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Original Research Article

Genetic Analysis of Resistance to Multiple Diseases in Maize (*Zea mays* L.) under Sub Temperate High Hill Conditions of Himachal Pradesh

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A B S T R A C T

This study was conducted to estimate general combining ability (GCA), specific combining ability (SCA) and genetic effects associated with Turcicum leaf blight (TLB), Maydis leaf blight (MLB) and Banded leaf and sheath blight (BLSB) in maize under natural and artificial epiphytotic conditions. The 60 F_1 hybrids generated from line × tester and 32 parents along with two local checks were evaluated for screening of disease resistance at CSK Himachal Pradesh Krishi Vishva Vidyalaya, Hill Agricultural Research & Extension Center, Bajaura (HP) during *Kharif*, 2016. Significant genetic variability was observed for resistance to all three diseases. Five inbred lines *viz*., L_{10}, L_{12}, L_{14}, L_{21}, L_{28} and one tester (T_1)were found most promising for resistant to TLB; Five lines namely L_{21}, L_{22}, L_{25}, L_{26} and L_{28} for MLB and L_5, L_6, L_9, L_{12}, L_{22} and T_1 for BLSB as they showed resistance against these particular diseases with significant GCA effects. These lines can be used as parent sources for resistance in further breeding programme. Five hybrids *viz*., $L_{17} \times T_1$, $L_{18} \times T_1$, $L_{23} \times T_2$, $L_{24} \times T_1$ and $L_{28} \times T_1$ were selected on the basis of disease reaction and significant SCA effects for one of the studied diseases. These cross combination can be commercialized after further evaluation for yield parameters at several locations. This offers scope for source population improvement for resistance to these TLB, MLB and BLSB as well as developing maize hybrids.

Keywords

Banded leaf and sheath blight, Maize, Maydis leaf blight, Turcicum leaf blight

Introduction

Maize (*Zea mays* L.) is one of the most widely grown crops in the world, ranking third next to wheat and rice occupying more than 33 million hectares each year (FAOSTAT, 2015). Maize is faced with many biotic stress factors in the tropics such as turcicum leaf blight, maydis leaf blight and banded leaf and sheath blight, maize streak

virus (MSV), grey leaf spot (GLS) and stem borers. Diseases are a potential threat to global food security but plants have evolved an extensive array of methodologies to cope with the invading pathogens. Therefore, identification of disease resistant germplasm is the primary and essential management practice of any crop. Maize also suffers from various diseases resulting in considerable losses in yield. Among them banded leaf and sheath blight (BLSB) disease incited by *Rhizoctonia solani* f.sp. *sasakii*, Turcicum leaf blight caused by *Helminthosporium turcicum* and Maydis leaf blight caused by *Helminthosporium maydis* are gaining considerable economic importance. Due to moderate low temperature and high humidity during the maize period, Turcicum Leaf blight (TLB) is major disease for highland maize farmers in the Himalayan region (Mir *et al.,* 2015). It is widely distributed, however, sporadic in nature and its development mostly depends on weather conditions, stage of plant growth and level of resistance in maize cultivars (Perkins and Pedersen, 1987). The pathogen has wide host range and a high pathogenic variability (Muiru *et al.,* 2010). Therefore, identification of disease resistant germplasm is the primary and essential management practice of any crop. Several studies have been reported which identified the germplasm resistant to various diseases in maize (Sharma and Saxena 2002; Sharma *et al.,* 2003; Meena 2004). Garg *et al.,* (2005) screened 29 tropical maize inbred lines for banded leaf and sheath blight under artificial inoculation in field conditions at three locations during three consecutive years. Many of the Indian and CIMMYT inbred lines displayed susceptibility to BLSB and CA00106 was the only inbred that revealed moderate resistance to the three BLSB isolates.

The success of any breeding programme largely depends on the choice of parents and breeding procedure adopted. Combining ability is a powerful tool to discriminate good as well as poor combiners and for crossing suitable inbred lines in hybridization programme. Maize breeders develop cultivars through cross breeding of elite inbred lines, and subsequently evaluate them in multiple environments to identify superior cultivars adapted to different agro-ecologies. The mean values of parents and F_1 combinations are important for estimating combining ability, evaluating performance of hybrids, and selecting superior parents. Identification of best parental combinations is crucial for successful development of disease resistant hybrids. Vimla *et al.,* (1988) did combining ability analysis of 15 single crosses across two locations to study the reaction to banded leaf and sheath blight and revealed that inbred line CM104 was the most promising for conferring resistance whereas inbreds CM601 and CM105, for susceptibility. Several workers conducted similar type of studies (Sharma *et al.,* 2005; Mir *et al.,* 2015, Chen *et al.,* 2013; Kumar *et al.,* 2013).So, this study was conducted to screen the maize germplasm for various diseases, estimate the combining ability effects and identification of promising lines and crosses.

Materials and Methods

The thirty selected inbred lines were crossed with two diverse testers in the field CSK Himachal Pradesh Krishi Vishva Vidyalaya, Hill Agricultural Research & Extension Center, Bajaura during *kharif*, 2015 using Line x Tester mating design. The list of the inbred lines and testers used in this experiment is given in Table 1. The resulting hybrid seed (F_1s) and their parents along with two commercial checks were evaluated in randomized block design (RBD) design with two replications under the natural and artificial epiphytotic conditions for disease reactions during *Kharif*, 2016.

Disease screening

The material was screened against turcicum leaf blight (TLB), maydis leaf blight (MLB) and banded leaf and sheath blight (BLSB) under natural condition in the main experimental trial. For the screening of material against TLB & MLB diseases under the artificial conditions, a separate single row trial in RBD with two replications in a plot size of 2.0 × 0.60 m (1.2 m^2) at a spacing of 60 × 20 cm was conducted during *Kharif*, 2016. The inoculation was done by dropping a pinch of inoculum by hand inside the whorl of the leaves when the crop was around 35 to 45 days old. This was followed by a spray of water from a knapsack sprayer directed in the whorl. The inoculation was done in the late afternoon. The artificial inoculation was done three times at a weekly interval. The plants were phenotyped for TLB, MLB and BLSB incidence at dough stage using standard 1-9 disease rating scale (Payak and Sharma, 1983). Based on this rating scale, the maize lines were classified into four groups namely, resistant (R) genotypes with a score ≤ 3.0; moderately resistant (MR)>3.0-5.0; moderately susceptible (MS) >5.0- 7.0 and susceptible (S) >7.0-9.0.

Results and Discussion

Disease reaction to Turcicum leaf blight, Maydis leaf blight and Banded leaf and sheath disease

The present study resulted in identification of fifty eight resistant crosses against TLB under artificial epiphytotic conditions. Among lines and testers L_2, L_4, L_7, L_9, L_{11}, L_{12}, L_{13}, L_{14}, L_{15}, L_{16}, L_{18}, L_{20}, L_{21}, L_{28}, L_{29}, L_{30} and T_2 were found resistant whereas two crosses i.e. $L_7 \times T_2$, $L_{24} \times T_2$ and ten lines viz., L_1, L_3, L_6, L_{10}, L_{17}, L_{19}, L_{22}, L_{23}, L_{24}, L_{25} and T_1 tester exhibited moderately resistant reaction. Four lines *viz.*, L_5, L_8, L_{26} and L_{27} were found moderately susceptible whereas, none of the cross and testers was found moderately susceptible/ susceptible to this disease (Table 2). Under natural epiphytotic conditions, fifty eight crosses were found resistant whereas, twenty five lines namely; L_1, L_2, L_3, L_4, L_7, L_9, L_{10}, L_{11}, L_{12}, L_{13}, L_{14}, L_{15}, L_{16}, L_{17}, L_{18}, L_{19}, L_{20}, L_{21}, L_{22}, L_{23}, L_{24}, L_{25}, L_{28}, L_{29}, L_{30} and both testers T_1 and T_2 were found resistant against TLB. Two crosses$L_7 \times T_2$, $L_{24} \times T_2$ and five lines *viz.*, L_5, L_6, L_8, L_{26} and L_{27} exhibited moderately resistant reaction. None of the cross and line was found moderatelysusceptible/susceptible to this disease. Many researchers had been done similar work in this field. Kumar and Salgotra (2015) evaluated seventy two F_1s along with twenty seven parents and one standard check for resistance against leaf blight (*Helminthosporium maydis* and *Helminthosporium turcicum*) under natural epiphytotic conditions. Chandrashekara *et al.*, (2014) screened 35 short-duration maize inbred lines against TLB under artificial inoculation and found twelve inbred lines were resistant against TLB. The new sources of TLB resistance and their combination identified in the present study will be helpful to involve in breeding program. The present study revealed fifty eight resistant and two moderately resistant cross against MLB under artificial epiphytotic conditions.

Among lines and testers twenty four lines and both testers were found resistant whereas two crosses *viz.*,$L_{17} \times T_1$, $L_{17} \times T_2$ and six lines *viz.*,L_4, L_6, L_{18}, L_{19}, L_{20} and L_{29} exhibited moderately resistant reaction. None of the cross, line and tester were found moderately susceptible/ susceptible (Table 2). Fifty nine crosses were resistant to MLB disease under natural epiphytotic conditions. Twenty eight lines *viz.*,L_1, L_2, L_3, L_4, L_5, L_6, L_7, L_8, L_9, L_{10}, L_{11}, L_{12}, L_{13}, L_{14}, L_{15}, L_{16}, L_{17}, L_{18}, L_{21}, L_{22}, L_{23}, L_{24}, L_{25}, L_{26}, L_{27}, L_{28}, L_{29}, L_{30} and tester T_1 showed resistant to MLB. The cross

L_{17}×T_2, two lines L_{19}, L_{20} and tester T_2 were found moderately resistant. None of the cross, line and tester were found moderately susceptible/susceptible.Similar work has been done in this field by many researchers. Balint-Kurti *et al.,* (2008) conducted a study to identify loci contributing to MLB resistance in two recombinant inbred line populations and to compare these to MLB resistance loci in other populations. The fifty crosses were found resistant and ten crosses showed moderately resistant reaction to BLSB. Fifteen lines *viz.*, L_2, L_3, L_5, L_8, L_9, L_{10}, L_{13}, L_{15}, L_{16}, L_{21}, L_{22}, L_{23}, L_{25}, L_{29}, $L_{30}$and tester T_2 were found to be resistant whereas ten crosses namely; L_1×T_1, L_1×T_2, L_{10}×T_2, L_{11}×T_1, L_{17}×T_2, L_{18}×T_2, L_{19}×T_1, L_{24}×T_2, L_{26}×T_1, L_{28}×T_2 and fifteen lines namely; L_1, L_4, L_6, L_7, L_{11}, L_{12}, L_{14}, L_{17}, L_{18},L_{19}, L_{20}, L_{24}, L_{26}, L_{27}, $L_{28}$and tester T_1 were found to be moderately resistant. None of crosses and lines was found moderately susceptible/susceptible reaction against Banded leaf sheath blight (Table 2). Mir *et al.,* (2015) screened ten lines and found three lines moderately resistant to TLB under artificial epiphytotic conditions.

Estimates of combining ability effects

General combining ability and SCA estimates can be useful for choosing breeding parents since they provide information about the potential parental value in crosses as well as describing gene action (Beyene *et al.,* 2017). The results for combining ability effects of this study were presented below.

Analysis for variance for combining ability

Analysis of variance for Line × Tester for three different diseases in natural as well as artificial conditions reveled that there was significant variability among the genotypes studied in the present investigation (Table 3). The mean sum of squares (MSS) due to genotype, cross, parent and female were significant for all the diseases in both epiphytotic conditions. MSS due to male was significant for all three diseases except TLB under natural epiphytotic condition. MSS due to male vs female was significant for MLB in artificial epiphytotic condition, and TLB and MLB in natural condition.

The analysis of variance for combining ability revealed significant differences among crosses, lines and testers used in the present study (Table 4). The mean squares due to line × tester interactions were found to be significant for these diseases suggested that inbred lines may have different combining ability patterns and performed differently in crosses depending on type of testers used.

General combining ability effects

Among thirty inbred lines, eight lines and one tester (T_1) exhibited negative and significant GCA effects for TLB under inoculated trial (Table 5). Highest negative GCA effect was exhibited by L_9 (-0.76), followed by L_{14} (-0.59), L_{28} (-0.59) and L_{10} (-0.51). Four lines and one tester (T_2) showed positive significant GCA with highest value of 0.99 (L_{24}).

The negative value implies that the inbred lines are good combiners as it indicates the more resistance and the reverse is true for those with positive GCA effects. For MLB in inoculated field, three lines exhibited negative and significant GCA effects with highest negative value of -0.51 (L_{22} and L_{29}). Whereas, three lines showed significant positive GCA effect for this disease.

Under natural epiphytotic condition, nine lines exhibited significantly negative GCA effects for TLB out of these line L_2, L_{21} and L_{28} (-0.57) showed the highest negative GCA effects followed by L_{10} (-0.45).

Table.1 Description of the lines, testers and checks used in the study

Code	Genotypes	Code	Genotypes
	Lines		
L1	BAJIM-12-01	L19	CML-337
L2	BAJIM-13-01	L20	CML-439
L3	BAJIM-13-02	L21	CML-465-B-B
L4	BAJIM-15-08	L22	DMRQPM-58
L5	BAJIM-15-09	L23	HKI-1040-7
L6	BAJIM-15-10	L24	HKI-1105
L7	BAJIM-15-11	L25	LQPM-15-01
L8	BAJIM-15-12	L26	MRCQPM-16
L9	BML-6	L27	MRCQPM-18
L10	BML-7	L28	TNAU/CBE—83
L11	CML-44	L29	TNAU/CBE-115
L12	CML-141	L30	V-334
L13	CML-269	Testers	
L14	CML-269-1	T1	BAJIM 08-26
L15	CML-292	T2	BAJIM 08-27
L16	CML-294	Checks	
L17	CML-334	Check-1	Bio 9544
L18	CML-336	Check-2	Palam Sankar Makka-2

Table.2 Disease reaction to TLB, MLB and BLSB under natural and artificial epiphytotic conditions

		Disease							disease				
		inoculated		Natural					inoculated		natural		
		TLB	MLB	TLB	MLB	BLSB			TLB	MLB	TLB	MLB	BLSB
1	T1	2.50	1.00	2.00	1.50	2.50	48	L8 × T2	2.00	2.00	1.50	1.50	2.00
2	T2	2.00	2.00	2.00	2.50	2.00	49	L9 × T1	1.50	1.50	1.50	1.50	1.50
3	L1	3.00	1.50	1.50	1.50	3.00	50	L9 × T2	1.50	1.50	1.50	1.50	2.00
4	L2	1.50	1.50	1.00	1.00	1.00	51	L10 × T1	1.50	1.50	1.50	1.50	2.00
5	L3	2.50	1.00	2.00	1.00	1.00	52	L10 × T2	1.50	1.50	1.50	1.50	2.50
6	L4	1.50	2.50	1.00	2.00	2.50	53	L11 × T1	1.50	1.50	1.50	1.50	2.50
7	L5	4.00	2.00	3.00	1.50	2.00	54	L11 × T2	2.00	1.50	2.00	1.50	2.00
8	L6	3.00	2.50	2.50	2.00	2.50	55	L12 × T1	1.50	1.50	1.50	1.50	1.50
9	L7	2.00	2.00	1.50	1.50	3.00	56	L12 × T2	1.50	1.50	1.50	1.50	2.00
10	L8	3.50	1.50	2.50	1.50	2.00	57	L13 × T1	1.50	1.50	1.50	1.50	2.00
11	L9	2.00	1.50	1.50	1.00	2.00	58	L13 × T2	2.00	1.50	2.00	1.50	2.00
12	L10	2.50	2.00	2.00	1.50	2.00	59	L14 × T1	1.50	1.50	1.50	1.50	2.00
13	L11	2.00	2.00	1.50	1.50	3.00	60	L14 × T2	1.50	1.50	1.50	1.50	2.00
14	L12	1.50	1.50	1.00	1.00	2.50	61	L15 × T1	1.50	1.50	1.50	1.50	2.00
15	L13	1.50	1.00	1.00	1.00	2.00	62	L15 × T2	1.50	1.50	1.50	1.50	2.00
16	L14	2.00	2.00	1.50	1.50	2.50	63	L16 × T1	1.50	1.50	1.50	1.50	2.00
17	L15	1.00	1.00	1.00	1.00	2.00	64	L16 × T2	2.00	1.50	2.00	1.00	2.00
18	L16	2.00	2.00	1.50	1.50	2.00	65	L17 × T1	2.00	2.50	1.50	1.50	2.00
19	L17	2.50	1.00	2.00	1.00	2.50	66	L17 × T2	2.00	2.50	2.00	2.50	2.50
20	L18	2.00	2.50	1.50	2.00	2.50	67	L18 × T1	2.00	1.50	2.00	1.50	1.50
21	L19	3.00	3.00	1.50	2.50	2.50	68	L18 × T2	2.00	2.00	1.50	1.50	2.50
22	L20	1.50	2.50	1.00	2.50	2.50	69	L19 × T1	2.00	1.50	2.00	1.50	2.50
23	L21	1.00	1.00	1.00	1.00	1.00	70	L19 × T2	2.00	1.50	2.00	1.50	2.00

24	L22	2.50	1.50	2.00	1.50	2.00	71	L20 × T1	2.00	1.50	2.00	1.50	2.00
25	L23	2.50	1.50	2.00	1.00	2.00	72	L20 × T2	2.00	2.00	2.00	2.00	2.00
26	L24	2.50	2.00	2.00	1.50	2.50	73	L21 × T1	1.50	1.50	1.50	1.50	2.00
27	L25	2.50	2.00	2.00	1.50	2.00	74	L21 × T2	1.50	1.50	1.50	1.50	1.50
28	L26	3.50	1.50	2.50	1.50	3.00	75	L22 × T1	2.00	1.50	1.50	1.50	1.50
29	L27	3.50	1.50	3.00	1.50	3.00	76	L22 × T2	2.00	1.50	2.00	1.50	1.50
30	L28	2.00	2.00	1.50	1.50	2.50	77	L23 × T1	2.00	1.50	2.00	1.50	2.00
31	L29	1.50	2.50	1.00	2.00	2.00	78	L23 × T2	1.50	1.50	1.50	1.50	2.00
32	L30	2.00	1.00	2.00	1.00	2.00	79	L24 × T1	2.00	1.50	1.50	1.50	2.00
33	L1 × T1	2.00	1.50	2.00	1.50	2.50	80	L24 × T2	2.50	1.50	2.50	1.50	2.50
34	L1 ×T2	2.00	1.50	2.00	1.50	2.50	81	L25 × T1	2.00	1.50	1.50	1.00	2.00
35	L2 × T1	1.50	1.50	1.50	1.50	2.00	82	L25 × T2	2.00	1.50	1.50	1.00	2.00
36	L2 × T2	2.00	1.50	1.50	1.50	2.00	83	L26 × T1	2.00	1.50	1.50	1.50	2.50
37	L3 × T1	1.50	1.50	1.50	1.50	1.50	84	L26 × T2	2.00	1.50	1.50	1.50	2.00
38	L3 × T2	2.00	1.50	1.50	1.50	2.00	85	L27 × T1	2.00	1.50	1.50	1.50	2.00
39	L4 × T1	2.00	2.00	1.50	1.50	1.50	86	L27 × T2	2.00	1.50	2.00	1.50	2.00
40	L4 × T2	2.00	2.00	1.50	1.50	2.00	87	L28 × T1	1.50	1.50	1.50	1.50	2.00
41	L5 × T1	1.50	1.50	1.50	1.50	1.50	88	L28 × T2	1.50	1.50	1.50	1.50	2.50
42	L5 × T2	2.00	1.50	2.00	1.50	2.00	89	L29 × T1	1.50	1.50	1.50	1.50	2.00
43	L6 × T1	2.00	1.50	2.00	1.50	1.50	90	L29 × T2	2.00	1.50	2.00	1.50	2.00
44	L6 × T2	2.00	2.00	1.50	1.50	2.00	91	L30 × T1	2.00	1.50	1.50	1.00	2.00
45	L7 × T1	2.00	1.50	2.00	1.50	1.50	92	L30 × T2	2.00	2.00	1.50	1.50	2.00
46	L7 ×T2	2.50	1.50	2.50	1.50	2.00	93	Check	1.00	1.00	1.00	1.00	2.00
47	L8 ×T1	2.00	1.50	2.00	1.00	2.00	94	Check	2.00	1.50	1.50	1.00	2.00

Table.3 Analysis of Variance for Line × Tester

		inoculated		natural		
SOURCE	DF	TLB	MLB	TLB	MLB	BLSB
Replication	1	0.1	0.17	0.1	0.05	0.11
Genotype	91	2.22**	1.01**	1.08**	0.62**	1.34**
Cross	59	0.53**	0.39**	0.52**	0.31**	0.73**
Parent	31	4.4**	2.1**	2.14**	1.2**	2.11**
Female	29	4.66**	2.12**	2.26**	1.09**	2.14**
Male	1	1.1**	2.25**	0.06	2.25**	3.06**
MalevsFemale	1	0.002	1.28**	0.74**	3.38**	0.25
Cross vs Parent	1	34.8**	3.48**	0.74**	1.06**	13.78**
Error	91	0.15	0.11	0.1	0.1	0.15

*Significant at 5% level of significance; **Significant at 1% level of significance

Table.4 Analysis of Variance for Combining Ability

		Inoculated		Natural		
SOURCE	DF	TLB	MLB	TLB	MLB	BLSB
Replication	1	0.01	0.24	0.21	0.3	0.13
Cross	59	0.53**	0.39**	0.52**	0.31**	0.73**
Line	29	0.74**	0.64**	0.61**	0.36**	0.81**
Tester	1	1.73**	0.41*	0.68*	0.68*	2.7**
Line x Tester	29	0.27**	0.15	0.43**	0.26**	0.57**
Error	59	0.11	0.1	0.11	0.1	0.16

*Significant at 5% level of significance; **Significant at 1% level of significance

Table.5 General combining ability effects for diseases under artificial and natural epiphytotic conditions

	Inoculated		Natural		
LINES	TLB	MLB	TLB	MLB	BLSB
L1	0.23	-0.13	0.43*	0.05	1.07**
L2	-0.34*	-0.18	-0.57**	-0.08	0.07
L3	0.06	-0.13	-0.32*	0.05	-0.43*
L4	0.23	0.62**	-0.08	-0.20	-0.18
L5	-0.27	-0.31	0.17	-0.20	-0.56**
L6	0.23	0.24	0.30	0.30	-0.56**
L7	0.86**	-0.13	0.93**	-0.08	-0.18
L8	0.23	0.37*	0.30	-0.32*	-0.06
L9	-0.76**	-0.13	-0.20	0.05	-0.56**
L10	-0.51**	-0.06	-0.45**	0.05	0.44*
L11	-0.07	-0.26	0.17	0.05	0.57**
L12	-0.51**	0.12	-0.32*	0.17	-0.43*
L13	-0.12	0.12	-0.08	0.05	0.07
L14	-0.64**	-0.13	-0.45**	-0.20	-0.18
L15	-0.51**	-0.13	-0.08	-0.08	0.07
L16	-0.07	-0.13	0.17	-0.45**	-0.06
L17	0.41*	1.69**	-0.08	0.80**	0.44*
L18	0.16	0.24	-0.08	-0.08	-0.06
L19	0.36*	-0.13	0.43*	0.17	0.69**
L20	0.23	0.24	0.55**	0.30	-0.06
L21	-0.59**	-0.38*	-0.57**	0.30	-0.31
L22	0.28	-0.51**	0.05	-0.20	-1.06**
L23	-0.21	-0.13	0.17	0.05	-0.06
L24	0.99**	-0.13	0.68**	0.05	0.57**
L25	0.28	-0.06	-0.45**	-0.82**	-0.18
L26	0.23	-0.01	-0.32*	0.30	0.57**
L27	0.23	-0.01	0.17	0.30	0.07
L28	-0.59**	-0.13	-0.57**	0.17	0.44*
L29	-0.09	-0.51**	0.30	-0.08	0.07
L30	0.23	0.12	-0.20	-0.45**	-0.18
TESTERS					
T1	-0.12**	-0.06	-0.08	-0.08	-0.15**
T2	0.12**	0.06	0.08	0.08	0.15**

*Significant at 5% level of significance; **Significant at 1% level of significance

Table.6 Specific combining ability effects for diseases under artificial and natural epiphytotic conditions

CROSS	Inoculated		Natural			CROSS	Inoculated		Natural		
	TLB	MLB	TLB	MLB	BLSB		TLB	MLB	TLB	MLB	BLSB
L1 × T1	0.19	0.18	0.07	-0.17	0.27	L16 × T1	-0.25	-0.07	-0.17	0.32	0.15
L1 × T2	-0.19	-0.18	-0.08	0.17	-0.28	L16 × T2	0.25	0.07	0.17	-0.33	-0.15
L2 × T1	-0.38	0.13	0.07	-0.05	0.03	L17 × T1	0.12	0.26	-0.42	-0.93**	-0.35
L2 × T2	0.38	-0.13	-0.08	0.05	-0.03	L17 × T2	-0.12	-0.26	0.43	0.93**	0.35
L3 × T1	-0.13	-0.07	0.07	-0.17	-0.22	L18 × T1	0.12	-0.44	0.57*	-0.05	-0.85**
L3 × T2	0.13	0.07	-0.08	0.17	0.22	L18 × T2	-0.12	0.44	-0.57*	0.05	0.85**
L4 × T1	0.19	0.18	0.08	0.08	0.03	L19 × T1	0.07	-0.07	0.07	-0.05	0.65*
L4 × T2	-0.19	-0.18	-0.08	-0.08	-0.03	L19 × T2	-0.07	0.07	-0.08	0.05	-0.65*
L5 × T1	-0.45	0.26	-0.17	0.08	-0.35	L20 × T1	0.19	-0.19	0.20	-0.43	0.15
L5 × T2	0.45	-0.26	0.17	-0.08	0.35	L20 × T2	-0.19	0.19	-0.20	0.42	-0.15
L6 × T1	0.19	-0.44	0.45	0.07	-0.35	L21 × T1	0.12	-0.07	0.07	0.07	0.65*
L6 × T2	-0.19	0.44	-0.45	-0.08	0.35	L21 × T2	-0.12	0.07	-0.08	-0.08	-0.65*
L7 × T1	-0.58*	-0.07	-0.43	-0.05	0.03	L22 × T1	0.25	0.06	-0.30	0.08	0.15
L7 × T2	0.58*	0.07	0.42	0.05	-0.03	L22 × T2	-0.24	-0.06	0.30	-0.08	-0.15
L8 × T1	0.19	-0.32	0.45	-0.30	0.15	L23 × T1	0.50*	0.18	0.33	0.08	0.15
L8 × T2	-0.19	0.32	-0.45	0.30	-0.15	L23 × T2	-0.50*	-0.18	-0.32	-0.08	-0.15
L9 × T1	0.04	0.18	-0.05	-0.17	-0.35	L24 × T1	-0.46	-0.07	-0.93**	0.32	-0.72*
L9 × T2	-0.05	-0.18	0.05	0.17	0.35	L24 × T2	0.46	0.07	0.93**	-0.33	0.73*
L10 × T1	0.04	0.01	0.20	0.32	-0.35	L25 × T1	0.25	0.01	0.20	0.20	0.28
L10 × T2	-0.05	-0.01	-0.20	-0.33	0.35	L25 × T2	-0.24	-0.01	-0.20	-0.20	-0.28
L11 × T1	-0.25	0.06	-0.17	-0.17	0.53	L26 × T1	0.19	0.06	0.32	0.07	0.53
L11 × T2	0.25	-0.06	0.17	0.17	-0.52	L26 × T2	-0.19	-0.06	-0.33	-0.08	-0.52
L12 × T1	0.19	-0.07	0.32	0.20	-0.22	L27 × T1	0.05	0.06	-0.42	0.07	0.28
L12 × T2	-0.20	0.07	-0.33	-0.20	0.22	L27 × T2	-0.05	-0.06	0.43	-0.08	-0.28
L13 × T1	-0.31	0.18	-0.42	0.08	0.03	L28 × T1	0.12	0.18	0.07	0.20	-0.60*
L13 × T2	0.31	-0.18	0.43	-0.08	-0.03	L28 × T2	-0.12	-0.18	-0.08	-0.20	0.60*
L14 × T1	0.07	0.18	0.20	0.08	0.03	L29 × T1	-0.38	0.06	-0.30	0.20	0.03
L14 × T2	-0.07	-0.18	-0.20	-0.08	-0.03	L29 × T2	0.38	-0.06	0.30	-0.20	-0.03
L15 × T1	0.04	-0.07	0.08	0.20	0.03	L30 × T1	0.05	-0.32	-0.05	-0.18	0.28
L15 × T2	-0.05	0.07	-0.08	-0.20	-0.03	L30 × T2	-0.05	0.32	0.05	0.17	-0.28

*Significant at 5% level of significance; **Significant at 1% level of significance

For MLB, four lines showed significantly negative GCA effects out of these line L_{25} (-0.82) had the highest negative GCA effects followed by L_{16} (-0.45), L_{30} (-0.45) and L_8 (-0.32).

These inbred lines are good general combiner for MLB. Six lines and one tester (T1) had significant negative GCA values for BLSB; indicating that these lines are good general combiner. The highest GCA value was recorded for L_{22} (-1.06), followed by L_5 (-0.56) and L_6 (-0.56). Whereas, eight lines and one tester (T2) exhibited significant positive GCA effects; indicating that there inbreds are poor general combiners for BLSB.

Specific combining ability effects

Among sixty hybrids, only two cross combinations L_7× T_1 (-0.58) and L_{23}×T_2 (-0.50) exhibited significant negative SCA effects for TLB under artificial epiphytotic conditions; and two hybrids L_7× T_2 (0.58) and L_{23}×T_1 (0.50) showed significant positive SCA effects (Table 6). None of cross combination exhibited significant negative and positive SCA effects for MLB under

artificial epiphytotic conditions; however thirty lines showed negative SCA effect for this disease. Under natural condition, two hybrids *viz*., L_{18}× T_2 (-0.57) and L_{24}× T_1 (-0.93) showed significant negative SCA effects for TLB. While two crosses L_{18}× T_1 and L_{24}× T_2 exhibited significant positive SCA effects. For MLB, one hybrid i.e. L_{17} X T_1 (-0.93) showed significant negative SCA effect and one hybrid i.e. L_{17}× T_2 (0.93) exhibited significantly positive SCA effect. Five cross combinations namely, L_{18}× T_1, L_{19}× T_2, L_{21}× T_2, L_{24}× T_1 and L_{28}× T_1 showed significant negative SCA effects for TLB in natural epiphytotic condition. These hybrids were good specific combiners for BLSB resistance. Five crosses *viz*., L_{18}× T_2, L_{19}× T_1, L_{21}× T_1, L_{24}× T_2 and L_{28}× T_2 exhibited significantly positive SCA effects which determined that these were poor specific combiners.

Results of the current study indicate that significant genetic variation for resistance to all three diseases exists in maize under mid hill conditions of Himachal Pradesh. Among the inbred lines evaluated the most promising ones wereL_{10}, L_{12}, L_{14}, L_{21}, L_{28} and T_1 for TLB; L_{21}, L_{22}, L_{25}, L_{26} and L_{28} for MLB and L_5, L_6, L_9, L_{12}, L_{22} and T_1 for BLSB as they showed resistance against these particular diseases with significant GCA effects. These lines can be used as parent sources for resistance in further breeding programme. Five cross combinations viz., L_{17}× T_1, L_{18}× T_1, L_{23}× T_2, L_{24}× T_1 and L_{28}× T_1 were selected on the basis of disease reaction and significant SCA effects for one of the studied diseases. These cross combination can be commercialized after further evaluation for yield parameters at several locations.

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