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Study of combining ability through diallel crosses in maize (*Zea mays* L.) for grain yield and protein content

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Abstract
The experiment comprised of twenty one maize hybrids generated from a 7 X 7 diallel cross, along with their parents and two standard check (Gujarat Maize 3 and HQPM 1). The analysis of variance for combining ability study revealed that the value of mean square for general and specific combining ability were highly significant which indicated involvement of both additive and non-additive gene actions with prime importance of non-additive genetic variance for the expression of all the characters. The estimates of *gca* effect revealed that lines CML 264 and GWL 24 appeared to be good general combiners for grain yield and its yield attributes, while line GWL 22 was good general combiner for protein content. The *sca* effect were estimated and it resulted that single crosses GWL 24 x CML 490, CML 264 x GWL 22 and GWL 24 x GWL 28 were outstanding for grain yield. The cross CML 264 x GWL 27 were found most promising for protein content. That outstanding crosses could be exploit commercially as single cross hybrid or further evaluated and utilized to get desirable segregants which will used to improve the synthetic/composite varieties under cultivation or to develop a segregating population.

Keywords: diallel crosses, GCA, grain yield, protein content, SCA, significant

Introduction
Maize (*Zea mays* L.) is one of the most important cereal crop after rice and wheat, contributing to agriculture economy in various ways finding its utility as a source of food for human being as well as a feed for animals and poultry across the world. It is a crop being commercially exploited extensively fetches the name "queen of cereals". Maize is staple food of Asian people and is also utilized in starch, oil, food and feed industries. Maize grain contains about 10 percent protein, 4 percent oil, 70 percent starch and 2.7 percent crude fibre. In India, about 55 percent of maize produced is used for food purposes, about 14 percent as livestock feed, 18 percent as poultry feed, 12 percent in wet milling industry (for starch and oil production) and 1 percent as seed. The recent trend is to go for single cross hybrid than for double crosses as the single cross hybrid show higher uniformity and heterosis than the double cross hybrid and three-way cross hybrid. Therefore a study was carried out with an objective to identify superior maize hybrids with high specific combining ability for yield and yield contributing characters.

Material and Methods
The experimental material comprised of seven white grained parental inbred lines and their 21 single cross hybrids developed by diallel mating scheme without reciprocals (Griffing method-II; Griffing, 1956) [4] crosses and two checks, Gujarat Maize 3 and HQPM 1. The seed of 21 hybrids were produced during 2012 by hand pollination at Anand Agricultural University, Anand. The inbred lines were maintained by sibbing. The crosses, parental inbred lines and checks were sown in Randomized Complete Block Design with three replications consisted of two rows of each treatment of 5 m length with inter and intra row spacing of 60 cm and 20 cm, respectively. The cultivation practices followed as per the recommendations to raise normal crop for optimum yield potential expression. The observations were recorded on randomly selected five plants per treatment in each replication for the thirteen characters *viz.* days to 50 % tasselling, days to 50 % silking, plant height (cm), ear height (cm), days to 75 % dry husk, ear length (cob length, cm), ear girth (cm), number of grain rows per ear, number of grains per row, 100-kernel weight (g), grain yield (g), shelling percentage and protein content (%) as per standard methods laid by Indian Institute of Maize Research, ICAR, New Delhi. Analysis of variance technique suggested by Panse and Sukhatme (1967) [7] was followed to test the differences among the genotypes for all the characters. Combining ability analysis was performed with the data obtained for parents and hybrids according to Model-I, Method-II proposed by Griffing (1956) [4].

Results and Discussion
The study involving seven parental lines with white kernels resulted highly significant values of mean square for general and specific combining ability indicated involvement of both additive and non-additive gene actions for the expression of all the characters except number of grain rows per ear where only non-additive gene action was responsible for expression of this trait (Table 1). The *SCA* variance component was observed to be higher than the respective *GCA* variance component for all the characters except days to 50 % tasselling, days to 50 % silking, ear girth and 100-kernel weight. The lower estimates of potence ratio and predictability ratio for all characters implied the predominant role of non-additive gene action and thus indicated specific combining ability played a greater role for the inheritance of the all the traits. The *gca* effect of parents for grain yield ranged from -10.95 to 7.41 (Table 2). The parent GWL 264 were best general combiner as it revealed highest significant and positive result. The parent also good general combiner for the characters days to 50% silking, days to 75 % dry husk, ear girth, 100-kernel weight and shelling percentage as it found significant and desirable results. Another parent GWL 24 (5.17) were also good general combiner for grain yield. The parents GWL 22 (0.37) and GWL 27 (0.33) proved to be good general combiners with positive significant effect for the character protein content. The *sca* effect for grain yield ranged from -41.11 to 73.61(Table 3). The hybrid GWL 24 x CML 490 observed highest positive and significant estimates of *sca*

effect. For all the traits except days to 75 % dry husk, the cross showed significant and desirable results. It means the cross flowered earlier and give highest grain yield and yield attributes, but it mature very late. Another cross, CML 264 x GWL 22 (30.43) observed significant estimates of *sca* effect in desirable direction for grain yield as well as days to 50 % silking, plant height, ear height, ear length, number of grains per row, 100-kernel weight, shelling percentage and protein content. The single cross hybrids, CML 264 x GWL 27 (2.53) CML 186 x GWL 28 (2.03) GWL 22 x GWL 24 (1.85) showed positive and significant estimates of *sca* effect for protein content. These results are in agreement with those obtained by Avinashe (2011) [1], Gichuru *et al.* (2011) [3], Jampatong *et al.* (2010) [5], Jebaraj *et al.* (2010) [6], Shanthi *et al.* (2010) [6, 10] and Silva *et al.* (2010) [10] for grain yield. The results obtained are also correspond with those of Dodiya and Joshi (2003) [2] and Premlatha *et al.* (2011) [8] for protein content. The parents, CML 264 and GWL 24 were observed to be good combiners for grain yield and yield attributes. Thus these could be used in the future breeding programmes and also to generate more number of desirable segregants. May some cross combinations would throw some desirable transgressive segregants in later generations. Therefore, these crosses may be further evaluated across the years and locations for grain yield and may be exploited for commercial cultivation.

Table 1: Analysis of variance for combining ability for various characters

Source	d.f.	DT	DS	PH	EH	DDH	EL	EG	GRE	NGR	KW	GY	SP	PC
GCA	6	21.54**	25.47**	205.51**	25.27**	8.72**	1.26**	1.10**	0.51	9.37**	17.83**	338.21**	14.00**	0.68**
SCA	21	14.17**	10.56**	306.80**	51.97**	10.49**	3.82**	0.94**	1.33**	17.83**	11.04**	633.58**	17.60**	1.57**
Error	54	0.92	0.82	12.99	3.55	0.75	0.23	0.15	0.29	1.70	0.73	41.90	0.13	0.02
$\delta^2 gca$		2.29**	2.73**	21.38**	2.41**	0.88**	0.11**	0.10**	0.02	0.85**	1.90**	32.92**	1.41**	0.07**
$\delta^2 sca$		13.24**	9.73**	293.90**	48.42**	9.74**	3.58**	0.78**	1.04**	16.12**	10.31**	591.67**	16.29**	1.55**
Potence Ratio		0.60	0.98	0.25	0.17	0.31	0.11	0.46	0.08	0.18	0.64	0.19	0.30	0.16
Predictability Ratio		0.25	0.36	0.12	0.09	0.15	0.05	0.21	-	0.09	0.26	0.10	0.14	0.08

Table 2: General combining ability (*gca*) effect of parents for various characters

Parents	DT	DS	PH	EH	DDH	EL	EG	GRE	NGR	KW	GY	SP	PC
CML 186	-1.13**	0.37	6.12**	-0.56	0.54*	0.52**	-0.23	-0.40*	1.16**	-0.62*	-1.09	2.29**	-0.14**
CML 264	-0.94**	-0.89**	-3.07**	-2.15**	-0.83**	-0.11	0.44**	0.13	-0.39	2.56**	7.41**	0.95**	-0.42**
GWL 22	-1.79**	-1.70**	-5.22**	-1.67**	-1.28**	-0.22	0.43**	0.39*	0.83*	0.04	3.68	0.16	0.37**
GWL 24	-0.94**	-2.37**	-5.77**	-0.34	-0.94**	-0.56**	0.10	-0.02	0.72	0.26	5.17**	-0.41	0.02
GWL 27	2.05**	1.26**	1.49	1.07	0.58*	0.18	-0.06	-0.07	-1.10**	-2.07**	-10.95**	-0.97**	0.33**
GWL 28	1.39**	1.22**	1.41	1.07	0.72**	-0.18	-0.16	0.02	-1.50**	0.45	-2.47	-1.11**	-0.04
CML 490	1.39**	2.11**	5.04**	2.59**	1.21**	0.36**	-0.52**	-0.06	0.28	-0.62*	-1.75	-0.92**	-0.12**
Range	-1.79 to 2.05	-2.37 to 2.11	-5.77 to 6.12	-2.15 to 2.59	-1.28 to 1.21	-0.56 to 0.52	-0.52 to 0.44	-0.40 to 0.39	-1.50 to 1.16	-2.07 to 2.56	-10.95 to 7.41	-1.11 to 2.29	-0.42 to 0.37
S. E. (g_i) ±	0.29	0.28	1.11	0.58	0.26	0.15	0.12	0.16	0.40	0.26	1.99	0.35	0.04

*, ** Significant at 5% and 1% levels, respectively. > When both *GCA* and *SCA* were significant then predictability ratio calculated
d.f. = degree of freedom DT = Days to 50 % tasselling DS = Days to 50 % silking PH = Plant height EH = Ear height
DDH = Days to 75 % dry husk EL = Ear length EG = Ear girth GRE = Number of grain rows per ear NGR = Number of grains per row KW = 100-kernal weight GY = Grain yield SP = Shelling percentage PC = Protein content

Table 3: Specific combining ability (*sca*) effect of hybrids for various characters

Hybrids/crosses	DT	DS	PH	EH	DDH	EL	EG	GRE	NGR	KW	GY	SP	PC
CML 186 x CML 264	5.22**	3.60**	-8.00*	-13.33**	-1.60*	3.28**	1.28**	0.44	3.95**	-0.31	16.67**	1.20	-0.51**
CML 186 x GWL 22	1.74**	0.42	-1.19	-0.48	-1.16	1.73**	0.90*	0.78	3.06**	-2.45**	3.26	0.88	-0.86**
CML 186 x GWL 24	0.56	-0.58	-9.96**	-7.48**	1.18	-1.64**	-1.04**	-1.40**	-4.49**	-4.01**	-41.11**	-4.87**	0.14
CML 186 x GWL 27	-0.44	0.45	10.44**	9.44**	1.66*	0.23	0.29	0.38	3.66**	-2.34**	-1.73	-1.52	-0.66**
CML 186 x GWL 28	-0.11	-4.18**	3.19	3.11	-2.49**	0.15	-0.11	0.15	0.06	-0.86	5.13	7.40**	2.03**
CML 186 x CML 490	-2.44**	-1.06	3.89	3.93*	0.36	-0.39	0.77*	0.63	-4.38**	2.21**	-10.03	1.32	1.72**
CML 264 x GWL 22	-1.11	-3.32**	16.00**	9.11**	5.88**	0.93*	0.13	-0.55	5.29**	2.69**	30.43**	2.57*	0.04**
CML 264 x GWL 24	-5.63**	-3.32**	26.89**	13.11**	-0.12	-0.07	0.02	-0.80	-3.94**	3.14**	-9.61	-4.23**	-0.85**
CML 264 x GWL 27	2.70**	2.05*	10.63**	-0.63	-0.64	0.16	1.04**	0.91	1.88	1.47	15.63**	3.21**	2.53**
CML 264 x GWL 28	-4.63**	-1.25	13.04**	1.37	-3.79**	0.55	0.18	-0.31	-0.38	5.95**	16.17**	4.38**	-1.85**
CML 264 x CML 490	-1.30	-2.14**	-2.93	3.85*	-3.94**	-3.02**	-0.47	1.03*	-1.82	-3.31**	-18.39**	-4.02**	-0.69**
GWL 22 x GWL 24	-3.44**	-5.84**	-9.96**	-9.70**	-3.68**	-1.12*	-1.19**	-0.66	-0.49	1.32	-3.63	2.66**	1.85**
GWL 22 x GWL 27	-0.78	0.86	9.44**	0.56	-1.53*	-0.96*	0.20	0.12	1.32	-2.01**	-5.68	0.92	0.74**
GWL 22 x GWL 28	-2.44**	-0.44	8.85**	9.22**	-1.68*	0.93*	0.80*	1.56**	-1.27	0.81	1.33	-0.73	-0.52**
GWL 22 x CML 490	-4.11**	2.68**	16.56**	-0.63	-1.82*	-0.45	0.09	-0.03	-0.05	-1.45	-7.76	0.00	-1.29**
GWL 24 x GWL 27	-4.63**	-3.47**	24.00**	0.56	-1.19	-1.62**	-0.27	0.54	2.56*	-1.23	-10.05	2.90**	-2.21**
GWL 24 x GWL 28	5.04**	4.23**	5.74	-2.11	5.66**	1.24**	1.33**	1.24**	5.18**	0.25	24.29**	-4.47**	-0.04
GWL 24 x CML 490	-1.96**	-3.99**	6.78*	5.04**	2.84**	5.46**	1.95**	2.12**	12.40**	2.32**	73.61**	7.54**	0.79**
GWL 27 x GWL 28	4.37**	1.94*	15.48**	6.15**	4.81**	1.86**	0.18	0.56	2.32*	3.92**	22.39**	-5.18**	0.17
GWL 27 x CML 490	-1.30	0.38	-13.48**	-5.04**	1.66*	-1.15**	0.60	1.11*	-1.79	-2.68**	-4.50	-7.42**	0.14
GWL 28 x CML 490	1.70**	2.42**	6.59*	0.63	4.18**	0.05	-0.93**	-0.52	-1.38	-5.53**	-30.68**	-1.98	-0.63**
Range of SCA effect	-5.63 to 5.22	-5.84 to 4.23	-13.48 to 26.89	-13.33 to 13.11	-3.94 to 5.88	-3.02 to 5.46	-1.19 to 1.95	-1.40 to 2.12	-4.49 to 12.40	-5.53 to 5.95	-41.11 to 73.61	-7.42 to 7.54	-2.21 to 2.53
Total significant cross	14	13	16	12	15	13	10	6	11	13	10	13	17
Positive	6	6	12	8	7	7	7	5	8	6	7	7	7
Negative	8	7	4	4	8	6	3	1	3	7	3	6	10
S. E. (S_{ij}) ±	0.86	0.81	3.23	1.69	0.77	0.43	0.35	0.48	1.17	0.76	5.81	1.02	0.13

*, ** Significant at 5% and 1% levels, respectively.

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