tasseling, DS: Days to 50% silking, DBH: Days to 75% brown husk, PH: Plant height, EH: Ear height, EL: Ear length, EG: Ear girth, GRE: No. of grain rows per ear, 100 GW: 100 grain weight, GY: Grain yield per plant, SY: Stover yield per plant, HI: Harvest index, GOC: Grain Oil content, SC: Starch content, GPC: Grain Protein content, TC: Tryptophan content, LC: Lysine content

Table 5. Five best hybrids identified on the basis of *per se* performance along with their sca effects for grain yield and quality traits.

S.N.	Hybrids	*Per se* performance for grain yield per plant (g)	sca/gca effects					
			Grain yield per plant (g)	Grain oil content (%)	Starch content (%)	Protein content (%)	Tryptophan content (%)	Lysine content (%)
1.	(P6 x P8)	107.67	34.59**	1.42**	4.40**	1.83**	0.23**	1.37**
2.	(P5 x P8)	104.00	31.22**	0.65**	2.53**	1.47**	0.20**	1.16**
3.	(P3 x P5)	100.00	28.72**	2.01**	0.24	1.31**	0.16**	0.56**
4.	(P5 x P7)	99.00	25.95**	0.05**	4.46**	0.94**	-0.01**	0.08**
5.	(P1 x P8)	98.00	25.66**	1.20**	5.07**	1.64**	0.27**	1.13**
6.	EIQ – 105 (P1)	35.33	-2.41**	-0.11**	-0.90**	-0.16**	-0.03**	-0.06**
7.	EIQ – 107 (P3)	34.67	-4.11**	-0.30**	0.33**	0.25**	0.01**	-0.12**
8.	EIQ – 109 (P5)	44.67	8.89**	0.15**	1.33**	0.30**	0.03**	0.13**
9.	EIQ – 110 (P6)	50.17	-1.38**	-0.02**	0.16	-0.11**	0.02**	-0.12**
10.	EIQ – 111 (P7)	49.33	-2.61**	0.14**	-0.18	0.03**	0.01**	0.02**
11.	EIQ – 112 (P8)	52.33	10.46**	0.36**	0.87**	0.33**	0.05**	0.27**
12.	HQPM-5	90.00	-	-	-	-	-	-

*, **; Significant at 0.05 and 0.01 levels of probability, respectively

brids P3 x P5 also exhibited positive significant sca effects for all yield and quality traits under study except for starch content. The positive significant sca effects for starch content were exhibited by twenty-three hybrids. The hybrid P1 x P8 showed highest positive significant sca effect for starch content (5.07). The hybrid P1 x P8 also exhibited positive significant sca effects for all yield contributing traits except for number of grain rows per ear and as well as for all quality traits under study. Hybrid P3 x P9 depicted highest positive significant sca effect for protein content (1.91). This hybrid also exhibited positive significant sca effects for grain yield per plant, stover yield per plant, grain oil content, starch content, grain protein content, tryptophan content and lysine content. Hybrid P1 x P8 depicted highest positive significant sca effect for tryptophan content (0.27). This was a cross between good x good gca effect parent. Hybrid P3 x P9 depicted highest positive significant sca effects for lysine content (1.46%). This was a cross between good x good gca effect parent for lysine content. In the present investigation, some inbred lines can be selected for the successful development of single cross hybrids since they possessed good general combining ability for grain yield per plant, other yield contributing traits and quality traits.

Conclusion

The hybrid P6 x P8 was the best specific combination for grain yield per plant followed by (P5 x P8), (P3 x P5), (P5 x P7) and (P1 x P8). Out of the best hybrids few hybrids also showed significant positive sca effects for oil content (P1 x P8, P3 x P5 and P6 x P8), for starch content (P1 x P8, P5 x P7 and P6 x P8), for protein content (P1 x P8, P3 x P5 and P5 x P7), for tryptophan content (P1 x P8, P3 x P5, P6 x P8 and P5 x P8) and for lysine content (P1 x P8, P5 x P8 and P6 x P8). They produced significant and desirable sca effects for most of the traits studied indicating potential for exploiting hybrid vigour in breeding programme. In general, a close association between sca effects, *per se* performance for grain yield per plant, oil content, protein content, tryptophan content and lysine content was observed among the best hybrids identified on the basis of sca effects.

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