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# Identification of resistant donors for turcicum leaf blight disease of maize among cold tolerant temperate germplasm

**ROOHI JAN[1], M ASHRAF AHANGAR[2], FAROOQ A. SHEIKH[2], SHAHEEN KAUSAR[1], KHALID RASOOL[1], SHAHEEN KAUSAR[1], FEHIM JEELANI[1] AND SHAZIA FAROOQ[1]**

[1]Faculty of Agriculture, Wadoora SKUAST-Kashmir, India

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## ABSTRACT

*Turcicum leaf blight disease of maize is the major biotic factor limiting maize production under temperate agro-climatic conditions of Kashmir. Deployment of disease resistant cultivars is the most effective, ecofriendly and cost-efficient disease management option under these conditions where chemical control of maize diseases is not adopted. In the present study, temperate maize germplasm was evaluated against Exherohilum turcicum causing turcicum leaf blight of maize. Among the evaluated maize genotypes some early maturing cold tolerant inbred lines registered high level of resistance (HR) with disease score 1 in 1 to 9 evaluation scale which can be used profitably in resistance breeding programme for the development of high yielding maize varieties resistant to turcicum leaf blight.*

**Key words:** *Exserohilum turcicum*, maize genotype, screening, disease resistance

## INTRODUCTION

Turcicum leaf blight caused by fungus *Exserohilum turcicum* (Pass) Leonard and Suggs, is most devastating disease of maize which occurs all the maize growing regions of the world particularly in areas where high humidity (75-90%) and moderate temperature (22-25$^0$C) exists during the growing season (Khatri 1993). The occurrence of this disease has risen the alarming proportions in many maize growing areas of the world and has great economic importance under Kashmir agro-climatic conditions. Maize is ravaged by this disease to the losses above economic thresh hold levels in the range of 27.6 to 90.7% of total grain yield (Chenula and Hora 1962). The maximum damage to maize crop occurs if the disease develops prior to silk emergence. The disease epidemics at an early stage cause premature death of blighted leaves thereby loss their fodder quality (Payak and Renfro 1968, Patil 2000). Deployment of disease resistant cultivars is most effective and cost-efficient way to control the Turcicum leaf blight. An important step to devise a programme for the development of disease resistant cultivars in many host-pathogen systems where major genes control resistance, is the evaluation of germplasm and identification of potential donors for disease resistance. The absence of resistance or tolerance in the local maize varieties against Turcicum leaf blight shaped the first approach towards an improvement of the maize crop and introduction of maize materials from different sources all over the world. In the present study an attempt was made to see the level of resistance and quantitative traits of different accessions of maize to know the resistance potential of different germplasm against Turcicum leaf blight under high altitude conditions (7500ft) of Kashmir. The Kashmir Valley (longitude 73.0-74.2$^0$E and latitude 33-34$^0$N) is agro-climatically a typical temperate region where maize is grown as sole crop or intercropped with pole type common beans at an altitude of 1850-2500 m above mean sea level. Major challenge to increase maize production primarily involves the predominance of cultivated land races which are more susceptible to various biotic stresses particularly Turcicum leaf blight which causes 28-91 per cent yield losses in maize (Singh et al 2014, Ahanger et al 2022). Use of disease resistant varieties against the major diseases of maize is the most common method of disease management in high altitude areas of Kashmir where maize is being cultivated mostly on hilly terrains of the state (Ahangar et al 2016). Farmers do not prefer chemical management in these areas where it is

[2]*Mountain Crop Research Station-Sagam, SKUAST- Kashmir, India,* [2]*Corresponding author E-mail:* *mashrafjs@gmail.com*

difficult to carry plant protection equipment and not feasible to utilize them profitably. The present work represents a comprehensive effort to identify and utilize maize germplasm with resistance to Turcicum leaf blight disease, particularly among cold-tolerant temperate varieties, with the aim of improving maize productivity and resilience in affected regions. Different inbred lines of maize from indigenous and exotic sources that were adopted for cold temperate conditions with inbuilt resistance to Turcicum leaf blight of maize were identified to be used in resistance breeding programs. By leveraging the genetic diversity present in these diverse germplasm pools, breeders can develop improved maize varieties that meet the challenges posed by specific environmental conditions while ensuring productivity and sustainability in agricultural systems.

## MATERIALS AND METHODS

### Screening of maize germplasm

A set of 48 maize germplasm lines consisting of indigenous and exotic inbred lines in advanced stages of maintenance along with popular commercial cultivars were screened under artificially inoculated field conditions during *Kharif* season 2021 and 2022. The inbred lines belong to high altitude adaptation, cold tolerant and early maturity group (125-135 days to maturity). The experiment was conducted at Mountain Crop Research Station, Larnoo (latitude 33.37° N, longitude 75.22° E, Altitude: 2286 m amsl) and at Mountain Research Centre for Field Crops Khudwani, SKUAST-Kashmir (latitude 34.09° N, longitude 74.79° E, Altitude: 1560 m amsl) under temperate agro-climatic conditions. The experiment was laid in augmented design with three replications. Test lines were planted in 2 row plots of 4m length with plant to plant and row to row spacing of 20 cm and 70 cm respectively. The susceptible checks were planted after every 10 rows and the plot was bordered by susceptible disease spreader rows on each side. Standard recommended agronomic and cultural practices were followed. Weeding was done properly, and fertilizers were applied at the rate of 60 kg N, 40 kg P and 20 kg K $ha^{-1}$ in two split doses one at planting and second as topdressing four weeks after planting.

### Preparation of inoculum and inoculation

Twenty isolates of *E. turcicum* were isolated from the diseased samples collected from diverse locations of maize growing areas of Kashmir valley. These isolates were evaluated for their pathogenic variability and race identification was done on seven maize differentials having Ht1, Ht2, Ht3 and HtN genes. Races 0 and 1 were found to infect maize under temperate conditions of Kashmir. Spore suspension of the isolates of race 0 and race 1 was prepared by washing the conidia with distilled water from 20 days old cultures. The spore concentration was maintained at $3x10^5$ spore $ml^{-1}$. Tween 20 was added @ 0.1% to the spore suspension. Spraying of spore suspension was done in evening by using a glass atomizer at three to four leaf stage of plants. Control plants were treated similarly with distilled water.

Symptom and disease development was visually assessed by observing the symptoms at 10 days intervals, starting from 20 days after inoculation. From each treatment 10 plants were randomly selected and tagged for subsequent monitoring. Disease spots were measured and the changes in size, shape and colour of the spots were observed. Disease severity was assessed by estimating the mean percentage leaf area affected by disease using 1-9 disease rating scale (Table-1). From this screening relatively resistant lines from various genetic backgrounds were selected and were further evaluated against the selected isolates of *E. turcicum* under controlled conditions.

$$PDI = \frac{\text{Sum of all individual ratings}}{\text{Number of plants observed x maximum disease grade}} \text{ x } 100$$

Table 1: 1-9 disease rating scale (Paterniani *et al.* 2000)

| Score | Disease intensity (%) | Disease reaction |
|---|---|---|
| 1 | <11.11 | Highly Resistant |
| 2 | 11.11-22.22 | Resistant |
| 3 | 22.22-33.33 | Moderately Resistant |
| 4 | 33.33-44.44 | |
| 5 | 44.44-55.55 | Moderately Susceptible |
| 6 | 55.55-66.66 | |
| 7 | 66.66-77.77 | Susceptible |
| 8 | 77.77-88.88 | |
| 9 | 88.88-99.99 | |

**Evaluation of selected maize genotypes against *E. turcicum* isolates under controlled conditions**: To validate the resistance, a selected set of 23 genotypes which showed resistant reaction against Turcicum leaf blight under field conditions, was further screened under controlled conditions against both the identified races of *E. turcicum*. Five seeds of each genotype were sown in pots, filled with sterilized potting medium prepared by mixing soil, FYM and sand at the ratio of 6:2:1, respectively. Fertilizers were applied as per recommendation and watering was done as per the moisture status of the potting medium. After germination one plant was maintained in each pot. The treatments were arranged in a completely randomized block design with three replications per treatment. Spore suspension of each isolate was prepared separately and sprayed separately by using a glass atomizer at three to four leaf stages of plants, grown in glass house. The disease severity scores were recorded at 20 days interval after inoculation and used to calculate the area under disease progress curve (AUDPC) as:

$$AUDPC = \sum_{i=1}^{n} [\frac{\text{Y i + Y i + 1}}{2}] \text{(T i + 1 – Ti)}$$

*i* = time of rust severity rating, Ti is the number of days after inoculation, and Yi is the rust severity.

**Data analysis:** Data were subjected to analysis of variance using a general linear model with OPSTAT Statistics software. The average data categorized into 1-9 scale was subjected to cluster analysis to identify the similarity pattern among genotypes. For this analysis, a similarity matrix was derived with the Simqual Programme (NTSYS 1993 pc, version 1.7) using simple matching coefficient of similarity. A dendrogram was produced by the unweight pair group method for arithmetic average (UPGMA) in the SAHN program.

## RESULTS AND DISCUSSION

### Screening of maize genotypes for disease resistance

In present study significant interactions were observed between Genotype x Environment and genotype x time which indicates that maize genotypes had varying disease severity scores in the different environments and during different years against turcicum leaf blight. The differential disease response of genotypes was due to the random environments with different agro-climatic conditions. Significant effects between maize genotypes and test environments were previously reported (Selvaraj and Ngaranjan 2011, Lozano-Ramirez et al 2015, Minliang Jin et al 2022, Nigus Belay 2022). Mountain Crop Research Station Larnoo is high altitude area situated at 2286 m amsl where temperature remains moderate with high humidity and frequent rainfall which are the main environmental factors conducive for turcicum leaf blight disease of maize. The disease was found more at high altitude regions of the valley as compared to the lower plain belts. In 2021, disease intensity of genotypes was more compared to 2022 (Fig. 1) as the environmental conditions were more favourable for disease development during year 2022. Disease prevalence in maize is closely correlated with pathogen resources, cultivated varieties, weather conditions, farming systems, and agricultural ecology (Yang et al 2017).

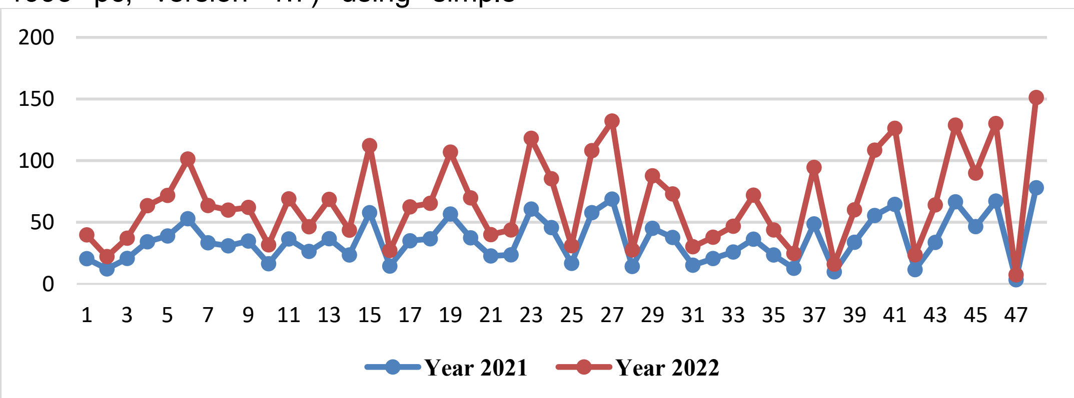


Fig. 1: Average disease intensity of maize genotypes over years

Table 2: Turcicum leaf blight disease reaction of temperate maize germplasm

| S. No. | Genotype | Source | PDI (Pooled) | Score | Disease Reaction |
|---|---|---|---|---|---|
| 1 | CML451 | CIMMYT | 12.2 | 2 | R |
| 2 | CML470 | CIMMYT | 33.4 | 4 | MR |
| 3 | CML472 | CIMMYT | 20.5 | 2 | MR |
| 4 | CML474 | CIMMYT | 30.9 | 3 | MR |
| 5 | CML563 | CIMMYT | 22.7 | 3 | MR |
| 6 | CML564 | CIMMYT | 20.7 | 3 | MR |
| 7 | CML578 | CIMMYT | 34.2 | 4 | MR |
| 8 | CML579 | CIMMYT | 14.5 | 2 | R |
| 9 | CML580 | CIMMYT | 16.4 | 2 | R |
| 10 | CML581 | CIMMYT | 57.8 | 6 | MS |
| 11 | CML582 | CIMMYT | 37.4 | 4 | MR |
| 12 | SMI-10 | SKUASK-K | 5.4 | 1 | HR |
| 13 | SMI 15C | SKUAST-K | 71.5 | 7 | S |
| 14 | SMI 27 | SKUAST-K | 23.0 | 3 | MR |
| 15 | SMI 43 | SKUAST-K | 6.2 | 1 | HR |
| 16 | SMI 60 | SKUAST-K | 58.6 | 6 | MS |
| 17 | SMI 90 | SKUASK-K | 7.8 | 1 | R |
| 18 | SMI 114-2 | SKUAST-K | 68.7 | 7 | S |
| 19 | SMI 161 | SKUAST-K | 30.4 | 3 | MR |
| 20 | SMI 510 | SKUAST-K | 16.2 | 2 | R |
| 21 | SMI 516 | SKUAST-K | 14.9 | 2 | R |
| 22 | SNL1914 | CIMMYT | 57.8 | 6 | MS |
| 23 | SNL1918 | CIMMYT | 14.2 | 2 | R |
| 24 | SNL1920 | CIMMYT | 68.8 | 7 | S |
| 25 | SNL1921 | CIMMYT | 60.7 | 6 | MS |
| 26 | SNL1945 | CIMMYT | 45.7 | 5 | MS |
| 27 | SNL18743 | CIMMYT | 16.7 | 2 | R |
| 28 | SNL172489 | CIMMYT | 23.6 | 3 | MR |
| 29 | CM 120 | CIMMYT | 45.1 | 5 | MS |
| 30 | CM 133 | CIMMYT | 37.7 | 4 | MR |
| 31 | CM 135 | CIMMYT | 15.2 | 2 | R |
| 32 | CM 138 | CIMMYT | 20.6 | 2 | R |
| 33 | CM 140 | CIMMYT | 25.9 | 3 | MR |
| 34 | CM 212 | CIMMYT | 36.3 | 4 | MR |
| 35 | CM 213 | CIMMYT | 23.5 | 3 | MR |
| 36 | DML-1 | DMR | 12.7 | 2 | R |
| 37 | DML-16 | DMR | 55.5 | 6 | MS |
| 38 | DML-112 | DMR | 48.7 | 5 | MS |
| 39 | DML-127 | DMR | 9.8 | 1 | HR |
| 40 | DML-134-2 | DMR | 33.8 | 5 | MS |
| 41 | DML-163-1 | DMR | 64.5 | 6 | MS |
| 42 | DML-170 | DMR | 11.6 | 2 | R |
| 43 | V 341 | VPKAS | 33.7 | 4 | MR |
| 44 | V 346 | VPKAS | 66.6 | 7 | S |
| 45 | V 372 | VPKAS | 46.5 | 5 | MS |
| 46 | V391 | VPKAS | 67.2 | 7 | S |
| 47 | A-632 HTN | USA | 3.4 | 1 | HR |
| 48 | Gurez Local | SKUAST-K | 78.0 | 8 | S |
| | CD (p<0.05) | | 3.62 | | |

The genotypes showed diverse disease response against turcicum leaf blight. The inbred lines of maize tested in present study showed highly resistant to susceptible disease reaction and the mean disease severity of maize genotypes ranged from 3.4 to 78.0 per cent (Table 2). Evaluation of forty-eight maize genotypes tested in the present study revealed that, five inbred lines exhibited the high level of resistance (HR) with disease score 1 in 1 to 9 evaluation scale. 12 genotypes with disease score of 2 showed resistant disease reaction against TLB and 8 genotypes showed moderately resistant disease reaction. The remaining genotypes were found moderately susceptible to susceptible against Turcicum leaf blight of maize. The inbred lines SMI-10, SMI-43, SMI-90 and DML-127 showed disease intensity of 5.4, 6.2, 7.8 and 9.8 per cent respectively against resistant check A632 HTN with disease intensity of 3.2 per cent. The identification of resistant genotypes against Turcicum leaf blight of maize is crucial for sustainable disease management and ensuring food security. 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. The genetic basis of resistance to TLB in maize is multifaceted, involving both major and minor genes with varying degrees of influence on resistance. Understanding the genetic mechanisms underlying TLB resistance is essential for breeding durable cultivars capable of withstanding the challenges posed by this devastating disease (Zhu et al 2021).

The prevalence of turcicum leaf blight has increased in recent years and new races of the pathogen have been reported worldwide. Turcicum leaf blight intimidation to maize production is mainly due to the presence of *S. turcicum* races and the potential of the pathogen for the development of new races (Ahangar et al 2022).

Using different disease score data and the data of area under disease progress curve (AUDPC) of turcicum leaf blight, the maize genotypes were grouped into three clusters using XLSTAT software (Fig. 2). Blue group represents highly susceptible and susceptible genotypes, red group represents moderately susceptible while as green group represents resistant, moderately resistant, and highly resistant maize genotypes. The genotypes which exhibited resistance or moderately resistant reaction were used in hybridization programme to evolve cultivars possessing desirable traits besides resistance to *Turcicum* leaf blight. Resistant sources and their utilization in regular breeding programs has been reviewed by Welz and Geiger (2000). Sustainable management of turcicum leaf blight with more resistance sources and their origins has well demonstrated by Hoda et al (2017). By integrating data from genetic variability assessments, molecular marker analyses, association mapping studies, and functional validation experiments, researchers can gain insights into the genetic basis of disease resistance in maize and facilitate the development of improved maize varieties with enhanced resistance to prevalent diseases (Bhiusal et al 2017).

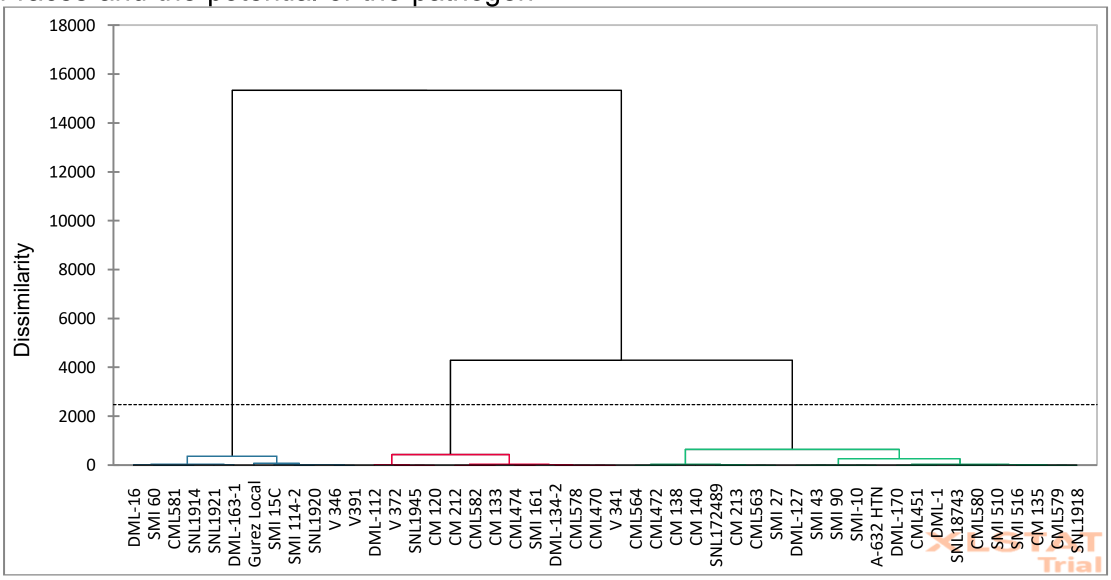

Fig. 2: Dendrogram of 48 inbred lines using XLSTAT software

To authenticate the resistance of genotypes screened under field conditions, 23 inbred lines which showed moderately resistant to highly resistant disease reaction under field screening were selected for further evaluation under controlled conditions along with resistant and susceptible check (Fig. 3). The genotypes *viz.*, SMI-10, SMI-43, SMI90 and SMI-127 were found highly resistant to turcicum leaf blight disease with disease grade of 1. The genotypes CML 451, CML 579, CML 580, SMI 510, SMI 516, SNL 1918, SNL 18743, CM 135, CM 138, DML-1 and DML170 were found resistant with disease grade of 2. These genotypes were efficiently utilized in breeding programme for the development of resistant varieties against turcicum leaf blight suitable for high altitude rainfed temperate regions. Natural germplasm resources, also known as genetic resources, showed extensive genetic diversity in terms of disease resistance. It is therefore necessary to conduct large scale collection and evaluation of maize germplasm before identifying importantly rare natural resistance genes and using them in resistant breeding program (Zhu et al 2021)

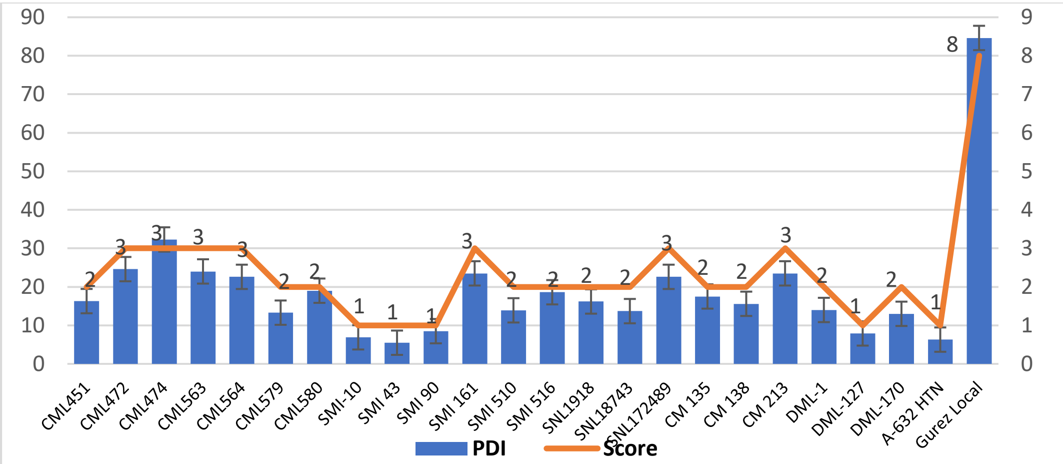

Fig.3: Evaluation disease score of maize genotypes under controlled conditions

The use of cultivars with genetic resistance is the most economical, effective, and practical method of obviating loss in crop yield due to diseases (Ribeiro et al 2016). Lot of germplasm has been developed, identified, and utilized worldwide with turcicum leaf blight resistance. The maize germplasm has been evaluated to identify new resistance sources and establish durability of known resistance against Turcicum leaf blight (Shikari and Zafar, 2009; Kumar et al 2011, Chandrashekara et al 2014, Muiru et al 2015, Ribeiro et al 2016, Garoma et al 2016, Setyawan et al 2016. To build up inherent resistance of crop plants to infection by a particular pathogen is the most economical and ecofriendly disease management decision. Turcicum leaf blight is the major biotic stress of maize under temperate agro-climatic conditions which reduces maize yield as well as fodder quality. Under temperate agroecosystem of Kashmir where chemical application for the control of maize diseases is not a common practice, development of resistant varieties is the most feasible approach for economical and ecofriendly maize production. Under temperate conditions of Kashmir few resistant/ tolerant lines have been identified earlier (Ahanger et al 2016). For the development of disease resistant varieties, it is essential to analyse the germplasm and identify the resistant donors to be utilized in breeding programme for the development of suitable resistant variety for a particular region, however for the develop disease-resistant cultivars, it is necessary to consider the structure of the population and the evolutionary potential in pathogens (Navarro et al 2021). In environments where there is a continuous change in the racial spectrum of the pathogen and the population is highly diverse, exploiting quantitative resistances are recommended (Bankole et al 2023). This can be achieved by using cultivar mixture and production of complex hybrids, like three-way and double-cross hybrids, with inbred lines varying in tolerance level (Kumar et al 2011). The qualitative resistance is typically recommended in locations where the pathogen diversity is low. Marker assisted backcrossing can result in the pyramiding of *Ht* genes in maize. Planting hybrids with good turcicum leaf blight resistance is an economical, effective, and sustainable method of avoiding yield losses in maize. Great efforts have been made worldwide to develop, identify, and utilize germplasm with TLB resistance (Setyawan et al 2016, Garoma et al 2016, Keerthana et al 2023).

## CONCLUSION

The identification of resistant donors for TLB among cold-tolerant temperate germplasm represents a critical step towards enhancing maize productivity and resilience in regions affected by this devastating disease. By harnessing the genetic diversity of maize germplasm and leveraging advances in biotechnology and breeding techniques, researchers can develop improved maize varieties that offer durable resistance to TLB while meeting the diverse needs of farmers and consumers. In the present study early maturing, cold tolerant inbred lines suitable for temperate ecologies registered high level of resistance (HR) against turcicum leaf blight of maize. These inbred lines can be used profitably as resistant donors for the development of improved high yielding resistant maize varieties suitable for temperate ecologies.

## REFERENCES

Ahangar, M.A., Bhat, Z.A., Sheikh, F.A., Dar, Z.A., and Ajaz, A. (2016) Pathogenic variability in *Exherohilum turcicum* and identification of resistant sources to turcicum leaf blight of maize (*Zea mays* L.). *Journal of Applied and Natural Science* **8**(3):1523–1529. DOI 10.31018/jans.v8i3.994.

Ahangar, M.A., Wani, S.H., Dar, Z.A., Roohi, J., Mohiddin, F. (2022) Distribution, Etiology, Molecular Genetics and Management Perspectives of Northern Corn Leaf Blight of Maize (*Zea mays* L.). *Phyton-International Journal of Experimental Botany* **91**, (10):2111–2133.

Bankole, FA., Badu-Apraku B, Salami AO, Falade TDO, Bandyopadhyay R, Ortega-Beltran, A. (2023) Variation in the morphology and effector profiles of *Exserohilum turcicum* isolates associated with the Northern Corn Leaf Blight of maize in Nigeria. *BMC Plant Biology* 23, 286. https://doi.org/10.1186/s12870-023-04385-7.

Bhiusal, TN., Lal, GM., Marker, S. Synrem, GJ. (2017) Genetic variability and traits association in maize (*Zea mays* L.) genotypes. *Annals of Plant and Soil Research* **19**(1), 59 – 65.

\Chandrashekara, C., Jha, S.K., Arukumar, R., Agrawal, P.K. (2014) Identification of new sources of resistance to turcicum leaf blight and maydis leaf blight in maize (*Zea mays* L.). *SABRAO Journal of Breeding and Genetics* **46** (1): 44-55.

Chenula, V.V., Hora, T.S. (1962) Studies on losses due to *Helminthosporium* blight of maize. *Indian Phytopathology* **15**, 235-237.

Garomaa B, Bitew T, Midekssa D, Temesgen D and Girma D. (2016) Evaluation of quality protein maize inbred lines for resistance to Turcicum leaf blight and grey leaf spot disease under field condition at mid altitude sub-humid agro-ecology of Ethiopia. *Scientific Journal of Crop Science* **5**(11): 137-145.

Hooda, K.S., Khokhar, M.K., Meena, Shekhar., Chikkappa, G.K., Bhupinder Kumar, Mallikarjuna, N., Devlash, M.K., Chandrashekara, C. (2016) Turcicum leaf blight—sustainable management of a re-emerging maize disease. *Journal of Plant Diseases and Protection*. DOI 10.1007/s41348-016-0054-8

Keerthana, D., Haritha, T., Sudhir Kumar, I., Ramesh, D. (2023) Field Screening of Maize (*Zea mays* L.) Genotypes against Turcicum Leaf Blight (TLB) under Artificial Conditions. *International Journal of Plant & Soil Science* **35,** (7): 1-11.

Khatri, N.K. (1993) Influence of temperature and relative humidity on the development of *Helminthosporium turcicum* on maize in Westeren Georgia. *Indian Journal of Mycology and Plant Pathology* **23**, 35-37.

Kumar, S., Gowd, P.K.T., Pant, S.K., Shekhar, M., Kumar, B. (2011) Sources of resistance to *Exherohilum turcicum* (Pass.) and *Puccinia polysora* (Underw.) incitant of Turcicum leaf blight and polysora rust of maize. *Plant Protection* **44**, 528-536.

Luenzzo De, O.R., García Von, P.R., Balestre, M., Ferreira, D.V. (2010) Evaluation of maize hybrids and environmental stratification by the methods AMMI and GGE biplot. *Crop Breeding and Applied Biotechnology* **10**, 247-253.

Minliang Jin, Haijun Liu, Xiangguo Liu, Tingting Guo, Jia Guo, Yuejia Yin, Yan Ji, Zhenxian Li, Jinhong Zhang, Xiaqing Wang, Feng Qiao, Yingjie Xiao, Yanjun Zan, Jianbing Yan. (2022) Complex genetic architecture underlying the plasticity of maize agronomic traits. *Plant Communications.* doi: https://doi.org/10.1101/2022.01.18.476828.

Muiru, W.M., Charles, A.K., Kimenju, J.W., Njoroge, K., Miano, D.W. (2015) Evaluation of resistance reaction of maize germplasm to common foliar diseases in Kenya. *Journal of Natural Science Research* **5**(1), 140-145.

Navarro, B.L., Ramos Romero, L., Kistner, M.B., Iglesias, J., Tiedemann, A. (2021) Assessment of physiological races of *Exherohilum turcicum* isolates from maize in Argentina and Brazil. *Tropical Plant Pathology* **46**, 371–380. DOI 10.1007/s40858-020-00417-x.

Nigus Belay. (2022) Genotype-by-Environment Interaction of Maize Testcross Hybrids Evaluated for Grain Yield Using GGE Biplots. *International Journal of Food Science and Agriculture* **6**(2), 216-227. DOI: 10.26855/ijfsa.2022.06.01.

Paterniani, M.E., Sawazaki, E., Dudienas, C., Duarte, A.P., Gallo, P.B. (2000) Diallel crosses among maize lines with emphasis on resistance to foliar diseases. *Genetics and Molecular Biology* **23**, 381-385.

Patil, S.J., Wali, M.C., Harlapur, Prasanth, S.I. (2000) Maize research in North Karnataka, pp. 54. University of Agricultural Science, Dharwad

Payak, M.M., Renfro, B.L. (1968) Combating maize disease. *Indian Farmer Disease* **1**: 53–58.

Ribeiro, R.M., Amaral Júnior, A.T., Pena, G.F., Vivas, M. (2016) History of northern corn leaf blight disease in the seventh cycle of recurrent selection of an UENF-14 popcorn population. *Acta. Sci. Agronomica* **38**, 1-10

Selvaraj, C.I., Nagarajam, P. (2011) Interrelationship and path-coefficient studies for qualitative traits, grain yield and other attributes among maize (*Zea mays* L.). *International Journal of Plant Breeding and Genetics* **5**, 209-223.

Setyawan, B., Irfan, S., Aswaldi, A., Etti, S. (2016) Resistance of eleven new hybrid maize genotypes to Turcicum leaf blight (*Exherohilum turcicum*). *Biodiversitas* **17**(2), 604-608.

Shikari, A.B., Zafar, G. (2009) Evaluation and identification of maize for turcicum leaf blight resistance under cold temperate conditions. *Maize Genetics Cooperation Newsletter* **83**, 1-8.

Singh, R., Srivastava, R.P., Mani, V.P., Khandelwal, R.S., Ram, L. (2014) Screening of maize genotypes against northern corn leaf blight. *Supplement on Genetics and Plant Brdeeding* **9**(4), 1689–1693. DOI 10.30848/PJB2019-5(10).

Welz, H. G., Geiger, H.H. (2000) Genes for resistance to northern corn leaf blight in diverse maize populations. *Plant Breeding* **119**(1), 1–14. DOI 10.1046/j.1439-0523.2000. 00462.x

Yang, Q., Balint-Kurti, P., Xu, M. (2017) Quantitative disease resistance: dissection and adoption in maize. *Molecular Plant* **10**(3), 402–413. https://doi.org/10.1016/j.molp.2017.02.004

Zhu, M., Tong, L., Xu, M., Zhong, T. (2021) Genetic dissection of maize disease resistance and its applications in molecular breeding. *Molecular Breeding* **41**, 32. https://doi.org/10.1007/s11032-021-01219-y.