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Research Article

Heterosis and Combining ability for yield and quality traits in Quality Protein Maize (*Zea mays* L.)

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Abstract
A study of diallel analysis (excluding reciprocal cross) involving 10 maize inbreds (P_1 to P_{10}) was carried out to identify high heterotic crosses and their relationship in terms of general and specific combining ability (GCA and SCA) for yield and quality traits in quality protein maize under four different environments. Analysis of variance exhibited highly significant difference among them for all the traits in all the environments. The ratio of gca/sca was less than unity there by indicating the preponderance of non-additive gene action in the expression of all the characters studied. The parents P_1, P_4 and P_{10} for kernel yield, P_1, P_3 and P_4 for oil content, P_6 and P_9 for protein content as well as tryptophan content, P_2, P_6 and P_9 for lysine content were identified as most promising parents due to having good general combining ability in all environments. Among the crosses significant and desirable sca effects were found in P1 x P9, P1 x P10, P2 x P7, P4 x P5, P5 x P9, P6 x P8 and P7 x P9 for kernel yield, P2 x P7, P3 x P5 and P1 x P7 for oil content and P1 x P8 and P5 x P9 for protein, tryptophan and lysine content, respectively. On the basis of heterosis, the hybrids P1 x P10, P2 x P7, P4 x P5 for kernel yield per plant, P3 x P5 for oil, P5 x P9 for protein as well as tryptophan and P1 x P10 for lysine content gave consistent performance in all the environments. Therefore, these crosses could be utilised for further selection of high kernel yield and quality progenies to achieve quantum jump in quality protein maize improvement.

Key words
Maize, *gca* and *sca* effects, heterobeltiosis, standard heterosis, yield, and quality traits

Introduction

Maize (*Zea mays* L.) is an important cereal crop next to rice and wheat and it is one of the principle sources of carbohydrate and proteins for nearly half of the people in the world. It is a highly cross pollinated crop and there is a wide scope for exploitation of hybrid vigor. A genetic approach to improve the nutritional quality of maize protein yielded the quality protein maize which contains *opaque-2*, a single gene mutation that alter the protein composition of the endosperm protein and nearly double the essential amino acids (Akande and Lamidi, 2006). Quality protein maize (QPM) contains two high quality amino acids *viz.*, lysine and tryptophan, which are two times higher in QPM than normal maize. With its high nutritional quality QPM can offer an easy and inexpensive source of high quality protein to the millions of poor. Development and adaptation of QPM would increase the nutritional quality of food and feed as well.

Information on heterotic patterns and combining ability among maize germplasm is essential in maximizing the effectiveness of hybrid development. Development of commercial QPM hybrid usually requires a good knowledge of combining ability of the breeding materials to be used. Selection of parents based on combining ability has been used as an important breeding approach in crop improvement. The success in commercial production of hybrid maize depends up on the availability of productive diverse quality protein maze inbred lines and clear knowledge of gene action for specific traits. Therefore, the present investigation was undertaken to study the combining ability and estimate the extent of heterosis for kernel yield and quality traits under different environments to check the consistency of superior cross combination.

Materials and Methods

Ten diverse inbred lines of QPM *viz.*, GWQPM 6-3, GWQPM 5-1, GWQPM 55-2, GWQPM 47-4, GWQPM 46-2, GWQPM 40-3, GWQPM 26-3, GWQPM 22-5, GWQPM 17-1 and GWQPM 11 were utilised to produce 45 F_1 hybrids using half diallel crossing system during *kharif* and *Rabi* 2011-12. The 45 hybrids along with their parents and checks (HQPM 1 and DHM 117) were evaluated in randomized block design with three replication in four different environments *viz*., E1: *Kharif* (1^{st} fortnight of July, 2012), E2: Semi *rabi* (2nd fort night of October, 2012), E3: *Rabi* (1^{st} fort night of December, 2012) and E4: Summer (2^{nd} fort night of January, 2013) at Agricultural Research Station, Anand Agricultural University, Sansoli, Ta: Mahemdavad, Dist.: Kheda (Gujarat). Each entry was consisted of a single row of 5.0 m length with distance of 60 cm between rows and 30 cm between plants within row. The data were recorded for kernel yield per plant, oil content (by Soxhlet method AOAC, 1995), protein content (Microkjeldahl method by Hawk 1951), tryptophan content (Colorimetric method by Hernandez and Bates, 1969) and lysine content (Colorimetric method by Tsai *et al*., 1972). The mean data were subjected to statistical

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analysis. The analysis of variance was carried out as per the method given by Panse and Sukhatme (1969), combining ability analysis (model-I and method -II) as suggested by Griffing (1956) as well as estimation of heterobeltiosis and economic heterosis as per the method given by Fonseca and Peterson (1968) and Meredith and Bridge (1972), respectively.

Results and Discussion

The analysis of variance revealed highly significant differences for all the characters studied (Table 1). The mean square due to parents differed significantly indicating the parents involved in the study were diverse for all the characters. The variance due to parents *vs* crosses differed significantly indicating the presence of high heterosis response in the material studied. The variance due to general and specific combining ability was highly significant for all the characters under study, indicating the influence of both additive and non-additive effects in the expression of these characters (Table 2). The influence of both types of gene effect was also observed by Amiruzzaman *et al*. (2011) and Avinashe (2011) in maize. Combining ability analysis revealed that estimates of specific combining ability (SCA) variances were higher than general combining ability (GCA) variances for all the traits under study in all the environments, suggesting preponderance of non-additive gene action for these traits.

GCA effects: The estimates of GCA effects (Table 5) showed that the parents GWQPM 6-3, GWQPM 47-4 and GWQPM 11 were found to be good general combiner for kernel yield per plant at least in three environments. The GCA effects for oil content revealed that, the parents GWQPM 6-3, GWQPM 55-2 and GWQPM 47-4 exhibited significant and positive GCA effects in all environments. The parents GWQPM 40-3 and GWQPM 17-1 possess positive significant GCA effects at least in three environments and proved to be a good general combiner for protein and tryptophan content, while the parents GWQPM 5-1, GWQPM 40-3 and GWQPM 17-1 were found to be good general combiner for lysine content in all the environments. Thus the inbred lines which exhibited good general combiner for at least one trait can be used as donor parents for the accumulation of favorable genes.

SCA effects: Specific combining ability effects for kernel yield per plant (Table 6) revealed that the range of SCA effects for these traits ranged from -29.45 to 42.77 in E_1, -17.19 to 34.11 in E_2, -39.51 to 49.67 in E_3 and -26.96 to 39.39 in E_4. Among the 45 crosses, the cross GWQPM 6-3 x GWQPM 17-1, GWQPM 6-3 x GWQPM 11, GWQPM 5-1 x GWQPM 26-3, GWQPM 47-4 x GWQPM 46-2, GWQPM 46-2 x GWQPM 17-1, GWQPM 40-3 x GWQPM 22-5 and GWQPM 26-3 x GWQPM 17-1 give the consistent performance in all the environments and proved to be good specific combiner for this trait. The number of crosses which depicted significant and positive SCA effects in all the environments were 12, 3, 9 and 11 for oil, protein, tryptophan and lysine content, respectively. Among them GWQPM 6-3 x GWQPM 26-3, GWQPM 5-1 x GWQPM 26-3, GWQPM 55-2 x GWQPM 46-2 for oil content and GWQPM 6-3 x GWQPM 22-5 and GWQPM 46-2 x GWQPM 17-1 for protein, tryptophan and lysine content found good specific combiners. In the present study, the cross which was found to be good for the respective characters had at least one parent with good or average general combiner. Therefore, in diallel analysis one must select hybrids of high specific combining ability in which one of the parents with good general combining ability.

Heterosis: The range of heterobeltiosis and standard heterosis for different traits is presented in Table 3. Considering the higher heterosis for kernel yield per plant, hybrids GWQPM 6-3 x GWQPM 11 and GWQPM 5-1 x GWQPM 26-3 were superior by giving consistent performance in all the environments. Whereas, cross GWQPM 47-4 x GWQPM 46-2 in E_1 and E_4, GWQPM 6-3 x GWQPM 17-1 in E_2 and GWQPM 6-3 x GWQPM 26-3 in E_3 were having better heterotic effects. Oil, protein, tryptophan and lysine content are important quality traits in quality protein maize. For these traits very less variation was observed between parents and crosses. Several crosses exhibited significant desirable heterosis for these traits. The cross GWQPM 55-2 x GWQPM 46-2 for oil content, GWQPM 46-2 x GWQPM 17-1 for protein as well as tryptophan content and GWQPM 6-3 x GWQPM 11 for lysine content recorded positive heterobeltiosis and standard heterosis in most of the environments. Thus heterosis breeding holds promise for improving quality traits in maize. In general, it is observed from the heterotic result that the cross which found superior for kernel yield and quality traits are different. This indicated that yield and quality have negative relationship i.e. when quality of hybrid increased side by side yield was decreased and vice versa (Amiruzzaman et al. 2011). The results are in agreement with Patel *et al.* (2007), Avinashe (2011) and Premlatha *et al.* (2011).

Thus it can be concluded that, parents GWQPM 6-3, GWQPM 47-4 and GWQPM 11 for kernel yield per plant whereas, GWQPM 40-3 and GWQPM 17-1 for quality traits (*viz*., oil, protein, tryptophan and lysine content) found good general combiners. The crosses GWQPM 6-3 x GWQPM 11, GWQPM 5-1 x GWQPM 26-3 and GWQPM 47-4 x GWQPM 46-2 were identified as

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outstanding for kernel yield per plant due to possessing high SCA and heterotic effects. Therefore, these hybrids and their parents may further utilize in future breeding programme.

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Table 1. Analysis of variance for kernel yield per plant, oil , protein, tryptophan and lysine contents in maize

Source of variance	df	Mean sum of squares																			
		Kernel yield/plant				Oil content				Protein content				Tryptophan content				Lysine content			
		E1	E2	E3	E4	E1	E2	E3	E4	E1	E2	E3	E4	E1	E2	E3	E4	E1	E2	E3	E4
Replications	2	178.04	74.39	24.64	35.47	0.001	0.007	0.013	0.002	0.04	0.01	0.10	0.02	0.0002	0.0002	0.0001	0.0001	0.0008	0.0001	0.0061	0.0001
Genotypes	56	663.53**	581.70**	1533.27**	573.07**	0.35**	0.36**	0.25**	0.27**	0.57**	0.59**	0.75**	0.57**	0.006**	0.005**	0.006**	0.006**	0.070**	0.077**	0.108**	0.049**
Parents (P)	9	380.22**	461.45**	112.51**	356.21**	0.24**	0.35**	0.09**	0.28**	0.31**	0.37**	0.30**	0.26**	0.005**	0.004**	0.006**	0.010**	0.082**	0.090**	0.119**	0.060**
Hybrids (H)	44	701.25**	564.97**	1712.44**	620.63**	0.33**	0.35**	0.26**	0.27**	0.55**	0.58**	0.82**	0.64**	0.006**	0.004**	0.006**	0.005**	0.066**	0.076**	0.107**	0.048**
P x H	1	1553.67**	2399.85**	6436.41**	432.07**	2.39**	0.62**	0.99**	0.45**	3.48**	2.83**	1.55**	0.32**	0.005**	0.029**	0.009**	0.019**	0.143**	0.041**	0.063**	0.001**
C x H.	1	1554.55**	1094.08**	1662.82**	1241.94**	0.02**	0.72**	1.12**	0.42**	0.013**	1.90**	8.53**	4.94**	0.007**	0.013**	0.042**	0.012**	0.497**	0.462**	0.677**	0.387**
Bet. Chk	1	97.07**	179.31**	3740.01**	489.45**	1.00**	0.30**	0.21**	1.92**	10.09**	11.68**	17.20**	9.88**	0.054**	0.073**	0.84**	0.084**	1.279**	1.915**	2.065**	2.030**
Error	112	51.18	75.23	72.80	59.53	0.001	0.002	0.005	0.003	0.05	0.05	0.06	0.06	0.0003	0.0002	0.0002	0.0003	0.0004	0.0004	0.0062	0.0002

Table 2. Analysis of variance for combining ability for kernel yield per plant, oil, protein, tryptophan and lysine contents in maize

Source of variance	df	Mean sum of squares																			
		Kernel yield/plant				Oil content				Protein content				Tryptophan content				Lysine content			
		E1	E2	E3	E4	E1	E2	E3	E4	E1	E2	E3	E4	E1	E2	E3	E4	E1	E2	E3	E4
Parents	9	228.2**	422.2**	622.2**	196.1**	0.13**	0.16**	0.07**	0.08**	0.19**	0.17**	0.38**	0.23**	0.002**	0.002**	0.003**	0.003**	0.04**	0.03**	0.05**	0.03**
Hybrids	44	219.8**	148.2**	488.9**	190.0**	0.12**	0.11**	0.09**	0.09**	0.18**	0.20**	0.22**	0.18**	0.002**	0.001**	0.002**	0.002**	0.02**	0.02**	0.03**	0.01**
Error	108	17.01	25.1	24.3	19.8	0.0002	0.0008	0.0016	0.0011	0.017	0.016	0.020	0.021	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001
Variance																					
GCA		0.77	24.9	12.1	0.55	0.0013	0.0043	-0.001	-0.001	0.001	-0.003	0.014	0.004	0.0001	0.0001	0.0001	0.0001	0.0021	0.0012	0.0025	0.0017
SCA		202.7	123.2	464.6	170.2	0.115	0.110	0.083	0.092	0.172	0.184	0.203	0.162	0.0017	0.0015	0.0019	0.0017	0.0194	0.0235	0.0293	0.0130
GCA/SCA		0.004	0.202	0.026	0.003	0.011	0.039	-0.012	-0.011	0.006	-0.016	0.068	0.024	0.058	0.066	0.052	0.058	0.11	0.051	0.085	0.13

Table 3. Range of heterobeltiosis and standard heterosis for yield and quality traits in maize

Traits	Range											
	HB				SH over HQPM 1				SH over DHM 117			
	E1	E2	E3	E4	E1	E2	E3	E4	E1	E2	E3	E4
KY	-25.55** to 43.21**	-21.63** to 45.23**	-29.25** to 60.66**	-27.94** to 48.16**	-29.35** to 34.30**	-24.92** to 18.77**	-30.38** to 56.61**	-29.66** to 48.22**	-34.01** to 25.44**	-31.17** to 8.88	-50.32** to 11.77**	-41.51** to 23.25**
OC	-17.87** to 21.43**	-22.46** to 22.26**	-13.15** to 23.31**	-19.55** to 23.47**	-21.92** to 6.91**	-17.07** to 20.17**	-9.37** to 23.75**	-21.83** to 7.02**	-5.62** to 29.22**	-7.45** to 34.11**	-0.81** to 36.29**	2.89* to 40.86**
PC	-14.79** to 4.97**	-9.67** to 5.42**	-8.05** to 7.36**	-9.61** to 8.78**	-17.88** to 0.89	-12.08** to 2.62	-13.95** to 4.47**	-11.31** to 6.48**	2.31 to 23.48**	11.44** to 30.07**	14.08** to 38.51**	11.02** to 33.29**
TC	-13.14** to 13.64**	-17.65** to 1.96	-18.32** to 8.23**	-18.18** to 6.38**	-18.00** to 3.20*	-17.00** to 2.17*	-18.11** to 3.54**	-19.46** to 1.56	6.22** to 33.68**	12.30** to 39.04**	13.66** to 43.72**	11.29** to 40.32**
LC	-14.69** to 14.10**	-20.05** to 7.92**	-25.22** to 6.17**	-11.82** to 8.82**	-18.29** to 4.73**	-23.98** to 0.60	-27.96** to 4.98*	-20.52** to 0.71	26.53** to 62.18**	28.08** to 69.49**	23.58** to 80.08**	35.63** to 71.86**

KY: kernel yield per plant, OC: oil content, PC-protein content, TC-tryptophan content, LC-lysine content

Table 4. Manifestation of heterobeltiosis (HB) and standard heterosis (SH) for quality characters in three top ranking crosses for kernel yield per plant in each environment

Characters		Heterobeltiosis (HB)			Standard heterosis (SH)					
					HQPM 1			DHM 117		
		P1 x P10	P2 x P7	P4 x P5	P1 x P10	P2 x P7	P4 x P5	P1 x P10	P2 x P7	P4 x P5
Kernel yield per plant	E_1	43.21**	23.67**	25.52**	34.30**	17.37**	13.74**	25.44**	9.62*	6.23
	E_2	15.66**	45.23**	13.06*	14.89*	18.77**	11.24	5.33	8.88	1.68
	E_3	60.66**	52.37**	37.59**	56.61**	49.92**	29.19**	11.77**	7.00	7.80
	E_4	48.16**	32.14**	27.36**	48.22**	30.40**	20.62**	23.25**	8.43	0.30
Oil content	E_1	9.57**	8.97**	15.25**	2.47**	3.59**	-1.48**	23.85**	25.21**	19.08**
	E_2	2.46**	15.70**	12.39**	13.27**	8.07**	10.47**	26.41**	20.61**	23.29**
	E_3	5.98**	6.17**	21.16**	10.60**	8.79**	23.75**	21.81**	19.82**	36.29**
	E_4	3.21**	13.39**	7.77**	0.28	-3.40**	-4.61**	32.00**	27.15**	25.56**
Protein content	E_1	-2.10	-1.60	-9.45**	-8.80**	-6.16**	-11.82**	13.62**	16.90**	9.86**
	E_2	-0.33	-1.25	-5.17**	-7.31**	-2.42	-4.74**	17.48**	23.68**	20.74**
	E_3	3.47*	6.19*	2.39	-1.16	-0.36	-0.36	31.04**	32.09**	32.09**
	E_4	-2.88	-0.54	1.92	-4.94**	-3.98*	0.00	19.00**	20.57**	25.18**
Tryptophan content	E_1	13.55**	5.51**	1.72	-2.8	-0.40	-5.6**	25.91**	29.02**	22.28**
	E_2	0.43	-1.20	-5.49**	-6.72**	-1.98	-4.74**	26.20**	32.62**	28.88**
	E_3	-0.79	3.20*	-2.29	-1.57	1.57	0.79	36.61**	40.98**	39.89**
	E_4	-1.70	-5.43**	-2.46	-10.12**	-5.06**	-7.39**	24.19**	31.18**	27.96**
Lysine content	E_1	14.10**	4.06**	10.94**	3.45**	1.53*	-1.41*	60.20**	57.23**	52.67**
	E_2	-0.67	7.92**	-5.17**	-10.67**	-0.36	-7.55**	50.51**	67.88**	55.76**
	E_3	5.90**	0.88	0.73	2.01	-5.21*	-2.25	75.00**	62.60**	67.68**
	E_4	7.54**	1.45**	3.32**	-5.22**	-8.78**	-7.59**	61.74**	55.67**	57.69**

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Table 5. General combining ability effects for kernel yield per plant, oil, protein , tryptophan and lysine contents in maize

Sl. No.	Parents	Envi.	Kernel yield/plant	Oil	Protein	Tryptophan	Lysine
1	GWQPM - 6-3	E_1	7.30 **	0.20 **	0.04	-0.01 **	-0.03 **
		E_2	12.95 **	0.13 **	-0.03	-0.01 **	0.02 **
		E_3	12.99 **	0.15 **	0.03	0.00	0.04 **
		E_4	7.38 **	0.11 **	0.15 **	-0.01 **	0.02 **
2	GWQPM - 5-1	E_1	2.60 *	-0.11 **	0.17 **	0.01 *	0.06 **
		E_2	0.21	-0.04 **	0.01	0.01 **	0.06 **
		E_3	1.17	-0.03 **	-0.06	0.00	0.03 **
		E_4	1.13	-0.04 **	0.00	0.01 **	0.02 **
3	GWQPM - 55-2	E_1	-6.87 **	0.12 **	-0.29 **	-0.02 **	-0.10 **
		E_2	-5.70 **	0.12 **	-0.14 **	-0.01 **	-0.07 **
		E_3	-10.05 **	0.03 **	-0.30 **	-0.02 **	-0.11 **
		E_4	-7.28 **	0.04 **	-0.13 **	-0.01 **	-0.07 **
4	GWQPM -47-4	E_1	5.11 **	0.03 **	-0.02	0.00	0.00
		E_2	7.16 **	0.14 **	0.13 **	0.00	-0.04 **
		E_3	-3.71 **	0.03 **	-0.03	0.00	-0.03 *
		E_4	3.32 **	0.06 **	0.00	-0.01 **	-0.02 **
5	GWQPM -46-2	E_1	-2.65 *	0.00	0.03	0.01 **	-0.02 **
		E_2	-3.36 *	0.01	0.13 **	0.01 **	0.00
		E_3	-4.79 **	0.07 **	0.10 *	0.01 **	0.01
		E_4	-2.79 *	0.00	-0.06	0.00	0.00
6	GWQPM -40-3	E_1	-3.47 **	-0.02 **	0.13 **	0.02 **	0.07 **
		E_2	-5.07 **	-0.02 *	0.02	0.01 **	0.06 **
		E_3	-9.60 **	0.04 **	0.25 **	0.02 **	0.09 **
		E_4	-3.03 *	-0.08 **	0.20 **	0.03 **	0.07 **
7	GWQPM -26-3	E_1	-1.20	0.03 **	-0.05	0.00	-0.04 **
		E_2	-1.59	-0.18 **	-0.01	-0.01 **	-0.03 **
		E_3	6.28 **	-0.04 **	-0.17 **	-0.01 **	-0.10 **
		E_4	-1.18	-0.15 **	-0.18 **	-0.01 **	-0.06 **
8	GWQPM -22-5	E_1	-0.79	-0.13 **	0.03	0.01 *	0.00
		E_2	0.01	-0.19 **	-0.01	0.01 **	0.00
		E_3	2.37	-0.07 **	0.10 *	0.00	0.05 **
		E_4	0.86	0.00	-0.04	0.00	-0.02 **
9	GWQPM -17-1	E_1	-2.91 *	0.00	0.04	0.01 **	0.09 **
		E_2	-5.04 **	0.03 **	0.15 **	0.02 **	0.08 **
		E_3	0.79	-0.09 **	0.23 **	0.02 **	0.08 **
		E_4	-1.07	0.10 **	0.20 **	0.02 **	0.09 **
10	GWQPM -11	E_1	2.87 *	-0.12 **	-0.07	-0.01 **	-0.03 **
		E_2	0.43	-0.01	-0.23 **	-0.02 **	-0.08 **
		E_3	4.55 **	-0.09 **	-0.15 **	-0.02 **	-0.05 **
		E_4	2.65 *	-0.02 *	-0.12 **	-0.02 **	-0.04 **
	SE	E_1	1.17	0.004	0.037	0.003	0.003
		E_2	1.42	0.008	0.036	0.002	0.003
		E_3	1.40	0.011	0.040	0.002	0.013
		E_4	1.27	0.009	0.042	0.003	0.002
	SE gi-gj	E_1	1.76	0.006	0.056	0.004	0.005
		E_2	2.14	0.012	0.055	0.003	0.005
		E_3	2.10	0.017	0.060	0.004	0.019
		E_4	1.90	0.014	0.062	0.004	0.003
	CD	E_1	3.49	0.012	0.111	0.008	0.010
		E_2	4.23	0.023	0.108	0.007	0.009
		E_3	4.16	0.034	0.120	0.007	0.038
		E_4	3.77	0.028	0.124	0.008	0.007

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Table 6. Range of specific combining ability effects for kernel yield per plant, oil, protein, tryptophan and lysine contents in maize

Sl. No.	Parents	Envi.	Kernel yield/plant	Oil	Protein	Tryptophan	Lysine
1	Range	E_1	-29.45 to 42.77	-0.65 to 0.66	-1.14 to 0.89	-0.09 to 0.07	-0.22 to 0.33
		E_2	-17.19 to 34.11	-0.53 to 0.64	-0.78 to 1.01	-0.09 to 0.06	-0.31 to 0.27
		E_3	-39.51 to 49.67	-0.47 to 0.65	-0.95 to 0.87	-0.10 to 0.08	-0.49 to 0.31
		E_4	-26.96 to 39.39	-0.53 to 0.69	-0.86 to 1.15	-0.08 to 0.07	-0.19 to 0.25
2	S.E.	E_1	3.78	0.01	0.12	0.009	0.011
		E_2	4.58	0.03	0.12	0.007	0.010
		E_3	4.51	0.04	0.13	0.008	0.041
		E_4	4.07	0.03	0.13	0.009	0.007
3	SE sij-sik	E_1	5.57	0.02	0.18	0.013	0.016
		E_2	6.75	0.04	0.17	0.010	0.015
		E_3	6.64	0.05	0.19	0.012	0.061
		E_4	6.01	0.04	0.20	0.013	0.011
4	CD	E_1	11.04	0.04	0.35	0.026	0.031
		E_2	13.38	0.07	0.34	0.021	0.029
		E_3	13.17	0.11	0.38	0.023	0.121
		E_4	11.91	0.09	0.39	0.026	0.021
5	SE sij-skl	E_1	5.28	0.02	0.17	0.013	0.015
		E_2	6.41	0.04	0.16	0.010	0.014
		E_3	6.30	0.05	0.18	0.011	0.058
		E_4	5.70	0.04	0.19	0.013	0.010
6	CD	E_1	10.47	0.04	0.33	0.025	0.030
		E_2	12.70	0.07	0.33	0.020	0.027
		E_3	12.49	0.10	0.36	0.022	0.115
		E_4	11.30	0.08	0.37	0.025	0.020
7	Positive	E_1	24	26	18	23	25
		E_2	23	22	22	20	21
		E_3	20	25	26	22	22
		E_4	22	23	21	21	24
8	Positive significant	E_1	11	23	8	14	20
		E_2	11	22	7	15	19
		E_3	18	21	17	19	14
		E_4	10	19	9	13	21
9	Negative	E_1	21	19	27	22	20
		E_2	22	23	23	25	24
		E_3	25	20	19	23	23
		E_4	23	22	24	24	21
10	Negative significant	E_1	13	18	14	14	18
		E_2	7	17	16	19	21
		E_3	13	15	14	20	18
		E_4	13	18	12	18	20