Plant Archives Vol. 26, No. 1, 2026 pp. 1703-1708 e-ISSN:2581-6063 (online), ISSN:0972-5210

Plant Archives

Journal homepage: http://www.plantarchives.org

DOI Url : https://doi.org/10.51470/PLANTARCHIVES.2026.v26.no.1.235

ADDITIONAL SOURCES OF RESISTANCE FOR TURCICUM LEAF BLIGHT (TLB), MAYDIS LEAF BLIGHT (MLB) AND BANDED LEAF AND SHEATH BLIGHT (BLSB) IN ELITE MAIZE (*ZEA MAYS* L.) INBREDS

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(Date of Receiving-04-02-2026; Date of Revision-29-03-2026; Date of Acceptance-11-04-2026)

ABSTRACT

Turcicum leaf blight (TLB), maydis leaf blight (MLB) and banded leaf and sheath blight (BLSB) are the major diseases of maize grown in the North-Western Himalayas, causing a drastic reduction in yield ranging from 15-30%, which may exceed up to 70% under favourable conditions. To overcome the losses due to these diseases, resistant genotypes need to be developed. Therefore, the identification of resistant sources of genes against these diseases is important in order to develop TLB, MLB and BLSB resistant genotypes. The present investigation was carried out to screen 30 elite maize inbred lines including two checks 'BAJIM-08-26' and 'BAJIM-08-27' against turcicum leaf blight (TLB), maydis leaf blight (MLB) and banded leaf and sheath blight (BLSB) under natural epiphytotic conditions at Palampur during *kharif*, 2024. The resistant reaction was noted in 10 genotypes for TLB, 8 genotypes for MLB and 7 genotypes for BLSB while 17 genotypes for TLB, 19 genotypes for MLB and 22 genotypes for BLSB exhibited moderate resistance. Among 30 diverse maize genotypes, five genotypes *viz.*, BML 7, CML 138, CML 442, IML 5 and KDM 323 exhibited resistance against all three diseases. These identified genotypes can be further used in maize breeding program as resistance sources against TLB, MLB and BLSB after testing their disease reaction at hot spots and also under artificial epiphytotic conditions.

Key words : Maize, Inbred lines, Resistance, TLB, MLB and BLSB.

Introduction

Maize (*Zea mays* L., 2n =20) also known as "Queen of cereals" is an annual C_4 crop which is cultivated all-around the world under a wide range of agro-ecologies. Its kernel contains 70% carbohydrates, 10.4% albuminoids, 10% protein, 4% oil, 2.3% crude fibre and 1.4% ash. It has significant amount of vitamin A, nicotinic acid and riboflavin. In Himachal Pradesh, maize is mostly grown as a '*kharif*' season crop, and the total area under maize cultivation is nearly 0.254 million hectares with total production of 0.62 million metric tonnes and productivity of 2.44 tonnes per hectare (Anonymous, 2023). The productivity of maize is substantially constrained by the incidence of fungal, bacterial and viral diseases, which adversely affect its yield performance.

There are 112 diseases which are reported to occur in maize worldwide. In India, 35 diseases are reported to affect maize production. Among the various diseases of maize, *Exserohilum turcicum* causing turcicum leaf blight, *Cochliobolus heterostrophus* causing maydis leaf blight and *Rhizoctonia solani* f.sp. *sasakii* causing banded leaf and sheath blight, are widely prevalent in different maize growing areas of Himachal Pradesh.

There are a variety of critical problems facing tropical maize cultivation, such as disease infestation, insect or pest and weed problems. Foliar diseases in particular cause significant losses in agricultural yield (Keerthana *et al.*, 2023). Turcicum leaf blight (TLB), maydis leaf blight (MLB) and banded leaf and sheath blight (BLSB) are the major foliar diseases of maize that severely affect maize productivity. These diseases progressively damage the foliage, causing a substantial reduction in leaf area and hindering the photosynthetic efficiency of maize. The resulting decline in assimilate production directly affects biomass accumulation and ultimately leads to significant grain yield losses. Their recurring incidence poses a serious challenge to sustainable maize cultivation, particularly in environments conducive to rapid disease development. Phenotyping of maize germplasm is one of the most decisive approaches which play complementary role in deciphering the genetic basis of TLB resistance and facilitating the development of resistant cultivars (Jan *et al.*, 2024).

Characteristic symptoms of TLB are the appearance of long, narrow, greyish or tan lesions initially on leaves that align with the midrib. These lesions later expand into an oblong or characteristic “cigar” or “spindle” shape and may also develop on husks. The disease is favoured by moderate, wet and humid weather conditions (18-27°C). The reduction of photosynthetic tissue causes yield losses from 25 to 90% of the total crop and a decline in silage quality.

MLB also known as southern corn leaf blight is prevalent in regions with warm temperatures (20-30°C) and high humidity (>80%), which initially appear as small elliptical spots or lesions with dark brown margins and a straw to light brown centre which start from the base of the plant up to the flag leaf eventually progressing to complete foliage blight (Kumar *et al.*, 2022).

BLSB begins as lesions on the lower leaf sheaths and adjoining leaf tissues. As the disease progresses upward, it can extend to the stalk and under severe conditions, may reach the ears, leading to ear rot or ear infection. Extensive grey, tan or brown snake-like, discoloured patches interspersed with dark brown bands appear on the affected parts. The disease is favoured by hot and humid weather and results in production losses of up to 60% in maize under natural conditions (Rai and Singh, 2018). The mode of spread of these three diseases is outlined in Table 1.

Although, chemical fungicides offer temporary relief in managing foliar diseases, their routine use is often neither economically viable for farmers nor environmentally sustainable. Moreover, indiscriminate application poses considerable risks to human and ecosystem health. Hence, ICAR strongly advocates the development and adoption of genetically resistant maize varieties as the most effective, ecologically sound and sustainable strategy for long-term disease management (Sharma *et al.*, 2022).

Table 1 : Mode of spread of TLB, MLB and BLSB in maize.

Disease	Primary spread	Secondary spread
TLB	Rain splash and air currents	Crop residues
MLB	Broken stalks and malformed or completely rotten cobs covered with greyish powder	Phytotoxins, pathotoxins and mycotoxins
BLSB	Sclerotia or mycelium in soil and grass hosts	Infected plant debris adjoining healthy plants

The genetic basis of resistance in maize to major foliar diseases such as turcicum leaf blight (TLB), maydis leaf blight (MLB) and banded leaf and sheath Blight (BLSB) has been extensively characterized over the years. Control by using resistant cultivars needs to be accompanied by an understanding of the epidemic components that influence the disease progression. This strategy was used as a preventive measure to control the TLB epidemic during the 1970s (Mirsam *et al.*, 2025). In case of TLB, qualitative resistance is governed by major genes such as *Ht1*, *Ht2* and *Ht3*, whereas durable quantitative resistance is polygenic in nature and associated with multiple QTLs, including *ZmWAK-RLK1* and *ZmREM6.3*. Resistance to MLB involves both monogenic and polygenic components, with the recessive gene *rhm-1* and several QTLs, notably *ZmCCoAOMT2*, contributing to enhanced tolerance (Kumar *et al.*, 2016; Jeevan *et al.*, 2020). For BLSB, resistance has been linked to functional alleles such as *ZmFBL41*, which plays a key role in lignin biosynthesis and restricts lesion expansion (Zhu *et al.*, 2021). However, the continuous dependence on a few resistant sources particularly major resistance (R) genes had narrowed the genetic base and poses a substantial risk to sustainable crop protection. Pathogens are genetically dynamic and can rapidly evolve into new virulent races capable of overcoming single-gene resistance, leading to resistance breakdown. A classic example is the catastrophic 1970 southern corn leaf blight epidemic in the USA, which was triggered by the widespread use of T-cytoplasm in hybrid maize production.

Therefore, to effectively counteract losses in maize production, it is important to broaden the genetic base of resistance by integrating multiple resistance genes, diverse germplasm sources and both vertical and horizontal resistance mechanisms into breeding programmes. Such diversification not only minimizes vulnerability associated with single gene dependence but also enhances the durability of resistance and ensures broad spectrum, stable protection across environments and against evolving pathogen populations. In this context, breeding for disease resistance i.e., development and deployment of resistant cultivars remain the most effective, economical and reliable strategy for sustaining maize productivity and safeguarding the crop under variable agro-ecological conditions (Stout and Davis, 2009; Lefebvre *et al*., 2020; Pathania *et al*., 2021).

Materials and Methods

The experimental material comprised 30 elite maize inbred lines including two checks *viz*., BAJIM-08-26 and BAJIM-08-27, which were obtained from different sources, were evaluated against TLB, MLB and BLSB under natural epiphytotic conditions in a randomized block design with three replications during *kharif*, 2024 at the Experimental Farm, Department of Genetics and Plant Breeding, Chaudhary Sarwan Kumar Himachal Pradesh Krishi Vishvavidyalaya, Palampur (Table 2). The weekly average maximum and minimum temperatures ranged from 25.9°C to 28.5°C and 12.8°C to 19.8°C, respectively, while the relative humidity ranged from 64 to 92.05% during the crop period.

Disease screening for TLB and MLB was carried out using the 0-9 scoring scale proposed by Mitiku *et al*. (2014), while disease reaction to BLSB was recorded following the scale developed by Muis and Quimio (2006). Disease severity was assessed on five randomly selected plants per genotype in each replication. The individual plant scores were averaged, and the mean score across three replications was used for classifying genotypes into resistant or susceptible categories. To study the inter-relationship among the diseases, correlation analysis was performed. The resistance scores of each genotype were subjected to correlation analysis to determine the degree and direction of association between the diseases.

Table 2 : List of maize inbred lines used in the present study.

S. no.	Inbred	Source
1	BAJIM-06-2	AICRP, HAREC, Bajaura
2	BAJIM-06-6	AICRP, HAREC, Bajaura
3	BAJIM-09-10	AICRP, HAREC, Bajaura
4	BAJIM-09-64	AICRP, HAREC, Bajaura
5	BML 7	AICRP, PJTSAU, Hyderabad
6	CML 40	ICAR-IIMR, New Delhi
7	CML 119	ICAR-IIMR, New Delhi
8	CML 138	ICAR-IIMR, New Delhi
9	CML 331	ICAR-IIMR, New Delhi
10	CML 442	ICAR-IIMR, New Delhi
11	CML 542	ICAR-IIMR, New Delhi
12	CML 564	ICAR-IIMR, New Delhi
13	CML 577	ICAR-IIMR, New Delhi
14	DML 194	ICAR-IIMR, Ludhiana
15	DML 313	ICAR-IIMR, Ludhiana
16	EC672693B-1-1-1	ICAR-IIMR, Ludhiana
17	IML 5	ICAR-IIMR, Ludhiana
18	IML-15-48	ICAR-IIMR, Ludhiana
19	IML-15-268	ICAR-IIMR, Ludhiana
20	IML-16-108	ICAR-IIMR, Ludhiana
21	KDM-323	AICRP, SKUAS&T, Srinagar
22	KDM-356	AICRP, SKUAS&T, Srinagar
23	KGI 3-1	AICRP, SAREC, Kangra
24	KGI 3	AICRP, SAREC, Kangra
25	KGI 75	AICRP, SAREC, Kangra
26	KGI 72	AICRP, SAREC, Kangra
27	LM 13	AICRP, PAU, Ludhiana
28	V 335	VPKAS, Almora
Check (s)		
1	BAJIM-08-26	AICRP, HAREC, Bajaura
2	BAJIM-08-27	AICRP, HAREC, Bajaura

Results and Discussion

The initial appearance of disease symptoms varied across the three foliar diseases. Symptoms of turcicum leaf blight (TLB) were first observed on the older, lower leaves of maize plants between 35-50 days after sowing (DAS). In contrast, symptoms of maydis leaf blight (MLB) appeared comparatively earlier, between 25-40 DAS. Banded leaf and sheath blight (BLSB) symptoms were recorded later in the crop growth cycle, typically between 40-60 DAS. The temporal variation in symptom onset among the diseases reflects differences in pathogen biology and environmental requirements for disease development.

Under natural epiphytotic conditions, ten genotypes exhibited resistance to TLB (Table 3, Fig. 1). Seventeen genotypes were found to be moderately resistant. Similar findings for TLB were also reported earlier by Sharma *et al*. (2021) and Sharma *et al*. (2022). Three genotypes displayed moderate susceptibility to TLB. This uniform resistance observed among the tested genotypes requires further detailed investigation into the genetic basis, suggesting the involvement of common resistance genes or defence mechanisms, which can be effectively exploited in maize breeding programmes for developing durable resistance.

For MLB, eight genotypes exhibited resistance with infection rates below 30% and nineteen genotypes were

Table 3 : Reaction of maize inbreds to TLB under natural field conditions.

Rating scale	**Reaction**	**No. of inbred lines**	**Inbred lines**
≤3.0	Resistant	10	CML 138, KDM 323, KDM 356, IML-15-48, BML 7, CML 577, IML 5, BAJIM-08-26, KGI 75 and CML 442
3.1-5.0	Moderately resistant	17	CML 40, CML 564, LM13, KGI 3, KGI 3-1, KGI 72, V335, BAJIM-06-6, BAJIM -09-10, BAJIM-08-27, DML 194, EC 672693B-1-1-1, CML 542, IML16-108, IML-15-268, CML331, BAJIM-06-2 and BAJIM-09-64
5.1-7.0	Moderately susceptible	3	CML 119, DML 313 and LM13
>7.0-9.0	Susceptible	-	-

Table 4 : Reaction of maize inbreds to MLB under natural field conditions.

Rating scale	**Reaction**	**No. of inbred lines**	**Inbred lines**
≤ 3.0	Resistant	8	BAJIM-06-2, BAJIM-08-26, BML 7, CML 138, KDM 323, IML 5, BAJIM-06-6 and CML 442
3.1-5.0	Moderately resistant	19	CML 564, CML 542, CML 331, CML 119, CML-577, DML 194, DML 313, EC672693B-1-1-1, IML-15-268, IML-15-48, IML-16-108, KGI 72, KGI 75, KGI 3, BAJIM-09-10, BAJIM-09-64, BAJIM-08-27, KDM 356 and KGI 3-1
5.1-7.0	Moderately susceptible	3	LM 13, CML 40 and V335
>7.0-9.0	Susceptible	-	-

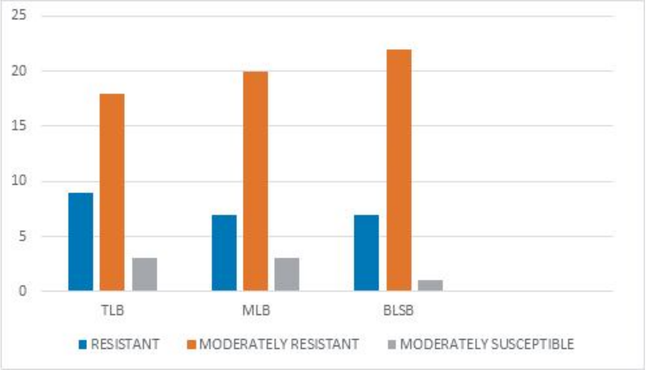
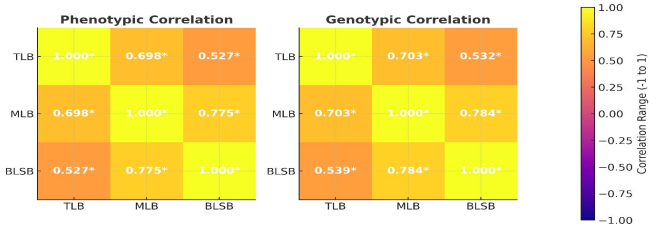


Fig. 1 : Number of maize inbreds that are resistant, moderately resistant and moderately susceptible to TLB, MLB and BLSB in the present study.

found to be moderately resistant (Table 4). Three genotypes had moderate susceptibility to MLB. The identified resistant maize inbred lines can be integrated into the active breeding material for making experimental cross combinations in order to develop improved MLB resistant hybrids in maize (Hooda *et al.*, 2024).

The higher number of resistant genotypes observed for TLB as compared to MLB suggests that resistance to TLB is likely more widespread within the evaluated germplasm pool. This variation in resistance distribution may reflect differences in evolutionary pressures, pathogen prevalence, or historical selection practices during the development of these maize inbred lines. The absence of highly susceptible genotypes for both TLB and MLB further highlights the inherent robustness of the genetic material against foliar blight pathogens. Such genotypes represent valuable resources for breeding programmes aimed at developing durable and broad-spectrum disease resistant maize varieties.



*Significance at P ≤ 0.05

Fig. 2 : Correlation between disease scores at (a) phenotypic and (b) genotypic levels.

Seven genotypes exhibited resistance to BLSB with infection levels up to 30%. Whereas, twenty-two genotypes were moderately resistant to BLSB and one genotype was moderately susceptible to BLSB (Table 5). Similar findings were also reported previously by Thakur *et al.* (2018).

The relationship between disease resistance scores was analysed to identify any potential correlations among the diseases. Understanding these associations can

Table 5 : Reaction of maize inbreds to BLSB under natural field conditions.

Rating scale	Reaction	No. of inbred lines	Inbred lines
d” 3.0	Resistant	7	CML 138, IML 5, KDM 323, CML 442, BML7, IML-15-268 and EC 6722693B-1-1-1
3.1-5.0	Moderately resistant	22	BAJIM-08-27, BAJIM-06-2, BAJIM-06-6, BAJIM-09-10, BAJIM-09-64, DML 194, DML 313, KGI 3, KGI 72, KGI 75, CML 119, CML 564, CML 40, IML-15-48, IML-16-108, KGI 3-1, CML 331, V335, KDM 356, CML 577, BAJIM-08-26 and CML 542
5.1-7.0	Moderately susceptible	1	LM 13
>7.0-9.0	Susceptible	-	-

provide valuable insights for selecting and breeding genotypes with improved resistance profiles. The analysis revealed that at the phenotypic level, TLB was found to be significantly and positively correlated with MLB and BLSB (Fig. 2). However, genotypic correlation coefficients showed a higher degree of association than their corresponding phenotypic correlation coefficients. This indicated that the traits under consideration had an inherent association and the environment had a smaller effect on these traits. TLB, MLB and BLSB exhibited significant and positive genotypic correlations among each other. The variation in resistance patterns across different diseases observed in the study presents varied opportunities for breeding. Genotypes that exhibited resistance to multiple diseases could serve as valuable foundation material for developing resistant maize inbred lines. Similar findings were also reported earlier by Godara *et al*. (2025).

Conclusion

The ubiquitous nature of maize has made it one of the important cereal crops across the globe. Proper management of these diseases require development of TLB, MLB and BLSB resistant inbred lines, which necessitates prior identification of resistant sources. For this, 30 inbred lines were evaluated against TLB, MLB and BLSB diseases. Among the 30 inbred lines, five inbred lines *viz.*, BML 7, CML 138, CML 442, IML 5 and KDM 323 exhibited resistance to all three diseases. These resistant inbred lines can serve as valuable sources of resistance genes for maize breeding programs. Following thorough evaluation at hot spots and under artificial epiphytotic conditions, these inbred lines can be further utilized to develop improved hybrids with enhanced and stable disease resistance. Incorporating these inbred lines into maize breeding programs will aid in building durable resistance, reducing yield losses and promoting sustainable maize production.

Acknowledgements

We express our thanks to the Department of Genetics and Plant Breeding, CSK HPKV, Palampur for providing the facilities and support during the research.

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