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Research Article

Gene action and combining ability analysis for kernel yield and its attributing traits in maize [*Zea mays* (L.)]

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Abstract

Eight maize (*Zea mays* L.) genotypes were crossed in a half diallel mating design. The analysis of variance for combining ability revealed that mean sum of squares due to general combining ability were found significant for all the traits except cob girth, whereas, the specific combining ability effects were found highly significant for all the characters except anthesis-silking interval. The low ratio (<1.0) of GCA to SCA variance for sixteen traits indicated that non-additive type of gene action was predominant in the expression of yield and component traits. Based on estimates of general combining ability effects revealed that four parents BLD-11 (5.19), CML-338 (4.28), VL-1032 (1.68) and VL-109178 (1.25) were found good general combiners because they registered significant and positive *gca* effects. The estimates of *sca* effects revealed that 23 hybrids were exhibited significant positive *sca* effects. The spectrum of differences in *sca* effects for this trait ranged from -2.70 (CBE-98 × CML-338) to 27.57 (CBE-98 × MRCN-3) and the top most three hybrids for kernel yield per plant on the basis of specific combining ability effects were CBE-98 × MRCN-3 (27.57), CBE-98 × BLD-11 (23.16) and CBE-26 × BLD-11 (21.20).

Keywords

Maize, diallel analysis, gene action, combining ability

Introduction

Maize (*Zea mays* L.; 2n=20) is one of the most important economic cereal crops of the world. Maize grain is gaining popularity and huge demand in our country due to nutritionally important and has multiple function of traditional farming system; it has diversified uses as food for human, live stocks and poultry. It is also a source of industrial raw material for the production of flour, flakes, corn starch, corn oil, corn syrup, glucose, alcohol, ethanol, gluten, dextrose, custard powder and many more products, besides these, it's also used for making glue, soaps, insecticides, toothpaste, shaving cream, rubber tires, rayon, model plastic, etc., (White and Johnson, 2003). Maize belongs to the grass family *Poaceae* (*Gramineae*), tribe *Maydeae* and out of four, maize is the only cultivated and economically important species of genus *Zea*. The word "Zea" (zela) was derived from an old Greek name for a food grass. The other *Zea* species referred to as teosinte [*Zea mexicana* (schrad.) Kuntze], is wild species.

Maize is a monoecious plant, that is, the reproductive organs are partitioned into separate pistillate (ear), the female flower and staminate (tassel) inflorescence, the male flower on the same

plant. It has a determinate growth habit and the shoot terminates into the inflorescences bearing staminate or pistillate flowers (Dhillon and Prasanna, 2001). Maize is generally protandrous, that is, the male flower matures earlier than female flower, however protogyny is not ruled out. In India, it is grown round the year in an area of 8.69 million hectares with the production of 21.81 million tonnes and 2509 kg/ha productivity (Anonymous, 2016).

The success of breeding procedure is determined by the useful gene combinations, organized in the form of good combining lines and isolation of valuable germplasm. Some lines produce outstanding progenies on crossing with others, while, others may look equally desirable but may not produce good progenies on crossing. The lines, which perform well in combination, are eventually of great importance to the plant breeders. Hence, investigation of general and specific combining ability would yield very useful information. Accordingly, a good knowledge of gene action involved in the inheritance of quantitative characters of economic importance is required in

order to form an efficient breeding plan leading to rapid improvement.

Material and Methods

The material used for this experiment consisted of eight parents (CBE-15, CBE-98, CBE-26, MRCN-3, CML-338, BLD-11, VL-1032 and VL-109178), their 28 half-diallel crosses and one check GAYMH-1. The seed of 28 hybrids were produced during *rabi*2016 at Department of Seed Technology, S.D. Agricultural University, Sardarkrushinagar. The seed of inbred lines were maintained by sibbing. A set of 37 genotypes comprising of eight parents and their 28 F₁ hybrids with single check (GAYMH-1) were sown in Randomized Block Design (RBD) with three replications, during *kharif*2017. Each entry sown in 3m length row and it was 70 cm away from another row and maintained 20 cm distance between plants within row. The recommended agronomical practices and plant protection measures were adopted for raising a good crop. The observations were recorded both as visual assessment (days to tasseling, days to silking, Anthesis-silking interval (ASI) and days to dry husk) and measurement on randomly selected five competitive individual plants (plant height, cob height, cob weight, cob length, cob girth, number of kernel rows per cob, number of kernels per row, 100-kernel weight, kernel yield per plant, shelling percentage, protein content and starch content). Where The cob height of the each tagged five plants per plot was measured in centimeter from the base of the plant to the base of the uppermost ear on the main stalk at a time of maturity. Where as Cob length was measured in centimeter from the end of the cob to the tip of the cob. The replication wise mean values of each entry for the sixteen traits were analysed using Randomized Block Design (RBD) as suggested by Sukhatme and Amble (1985).

Results and Discussion

The analysis of variance for combining ability was performed as per method suggested by Griffing (1956) Model-I and method-2. The analysis of variance for combining ability for sixteen traits were presented in table 1. The results revealed that mean sum of squares due to general combining ability were found significant for all the traits except cob girth, whereas, the specific combining ability effects were found highly significant for all the characters except anthesis-silking interval. The low ratio (<1.0) of GCA to SCA variance for sixteen traits indicated that non-additive type of gene action was predominant in the expression of yield and component traits.

The parents were classified as good, average and poor general combiner for different characters

based on estimates of *gca* (Table 2 and Table 3). The *gca* effects of parents revealed that none of the parents consistently good general combiner for all the characters under study. The parents, BLD-11, CML-338, VL-1032 and VL-109178 were good general combiner for kernel yield per plant. In addition to kernel yield, parent BLD-11 was also found good general combiners for cob weight, cob length, number of kernels per row, 100-kernel weight and shelling percentage. The parent CML-338 was found good general combiner for traits like days to tasseling, days to silking, days to dry husk, ear height, number of kernel rows per cob and shelling percentage. The parent, VL-1032 was good general combiner for days to dry husk, cob weight, cob length, 100-kernel weight. While, parent VL-109178 was also observed good general combiner for days to tasseling, days to silking and starch content.

When the estimates of general combining ability compared with the *per se* performance of parents, it was observed that the parents which were good general combiner for kernel yield and component and also superior in their *per se* performance, which indicates that predominant role of additive and additive x additive types of gene action. Thus, selection of parent for kernel yield and components based on *per se* performance may be effective. Hence, high yielding parents with good attributes for different kernel yield attributes may be inter crossed to combine the gene in positive direction to augment the yield potential. These results are agreement with those obtained by Krishna *et al.* (2003), Mathur and Bhatnagar (2003), Malik *et al.* (2004), Muraya *et al.* (2006), Bello and Olayo (2009), Avinash (2011), Soni (2012), Adebayo *et al.* (2014), Gami *et al.* (2018a) and Gami *et al.* (2018b).

The estimates of *sca* effects for kernel yield per plant (g) revealed that among 28 hybrids, 23 hybrids were exhibited significant positive *sca* effects (Table 4). The spectrum of differences in *sca* effects for this trait ranged from -2.70 (CBE-98 × CML-338) to 27.57 (CBE-98 × MRCN-3) and the top most three hybrids for kernel yield per plant on the basis of specific combining ability effects were CBE-98 × MRCN-3 (27.57), CBE-98 × BLD-11 (23.16) and CBE-26 × BLD-11 (21.20). A perusal of data revealed that none of the crosses had high-ranking *sca* effects for all the characters. The data revealed that the top ranking *sca* for most of the trait where accompanied by top ranking *per se* performance, which showing predominant role of non-additive gene effects in expression of kernel yield and component traits. Thus, for improvement of kernel yield and component traits, heterosis breeding may be more rewarding.



The general combining ability effects of parents revealed that none of the parents consistently good general combiner for all the characters under study. The parents, BLD-11, CML-338, VL-1032 and VL-109178 were good general combiners for kernel yield per plant. In addition to kernel yield, parent BLD-11 was also good general combiner for cob weight, cob length, number of kernels per row, 100-kernel weight and shelling percentage.

The hybrids exhibited high *sca* effects irrespective of the *gca* effects of the parents indicating important role of dominance and epistatic gene effects. The estimates of *sca* effects revealed that the cross combinations CBE-98 × MRCN-3, CBE-98 × BLD-11 and CBE-26 × BLD-11 were observed most promising hybrids for kernel yield and some of its related traits. This showed important role of intra allelic gene interaction, *i.e.*, additive x dominance of these hybrids having high *sca* effects and also top among *per se* performance. These hybrids with good attributes can be evaluated under multilocations and can be developed as commercial hybrids.

Reference

- Adebayo, M. A.; Menkir, A.; Blay, E.; Gracen, V. and Danquaha, E. Y. 2014. Performance based grouping of adapted and exotic drought tolerant maize (*Zea mays* L.) inbred lines under stressed and non-stressed conditions. *Maydica*. **59**: 115-123.
- Anonymous, 2016. Agricultural Statistics at a glance 2014, 1stEdn. Oxford University Press, New Delhi, pp., 88-90.
- Avinashe, H. A. 2011. Heterosis and combining ability studies in quality protein maize (*Zea mays* L.). M.Sc. (Agri.) Thesis (Unpublished). Anand Agricultural University, Anand.
- Bello, O. B. and Olaoye, G. 2009. Combining ability for maize grain yield and other agronomic characters in a typical southern guinea savanna ecology of Nigeria. *African Journal of Biotechnology*. **8** (11): 2518-2522.
- Dhillon, B. S. and Prasanna, B. M. 2001. Maize. In Breeding Field Crops; Theory and Practice edited by V. L. Chopra (ed.). Oxford and IBH, New Delhi. Pp 147-189.
- Gami, R. A.; Patel, P. C.; Patel, M. P.; Chaudhary, S. M. and Soni, N. V. 2018^a. Study of gene action and heterosis effects of different genotypes for yield and yield attributing traits in maize (*Zea mays* L.). *Advances in Research*. **14** (4): 1-7.
- Gami, R. A.; Soni, N. V.; Chaudhary, S. M.; Solanki, S. D. and Patel, P. C. 2018^b. Genetic studies of the kernel yield and attributing traits of single cross hybrid in yellow maize (*Zea mays* L.). *International Journal of Plant & Soil Science*. **22** (4): 1-7.
- Griffing, B. 1956. Concept of general combining ability and specific combining ability in relation to diallel crossing system. *Australian Journal of Biological Sciences*. **9**: 463- 493.
- Krishna, M. S. R.; Malhi, N. S. and Singh, H. 2003. Development of hybrid oriented source germplasm in maize (*Zea mays* L.). *Indian Journal of Agricultural Sciences*. **73** (7): 407-410.
- Malik, S. I., Malik, H. N., Minhas, N. M. and Munir, M. 2004. General and specific combining ability studies in maize diallel crosses. *International Journal of Agriculture and Biology*. **6** (5).
- Mathur, R. K. and Bhatnagar, S. K. 2003. Genetics of harvest index in white seeded maize (*Zea mays* L.). *Crop Research*. **26** (3): 468-472.
- Muraya, M. M.; Ndirangu, C. M. and Omolo, E. O. 2006. Heterosis and combining ability in diallel crosses involving maize (*Zea mays* L.) S₁ lines. *Australian Journal of Experimental Agriculture*. **46** (3): 387-394.
- Soni, N. V. 2012. Heterosis and combining ability of diallel crosses of popcorn (*Zea mays* var. *evarta*). M.Sc. (Agri.). Thesis (Unpublished). Anand Agricultural University, Anand.
- Sukhatme, P.V and Amble, V.N. 1985. Statistical methods for agricultural workers. 4th ed. ICAR, New Delhi.
- White, P.J. and Johnson, L.A. 2003. Corn Chemistry and Technology 2ndEdn, American Association of cereal chemists, St. Paul, MN., USA, ISBN-13:9781891127335, 892.



Table 1. Analysis of variance for combining ability of sixteen traits in maize

Sources of variation	d.f.	Days to tasseling	Days to silking	ASI	Days to dry husk	Plant height	Cob height	Cob Weight	Cob length
<i>Gca</i>	7	11.67**	10.49**	0.52*	2.67**	6.51*	15.61**	347.96**	0.42**
<i>Sca</i>	28	9.40**	10.26**	0.39	1.31**	870.86**	210.30**	1435.77**	4.45**
Error	70	0.55	0.65	0.24	0.47	2.63	1.96	10.55	0.11
$\delta^2 gca$		1.11	0.98	0.03	0.22	0.39	1.36	33.74	0.03
$\delta^2 sca$		8.84	9.61	0.15	0.84	868.23	208.34	1425.22	4.34
$\delta^2 gca / \delta^2 sca$		0.12	0.10	0.18	0.26	0.00	0.01	0.02	0.01

* P ≤ 0.05, ** P ≤ 0.01, Where: ASI= AnthesisSilking Interval

Sources of variation	d.f.	Cob Girth	Number of kernel rows per cob	Number of kernels per row	100-kernel weight	Kernel yield per plant	Shelling Percentage	Protein content	Starch content
<i>Gca</i>	7	0.15	0.58**	3.89**	4.35**	254.20**	29.61**	0.02**	0.26**
<i>Sca</i>	28	2.15**	0.55**	23.68**	3.67**	616.86**	35.78**	0.01**	0.23**
Error	70	0.09	0.14	0.42	0.72	3.12	3.41	0.004	0.09
$\delta^2 gca$		0.006	0.04	0.35	0.36	25.10	2.62	0.001	0.02
$\delta^2 sca$		2.06	0.41	23.26	2.95	613.74	32.37	0.01	0.14
$\delta^2 gca / \delta^2 sca$		0.003	0.11	0.01	0.12	0.04	0.08	0.11	0.13

* P ≤ 0.05, ** P ≤ 0.01 Where: ASI= AnthesisSilking Interval

Table 2. General combining ability (*gca*) effects for sixteen traits in maize

Parents	Days to tasseling	Days to silking	ASI	Days to dry husk	Plant height	Cob height	Cob weight	Cob length
CBE-15	-0.48*	-0.81**	-0.33*	-0.33	-1.08*	-2.46**	-13.34**	-0.23*
CBE-98	1.36**	1.36**	0.00	0.73**	0.65	0.21	3.96**	0.09
CBE-26	1.96**	1.79**	-0.17	0.57**	1.31**	0.86*	-2.40*	-0.19
VL-1032	-0.28	-0.01	0.27	-0.53*	0.29	1.18**	3.54**	0.27**
CML338	-1.14**	-0.78**	0.37*	-0.53*	-0.85	-1.23**	0.34	-0.03
VL-109178	-0.84**	-0.88**	-0.03	-0.03	0.43	0.77	1.32	-0.02
BLD-11	-0.24	-0.21	0.03	0.47*	-0.31	-0.07	5.28**	0.29**
MRCN-3	-0.34	-0.48	-0.13	-0.33	-0.44	0.76	1.31	-0.19
S. E. (g_i) ±	0.22	0.24	0.14	0.20	0.47	0.41	0.96	0.09

* P ≤ 0.05, ** P ≤ 0.01 Where: ASI= AnthesisSilking Interval

Parents	Cob girth	Number of kernel rows per cob	Number of kernels per row	100-kernel weight	Kernel yield per plant	Shelling percentage	Protein content	Starch content
CBE-15	0.20*	-0.24*	-1.46**	-0.25	-11.23**	-1.46**	0.03	-0.10
CBE-98	0.08	0.24*	0.07	-0.15	-1.28*	-2.77**	-0.08**	-0.26**
CBE-26	-0.19*	-0.12	0.50*	-1.24**	-0.48	0.42	0.04	0.10
VL-1032	-0.08	-0.23*	0.16	0.74**	1.68**	-0.33	-0.03	0.15
CML-338	0.08	0.35**	0.11	0.18	4.28**	2.85**	-0.01	-0.17
VL-109178	-0.11	-0.25*	-0.12	0.12	1.25*	-0.05	-0.02	0.19*
BLD-11	0.02	0.09	0.44*	0.87**	5.19**	1.58**	0.02	-0.01
MRCN-3	0.02	0.17	0.32	-0.27	0.58	-0.24	0.04*	0.11
S. E. (g_i) ±	0.08	0.11	0.19	0.25	0.52	0.54	0.01	0.08

±

* P ≤ 0.05, ** P ≤ 0.01



Table 3. Classification of parents with respect to general combining ability effects for various characters

Characters	Parents							
	CBE-15	CBE-98	CBE-26	VL-1032	CML- 338	VL-109178	BLD-11	MRCN-3
Days to tasseling	G	P	P	A	G	G	A	A
Days to silking	G	P	P	A	G	G	A	A
ASI	G	A	A	A	P	A	A	A
Days to dry husk	A	P	P	G	G	A	P	A
Plant height	G	A	P	A	A	A	A	A
Cob height	G	A	P	P	G	A	A	A
Cob weight	P	G*	P	G*	A	A	G*	A
Cob length	P	A	A	G*	A	A	G*	A
Cob girth	G	A	P	A	A	A	A	A
Number of kernel rows per cob	P	G	A	P	G*	P	A	A
Number of kernels per row	P	A	G	A	A	A	G	A
100-kernels weight	A	A	P	G*	A	A	G*	A
kernel yield per plant	P	P	A	G*	G*	G	G*	A
Shelling percentage	P	P	A	A	G*	A	G*	A
Protein content	A	P	A	A	A	A	A	G
Starch content	A	P	A	A	A	G	A	A

G = Good general combiner; G* = Very good combiner; A = Average general combiner; P = Poor general combiner



Table 4. Specific combining ability (*sca*) effect of hybrids for various characters in maize

Sr No.	Hybrid (F ₁)	Days to tasseling	Days to silking	ASI	Days to dry husk	Plant height	Cob height	Cob weight	Cob length
1	CBE-15 × CBE-98	-0.49	-0.30	0.19	0.56	13.03**	7.39**	13.06**	1.72**
2	CBE-15 × CBE-26	-4.42**	-4.07**	0.35	0.40	10.80**	6.10**	15.28**	0.06
3	CBE-15 × VL-1032	-2.19**	-1.93*	0.25	0.50	12.55**	5.44**	3.89	1.17**
4	CBE-15 × CML-338	-1.32	-1.83*	-0.52	-0.17	13.90**	6.62**	17.53**	1.35**
5	CBE-15 × VL-109178	-2.29**	-2.07**	0.22	-1.00	12.92**	6.51**	11.46**	1.86**
6	CBE-15 × BLD-11	-1.22	-0.40	0.82	0.16	16.10**	4.00**	1.24	1.05**
7	CBE-15 × MRCN-3	-1.45*	-1.80*	-0.35	-2.37**	15.00**	2.57	8.07*	0.13
8	CBE-98 × CBE-26	-2.25**	-1.23	1.02*	-1.34*	11.30**	1.00	-4.23	0.26
9	CBE-98 × VL-1032	-1.02	-1.10	-0.08	-0.57	15.15**	3.53**	27.87**	0.92**
10	CBE-98 × CML-338	1.85*	1.67*	-0.18	2.10**	13.74**	5.28**	-3.10	0.53
11	CBE-98 × VL-109178	-0.45	-1.23	-0.78	-0.40	17.18**	10.21**	24.78**	1.13**
12	CBE-98 × BLD-11	-1.39*	-1.57*	-0.18	-1.24	17.01**	10.39**	27.52**	1.09**
13	CBE-98 × MRCN-3	-1.62*	-1.30	0.32	1.23	10.66**	10.65**	43.95**	2.03**
14	CBE-26 × VL-1032	-1.62*	-1.87*	-0.25	0.26	15.55**	10.11**	23.61**	1.11**
15	CBE-26 × CML-338	-1.09	-1.10	-0.02	-0.74	16.13**	6.97**	11.22**	0.91**
16	CBE-26 × VL-109178	-2.72**	-2.33**	0.39	0.76	16.44**	11.94**	24.30**	1.55**
17	CBE-26 × BLD-11	-1.65*	-2.33**	-0.68	-0.74	16.84**	7.64**	41.72**	1.09**
18	CBE-26 × MRCN-3	-2.55**	-2.40**	0.15	-0.94	15.53**	8.76**	19.11**	0.94**
19	VL-1032 × CML-338	-1.19	-1.30	-0.12	-0.64	12.54**	8.00**	18.59**	1.03**
20	VL-1032 × VL-109178	-0.15	-0.20	-0.05	-1.14	13.75**	6.45**	8.17**	0.47
21	VL-1032 × BLD-11	-0.75	-1.20	-0.45	0.36	11.34**	6.15**	2.34	0.53
22	VL-1032 × MRCN-3	-1.65*	-2.27**	-0.62	-0.17	15.84**	8.40**	28.99**	0.95**
23	CML-338 × VL-109178	-1.29	-2.10**	-0.81	-2.14**	11.77**	5.37**	17.56**	1.00**
24	CML-338 × BLD-11	-1.55*	-2.43**	-0.88	-1.30*	13.15**	6.78**	12.28**	-0.24
25	CML-338 × MRCN-3	-1.45*	-1.83*	-0.38	0.16	14.79**	2.06	14.60**	0.87**
26	VL-109178 × BLD-11	0.15	0.33	0.19	0.20	12.29**	3.50*	32.55	1.39**
27	VL-109178 × MRCN-3	0.58	0.27	-0.32	1.00	11.87**	6.22**	14.42**	0.46
28	BLD-11 × MRCN-3	-0.02	-0.40	-0.38	0.50	11.37**	9.40**	11.35**	1.44**
S. E. (S_{ij}) ±		0.59	0.64	0.39	0.54	1.28	1.11	2.56	0.26

* P ≤ 0.05, ** P ≤ 0.01



Table 4Contd.....

Sr No.	Hybrid (F₁)	Cob girth	No. of kernel row/cob	No. of kernels per row	100-kernel weight	Kernel yield per plant	Shelling percentage	Protein content	Starch content
1	CBE-15 × CBE-98	0.78**	-0.14	2.45**	0.50	7.88**	-2.10	0.16*	-0.09
2	CBE-15 × CBE-26	1.23**	0.74*	0.09	1.26	7.64**	-2.16	0.09	-0.13
3	CBE-15 × VL-1032	1.29**	-0.08	2.19**	1.82*	5.33**	0.99	-0.03	0.33
4	CBE-15 × CML-338	0.40	0.67	2.81**	-0.36	-0.38	-10.09**	-0.05	0.71*
5	CBE-15 × VL-109178	1.07**	0.61	1.76**	0.31	13.07**	3.27	-0.10	-0.28
6	CBE-15 × BLD-11	0.94**	0.40	1.11	0.92	5.76**	2.44	0.13*	-0.21
7	CBE-15 × MRCN-3	0.56*	-0.21	-0.03	0.13	6.47**	-0.23	-0.15*	-0.35
8	CBE-98 × CBE-26	0.13	0.13	1.13	0.40	-2.00	0.05	0.19**	0.09
9	CBE-98 × VL-1032	1.34**	0.24	2.43	2.09*	1.41	-12.52**	-0.10	0.25
10	CBE-98 × CML-338	0.42	-0.07	0.95	0.28	-2.70	-1.38	-0.09	-0.52
11	CBE-98 × VL-109178	0.74*	-0.001	2.07**	1.48	15.41**	-2.50	-0.26**	0.14
12	CBE-98 × BLD-11	0.37	0.32	3.42**	-0.05	23.16**	-0.06	-0.04	0.07
13	CBE-98 × MRCN-3	0.70*	0.78*	1.11	1.10	27.57**	-3.30	-0.01	-0.37
14	CBE-26 × VL-1032	0.38	-0.34	4.30**	1.14	16.18**	-1.81	0.01	0.39
15	CBE-26 × CML-338	0.70*	0.25	3.35**	1.13	18.69**	6.71**	-0.09	0.10
16	CBE-26 × VL-109178	0.45	0.52	3.24**	2.26**	18.64**	-0.05	0.10	0.36
17	CBE-26 × BLD-11	0.59*	0.28	4.22**	-0.53	21.20**	-7.11**	-0.05	-0.37
18	CBE-26 × MRCN-3	1.33**	0.86*	2.54**	0.25	20.10**	3.27	-0.09	0.04
19	VL-1032 × CML-338	0.41	0.53	1.79**	1.15	16.11**	-0.08	-0.08	-0.73*
20	VL-1032 × VL-109178	0.73*	0.87*	1.94**	1.49	10.62**	2.03	0.29**	0.62*
21	VL-1032 × BLD-11	0.25	-0.54	1.89**	-0.24	4.55**	-0.08	-0.05	1.12**
22	VL-1032 × MRCN-3	0.90**	0.58	2.38**	1.57	10.23**	-8.00**	0.10	-0.48
23	CML-338 × VL-109178	0.75*	0.55	2.56**	2.08*	12.61**	-1.32	0.20**	-0.08
24	CML-338 × BLD-11	0.04	-0.06	0.28	-0.35	2.53	-6.26	0.03	-0.21
25	CML-338 × MRCN-3	0.63*	0.13	4.33**	0.66	12.72**	0.07	0.13**	0.71*
26	VL-109178 × BLD-11	0.65*	0.15	2.37**	1.12	13.83**	-7.75**	0.07	0.14
27	VL-109178 × MRCN-3	0.25	0.33	1.29*	-2.27**	10.76**	-0.75	-0.04	0.38
28	BLD-11 × MRCN-3	0.52	0.66	3.74**	1.34	8.17**	-1.80	-0.04	-0.48
S. E. (S_{ij}) ±		0.24	0.30	0.51	0.67	1.39	1.46	0.05	0.24

* P ≤ 0.05, ** P ≤ 0.01



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