

Novel sources of resistance against foliar diseases identified among the newly derived tropical inbreds of field corn

Jayant S. Bhat¹ · Ganapati Mukri² · Shwetha B.³ · Priya S.³ · R. N. Gadag² · Venkatesh Kukarni⁴ · Raju Shyadambi³ · Rajeshwari Teli³ · Krishnanand Iliger⁴

Abstract: The investigation was carried out at ICAR-IARI, Regional Research Centre, Dharwad, with the objectives to screen newly developed inbred lines against turicum leaf blight (TLB), curvularia leaf spot (CLS) and maydis leaf blight (MLB) and common rust (CR) to identify new sources of resistance during *Kharif* 2020 and 2021. The grain yield, and flowering traits were recorded on 45 newly developed inbred lines. The results revealed that none of the inbred is immune to any of the four foliar diseases. However, highly resistant lines are identified against TLB (5 lines viz., PDM 4641, PDIM 638, PDIM 639, PDIM 697, PDIM 635), CLS (5 lines viz., PDIM 697, LM-14, C-79, CDM-1105, TC-6), MLB (6 lines viz., C-79, CDM-1105, PDM-10, C-83, PDM-134, C-2765) and CR (7 lines viz., C-79, CM 202, PDIM 635, PDIM 805, PDIM 697, PML-50, C-67). Among these, PDIM 635 and PDIM 697 displayed resistance against all the four diseases studied, while PDIM 638 and PDIM 639 exhibited resistance against TLB, CLS, and MLB, and C 79 and C 67 showed resistance against CLS, MLB, and CR. Further, there are a few more inbreds that displayed resistance against two of the four diseases studied. The distribution

of inbred lines with respect to disease scores showed similar trends for foliar diseases implying the possible linkage of resistance genes against different foliar diseases or multiple disease resistance. Further, the analyses of genetic parameters revealed high PCV, GCV, heritability, and GAM of the traits studied. Based on the results it was suggested to select inbreds for hybrid breeding in the short run and to improve foliar disease resistance through population improvement approaches such as recurrent selection methods.

Keywords: CLS · CR · Inbred · GAM · MLB · TLB

Introduction

Maize (*Zea mays* L.) is an important tropical cereal and staple food crop of the world that originated in Mexico (South America) around 5,000 BC. It is now one of the most widely grown crops around the world in both temperate and tropical regions. It is physiologically more efficient and has the highest genetic yield potential among food grain crops because of its C₄ pathway. It is the most versatile photo-insensitive crop with high adaptability cultivated throughout the year. Globally, maize stands fifth among the cereals in the area, fourth in production, and third in productivity. As per the latest reports by USDA maize has an area of 202 m ha with a production of 1162 m t and with a productivity of 5544 kg/ha (FAOSTAT, 2020). In India, it is the third most important food crop after rice and wheat with an area, production, and productivity of 9.86 m ha, 30.16 m t, and 3058 kg/ha, respectively (FAOSTAT, 2020).

Despite its high yield potential, adaptability and versatility, maize productivity is limited by biotic and

✉ Ganapati Mukri: ganapati4121@gmail.com

¹ICAR-Indian Agricultural Research Institute, Regional Research Centre Dharwad-580 005, Karnataka, India

²ICAR-Indian Agricultural Research Institute, New Delhi-110 012, India

³Department of Genetics and Plant Breeding, UAS, Dharwad-580 005, Karnataka, India

⁴Department of Plant Pathology, UAS, Dharwad-580 005, Karnataka, India

abiotic factors (Shah, 2016). Approximately, 65 pathogens infect maize, causing substantial yield loss. This necessitates the development of high-yielding and disease-resistant hybrids to meet the country's ever-growing food demands (Barakat *et al.*, 2009). Among the maize diseases, foliar diseases such as turicum leaf blight (TLB), curvularia leaf spot (CLS) maydis leaf blight (MLB), and common rust (CR), caused by *Exserohilum turicum*, *Curvularia spp.*, *Bipolaris maydis* and *Puccinia sorghi*, respectively, are important in India. Although these diseases have widespread distribution in cold humid regions with heavy dew conditions and appears in a sizeable form in Karnataka, Maharashtra, Andhra Pradesh, and Himalayan regions with the reduction of grain yield by 28 to 91% (Harlapur *et al.*, 2000). In addition, the incidence of foliar diseases reduces the fodder quality of maize stalks and leaves. The management practices like crop rotation, seed treatment, and the application of fungicides have been recommended (Reddy *et al.*, 2013) to reduce the losses due to foliar diseases. However, host plant resistance (HPR) has been considered the most appropriate and economical strategy due to several advantages, it is environmentally friendly and convenient to adapt at the farmers' level. Hence, resistance breeding in maize has been emerging as an important area of research in recent years due to the recent surge in losses due to disease incidence. Identifying resistant genes and genotypes to foliar diseases and combining them with yield traits has now become an essential objective of maize breeding programs. It is important, therefore, to identify more diverse sources of resistance to foliar diseases, as the increase in the disease severity has the potential of threatening maize grain productivity with a negative influence on food production (Sibiya *et al.*, 2013; Hooda *et al.*, 2017). While breeding for disease resistance, prior knowledge of the genetics of resistance in the population and lines that would be utilized for developing high-yielding resistant varieties is essential.

Keeping these points in mind, the present study was conducted with the 42 new inbred lines developed from diverse sources were screened along with resistant (LM 13 and LM 14) and susceptible check (CM 202) against foliar diseases during two consecutive *Kharif* seasons during 2020 and 2021 with the objective identifying novel sources of resistance and to understand the variability and other genetic parameters in the inbred pool selected.

Materials and methods

The base material for the study consisted of 45 new inbred lines derived from diverse sources. These 45 inbreds were selected based on the disease scores (<6.0) under natural epiphytotics. The list of inbred lines and their pedigree is presented in Table 1.

Table 1. List of inbreads used for the present study during *kharif* 2020 and 2021

S.No.	Inbred line	Pedigree
1	C-79	VL144287 (VL1110435/CML4
2	CM 202	CI21
3	PDIM	(CA34505/CA0
4	PDIM 805	IC 470150
5	PDIM 697	VL175899 (((CML161xCML45
6	PML-50	P-3501-5-2-K-2-K-2-50
7	C-67	ZL155281 ((Pop61C C1QPMTE
8	C-74	VL183808 (CML451 (ZPop1W
9	PDM-134	(MDRxPC-3xComp 85164
10	JK-1553	IMLSB-2012
11	C-2765	((CTSO II 072/P3 1 C4S58-
12	C-62	VL18352 (CLQRCYQ44-
13	C-8	VL18300 (CLQRCYQ44-
14	DT-2	(DT/LN/EM-46-3-1xCML311-2-
15	BGD-48Y	BGD comp--48(Y)
16	C-14	VL18242 ((CL02450/OFP67//C
17	JK1800	EC 697148
18	C-2760	Pop61 C1 QPMTEYF-40-
19	C-78	Vl18260 Composite 14-BBB-1-
20	DDM-2313	MWN-2956
21	PDM-10	(O pool x Comp85134 x
22	PML-18 B	RMH-3591-4-1-1-K-1-K-1-18
23	TC-12	Tmap-3-F3-1 Op #-3-1-2-1
24	TC-6	GB-OP sel-2-1-2-1
25	C-12	VL181017 (CLQRCYQ44-
26	PDM-59	PS-11-2-8-1-1-1-2-1-1-1
27	PML-102_1	KDMH-755-2-1-1-1-1-1
28	PML-25	KMH-218PLUS-1-1-3-R-1
29	DT-5_1	DTPYC9-F103-5-4-1-2-1-2-1-
30	PDIM 639	(PMH-1 x PMH-3)-4-2-1-2-3-1-1-
31	CDM-1105	(DMSyn-C I) 18-1-8
32	DIM-204 B	Advanta 7074-1-2-1-1-1
33	DIM-316	PHB-14-1-1-3-2-K-2
34	PDM 4641	(Agti 76 X Comp 8527
35	PDM-114-2	(Comp8527xComp
36	C-23	VL19190 ((CML466/CML1
37	C-83	VL18214 ((CL02450Q/OFP

Table 1 contd...

S.No.	Inbreed line	Pedigree
38	CML-582	CAL1819-2-1-3-2-3-1
39	D-2282_1	PMH-1-1 Bulk-Bulk-1-2-1-1
40	JK-370	EC699496ÄÄÄÄ
41	BLSB-2 B	MDR pool bpm-2
42	C-25	VL18149 AMDROUT(5x6)
43	PDIM 638	PMH-1 x LM-13-3-2-2-3-2-2-
44	LM-14	CA 00310-xb-xb-xb-1-1-1-1-
45	PML-85	IML307-3-1-1---85

The inbred lines were screened against foliar diseases across two consecutive seasons, viz., *Kharif* 2020 and 2021, and they were also evaluated for yield and flowering traits during *Kharif* 2021. The separate sets of experiments were carried out to screen for different foliar diseases through artificial epiphytotics. The evaluation and screening of inbreds were carried out in randomized complete block designs with two replications with susceptible check CM 202. Each genotype was planted in two rows of 3 m length with a spacing of 60 × 20 cm with two seeds per hill. Finally, one plant per hill was retained and recommended package of practices was followed to raise a healthy crop. The spreader rows (susceptible genotypes) were planted at regular intervals to help create high disease pressure in the experimental plots.

Creation of artificial epiphytotics

After isolating the maize foliar disease pathogen and

obtaining the pure culture, the mass multiplication of *E. turcicum*, *B. maydis* and *C. spp.* was done on sterilized sorghum grains. For each pathogen, one hundred grams of sorghum grains were soaked in tap water for 24 hours in a 500 ml conical flask. The excess water was drained off and the material was sterilized twice in the autoclave at 24-hour intervals. To prevent the clumping of the material the flasks were shaken thoroughly. The flasks were inoculated with respective pathogen culture aseptic conditions and incubated at 25±10°C for 20 days. To avoid clumping, the flasks were shaken every alternate day. Within three weeks the mycelial growth and conidia of the fungus were observed on the sorghum grains. A fully colonized sorghum grains culture was used for creating artificial epiphytotic conditions in the field following the whorl method of inoculation. The inoculation of mass multiplied culture was done at 35 and 45 days after sowing and light irrigation was given to create humid conditions to facilitate the growth of the pathogen. Observations were recorded on five randomly selected plants in each replication for disease score, percentage disease index, and characters such as days to 50% tasseling, days to 50% silking, and grain yield (t/ha). The screening was based on the 1-9 scoring method given by IIMR, Ludhiana. Common rust was scored under natural epiphytotic conditions. The data on both disease scores and yield component traits were subjected to statistical analyses using AGRISTAT (V.6.2003) software.

Table 2. Disease scoring scale for turicum leaf blight disease

Rating scale	Degree of infection	Disease reaction
1	Nil to very slight infection (<10%)	Resistant (Score: < 3.0)
2	Slight infection, a few lesions scattered on two lower leaves (10.1–20%)	
3	Light infection, a moderate number of lesions scattered on four lower leaves (20.1–30%)	
4	Light infection, a moderate number of lesions scattered on lower leaves, a few lesions scattered on middle leaves below the cob (30.1–40%)	Moderately resistant (Score: 3.1–5.0)
5	Moderate infection, an abundant number of lesions scattered on lower leaves, a moderate number of lesions scattered on middle leaves below the cob (40.1–50%)	
6	Heavy infection, an abundant number of lesions scattered on lower leaves, moderate infection on middle leaves, and a few lesions on two to four leaves above the cob (50.1–60%)	Moderately susceptible (Score: 5.1–7.0)
7	Heavy infection, an abundant number of lesions scattered on lower leaves, and a moderate number of lesions on two to four leaves above the cob (60.1–70%)	
8	Very heavy infection, lesions abundant scattered on lower and middle leaves and spreading up to the flag leaf (70.1–80%)	Susceptible (Score: > 7.0)
9	Very heavy infection, lesions abundant scattered on almost all the leaves, plant prematurely dried and killed (> 80%)	

Results

Screening of maize inbreds against foliar diseases

The screening of inbred lines for foliar diseases was carried out under artificial epiphytotic conditions. The inoculation of pathogen and planting of spreader rows ensured sufficient inoculum load in test plots as revealed by the highly susceptible reactions of susceptible check CM 202 and spreader rows. The ANOVA for the response of inbred lines against foliar diseases revealed that the mean sum of squares due to genotypes was highly significant during both *Kharif* 2020 and 2021 for all the foliar diseases studied (Table 3). Besides, during *Kharif* 2021, grain yield, days to 50% tasselling, and days to 50% silking were also recorded. The ANOVA for these traits in *Kharif* 2021 also showed a significant mean sum of squares due to genotypes in the newly developed inbred lines.

Response of inbred lines against foliar diseases

The inbred lines exhibited differential responses against foliar diseases, where disease scores varied from 1–9. Most of the genotypes showed disease scores of less than 6 and only a few recorded susceptible reactions. The pooled disease scores along with grain yield and flowering traits of the different inbred lines are given in Table 5.

Among the 42 inbreds screened against different foliar diseases, five inbreds each were highly resistant against TLB and CLS, six against MLB, and seven against common rust. However, more resistant inbreds were observed against MLB. In all four foliar diseases, the moderate resistant category contained more inbreds

compared to the resistant category and susceptible category.

Grain yield and maturity behavior of inbreds studied

The inbreds showed a wide range of values for grain yield, days to 50% tasselling, and days to 50% silking. The grain yield ranged from 1.3 (DIM 316) to 5.5 t/ha (PML 102) and 25 inbreds recorded more than 3.0 t/ha (Table 5). For flowering traits, the DFT varied from 50.5 (DT 5–1) to 70.5 (PDIM 635). However, more than 50% of inbreds studied showed days to 50 tasseling in the range 59–65 days, among them 10 inbreds flowered in more than 65 days and four inbreds flowered in less than 54 days.

Genetic variability and genetic parameters under foliar diseases of maize

The analyses were carried out to generate information on genetic variability, heritability, and genetic advance in the traits studied in each season (*Kharif* 2020 and 2021) and are presented in Tables 6 and 7. The results revealed that the pool of inbred lines used for the study recorded high PCV, GCV, heritability(bs), and genetic advance as percent of the mean (GAM) for all the foliar diseases in *Kharif* 2020 and for grain yield, flowering traits and foliar diseases in *Kharif* 2021.

Discussion

The diseases of maize, especially foliar diseases, cause severe losses in India and around the world. The diseases of economic scale vary across growing ecologies and

Table 3. ANOVA for the scores of foliar diseases in maize inbred lines during *Kharif* 2020

Source of variation	df	TLB score (1–9)	CLS score (1–9)	MLB score (1–9)	Rust score (1–9)
Replication	1	0.01	0.01	0.02	0.28
Treatments	24	6.43**	6.14**	4.90**	8.62**
Error	24	0.12	0.28	0.34	1.21

df : Degrees of freedom; DFS : Days to 50% silking; DFT : Days to 50% tasseling

Table 4. ANOVA for the scores of foliar diseases along with grain yield and maturity traits in maize inbred lines during *Kharif* 2021

Source of variation	df	TLB score (1–9)	CLS score (1–9)	MLB score (1–9)	Rust score (1–9)	Grain yield	DFT	DFS
Replication	1	5.88**	1.68	0.18	0.10	0.47**	80.71**	62.40**
Treatments	24	7.35**	4.93 **	4.67**	8.49**	1.99**	44.16**	45.01**
Error	24	0.99	0.88	0.31	1.21	0.07	9.28	9.88

** : significant at 1% probability * : significant at 1% probability df: Degrees of freedom DFT and DFS: Days to 50% tasseling and silking

Table 5. Response maize inbred lines against foliar disease during *Kharif* 2020 and *Kharif* 2021

Inbred line	Grain yield	DFT	DFS	Mean Disease scores [K2020 and 2021 (1–9)]			
				TLB	CLS	MLB	CR
BGD 48Y	4.2	54.5	56.5	7.3	6.0	2.0	3.5
BLSB 2 B	2.4	57.0	59.0	6.8	3.3	5.0	6.5
C 12	2.0	59.0	61.5	7.0	4.0	1.5	4.5
C 14	2.0	64.5	66.5	7.3	2.3	4.0	3.5
C 23	1.9	67.5	70.5	6.8	3.8	1.3	6.0
C 25	3.1	58.0	60.0	6.0	3.8	1.3	6.5
C 2760	3.6	66.5	68.5	5.8	3.8	1.3	4.0
C 2765	2.9	64.0	66.0	5.0	4.5	1.0	3.0
C 62	2.1	61.0	63.0	6.8	4.5	6.0	3.0
C 67	3.6	61.0	63.0	5.3	3.0	1.8	2.0
C 74	2.6	64.5	66.5	7.3	4.3	1.5	2.0
C 78	3.5	61.0	61.0	5.5	2.0	1.8	4.0
C 79	5.0	61.0	63.0	3.8	1.8	1.0	0.0
C 8	3.4	64.0	65.5	4.8	4.8	4.0	3.0
C 83	2.5	57.5	59.5	4.8	3.5	1.0	6.0
CDM 1105	3.6	57.5	59.5	3.8	1.8	1.0	5.5
CM 202	3.1	55.5	58.0	7.5	7	8.5	0
CML 582	4.2	69.0	71.0	3.8	3.3	3.8	6.0
D 2282_1	3.1	60.0	62.0	5.3	4.0	4.0	6.0
DDM 2313	4.3	66.0	67.0	5.5	3.8	2.0	4.0
DIM 204 B	1.6	63.5	65.5	7.0	4.5	1.8	5.5
DIM 316	1.3	66.0	68.0	6.3	4.8	1.3	5.5
DT 2	1.8	54.0	56.0	6.5	4.0	2.0	3.0
DT 5 _1	4.3	50.5	51.0	7.0	4.3	1.3	5.0
JK 1553	3.3	51.5	53.5	6.3	3.3	1.8	2.5
JK 1800	3.4	57.5	59.5	6.5	3.0	1.5	3.5
JK 370	3.1	58.5	61.0	6.8	3.3	1.3	6.0
LM 14	3.2	62.0	64.0	4.3	1.5	2.0	7.0
PDIM 635	4.7	70.5	72.0	2.0	2.3	1.5	0.0
PDIM 638	2.7	67.5	69.0	2.0	2.0	2.8	6.5
PDIM 639	4.3	68.5	70.5	2.0	3.3	2.3	5.0
PDIM 697	2.9	66.0	67.5	2.0	1.3	1.3	1.0
PDIM 805	3.0	57.5	59.0	4.0	6.8	4.5	0.0
PDM 4641	3.7	59.5	61.5	1.8	6.5	3.3	5.5
PDM 10	2.9	57.0	59.0	6.8	2.5	1.0	4.0
PDM 114 2	2.6	59.0	59.0	8.3	4.3	3.3	5.5
PDM 134	3.3	62.5	65.0	5.0	3.8	1.0	2.0
PDM 59	2.6	59.5	62.0	7.3	3.3	1.5	4.5
PML 102 _1	5.5	65.0	67.0	5.8	6.0	1.5	4.5
PML 18 B	2.4	59.0	61.0	6.3	3.5	1.3	4.0
PML 25	5.2	63.0	66.0	6	4	1.5	4.5
PML 50	2.1	59.5	61.5	7.5	4.0	1.5	1.0
PML 85	1.4	63.0	65.0	7.0	2.3	1.5	9.0
TC 12	2.4	53.5	56.5	6.5	2.5	2.0	4.0
TC 6	4.0	62.0	64.5	8.5	1.8	1.8	4.0
Mean	3.0	63.3	65.2	5.7	3.6	2.4	4.1
SEm±	0.2	0.9	0.9	0.3	0.2	0.2	0.3
CD	0.4	2.5	2.5	0.7	0.5	0.6	0.8
CV	8.5	13.9	13.8	3.8	3.0	3.4	4.6

Table 6. Genetic parameters for foliar diseases in *Kharif* 2020

Genetic parameter	TLB	CLS	MLB	Rust
Phenotypic variance	3.28	3.21	2.62	4.91
Genotypic variance	3.15	2.93	2.28	3.70
Environmental variance	0.12	0.28	0.34	1.21
PCV (%)	33.87	43.00	73.55	54.66
GCV (%)	33.22	41.06	68.59	47.46
h ² (%)	96.19	91.16	86.98	75.39
GAM (%)	67.11	80.75	131.78	84.88

breeding climate smart maize is a major challenge that also requires breeding and deployment of genetic resistance against diseases (Reynolds and Ortiz, 2010). The development and identification of new sources of resistance against important diseases are very crucial and require continuous breeding efforts. The challenge is exacerbated by the changing climates that will affect the diversity and responsiveness of maize diseases as well (Singh *et al.*, 2021). Thus, breeding biotic stress resistance in maize during the era of climate change is the need of the hour. In this direction, ICAR-IARI Regional Research Centre Dharwad has developed new inbred lines from diverse sources. The fixed inbred lines were initially screened against foliar diseases under natural epiphytotics. Dharwad being a hot spot for the diseases like TLB and other foliar diseases, the screening of germplasm against foliar diseases could be accomplished and the genetic resistance sources can be identified under both natural and artificial epiphytotics. In the present study, 45 newly developed inbred lines, which were selected from screening under natural epiphytotics, were subject to artificial epiphytotics. The responses of these inbreds and the salient findings of the study have been discussed below.

Performance and distribution of maize inbreds against foliar diseases and for grain yield

The highly significant mean sum of squares due to

genotypes for grain yield, flowering, and foliar diseases suggested the existence of substantial variability among the inbred lines (Table 3). The results indicated the possibility of the selection of desirable genotypes from this pool of inbreds and also the possibility of further improvement by devising appropriate breeding strategies.

The distribution of genotypes with respect to disease scores showed that the majority of the inbreds exhibited resistant to moderately resistant responses against these foliar diseases (Table 8 and Figure 1). This was expected as the inbred lines selected for the screening were initially screened under natural epiphytotics in Dharwad and those with scores of < 6.0 were subject to artificial screening. The disease scores of > 6.0 under artificial epiphytotics from among the inbreds with < 6.0 score implied that the disease pressure and inoculum load were sufficient enough to rule out the disease escape by the inbreds. The extent of disease pressure in the screening plots can also be seen in Figure 2 for TLB, CLS, and MLB. The trend of disease distribution indicated the possible linkage among the two or more resistance genes against different diseases (Figure 1).

In addition, the evaluation of inbred lines for yield and maturity traits, identified 25 productive inbred lines (> 3.0

Table 8. Distribution of inbred lines w.r.t. diseases scores against different foliar diseases

Disease Score	Number of inbreds (Based on average disease scores of K 2020 and 21)			
	TLB	CLS	MLB	Rust
1	0	1	14	2
2	5	9	20	3
3	0	10	3	5
4	5	15	4	10
5	6	5	2	6
6	9	2	1	10
7	16	3	0	4
8	3	0	0	0
9	1	0	1	1

Table 7. Genetic parameters grain yield and foliar diseases during *Kharif* 2021

Genetic parameter	Grain yield	DFT	DFS	TLB	CLS	MLB	Rust
Phenotypic variance	1.0	31.7	32.4	4.2	1.9	2.5	4.9
Genotypic variance	1.0	12.4	12.6	3.2	1.0	2.2	3.6
Environmental variance	0.1	19.3	19.9	1.0	0.9	0.3	1.2
PCV (%)	32.6	9.2	9.1	34.2	44.9	71.1	54.6
GCV (%)	31.5	5.8	5.6	29.9	32.9	66.4	47.3
h ² (%)	93.3	39.2	38.7	76.2	53.7	87.4	75.0
GAM (%)	62.6	7.5	7.2	53.7	49.6	127.9	84.3

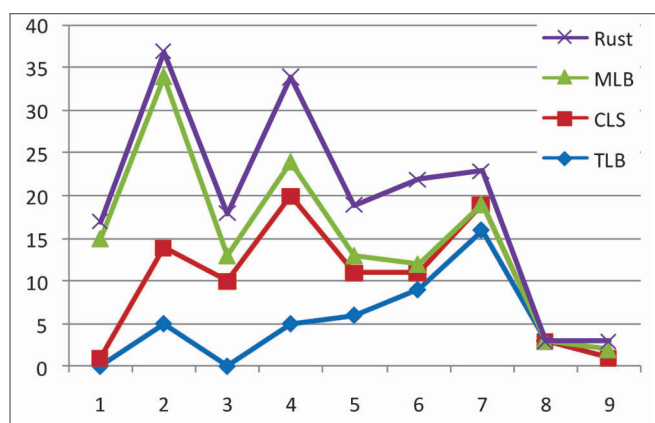


Figure 1. Distribution of inbred lines with respect to disease scores against foliar diseases

t/ha) that fall into different maturity categories. One of the inbred which was most notable is a late inbred line PDIM 635 with a productivity of 4.7 t/ha and resistance against all four diseases studied. The inbred lines C 79 and C 67 had a yield level of 5.0 t/ha and 3.6 t/ha, respectively with resistance against CLS, MLB, and CR. Few more inbreds displayed higher productivity and resistance against more than one foliar disease. For

instance, such results have been earlier reported from the studies on different foliar diseases by Craven and Fourie (2011), Ram Dutta *et al.* (2012), Wisser *et al.* (2006), Bindhu *et al.* (2017) and Kuselan *et al.* (2017).

The study identified novel sources of resistance and sources of multiple resistance

The results of the screening against foliar diseases identified novel sources of resistance. The summary of the results is given in Table 9. It identified 5 resistant inbred lines against TLB (PDM 4641, PDIM 638, PDIM 639, PDIM 697, PDIM 635), 14 against CLS (PDIM 697, LM-14, C-79, CDM-1105, TC-6, PDIM 638, C-78, PDIM 635, PML-85, C-14, TC-12, PDM-10, C-67, JK-1800), 35 against MLB and 7 against CR (C-79, CM 202, PDIM 635, PDIM 805, PDIM 697, PML-50, C-67). Among these, PDIM 635 and PDIM 697 displayed resistance against all the four diseases studied, while PDIM 638 and PDIM 639 exhibited resistance against TLB, CLS, and MLB and C 79 and C 67 showed resistance against CLS, MLB, and CR. Further, there are a few more inbreds that displayed

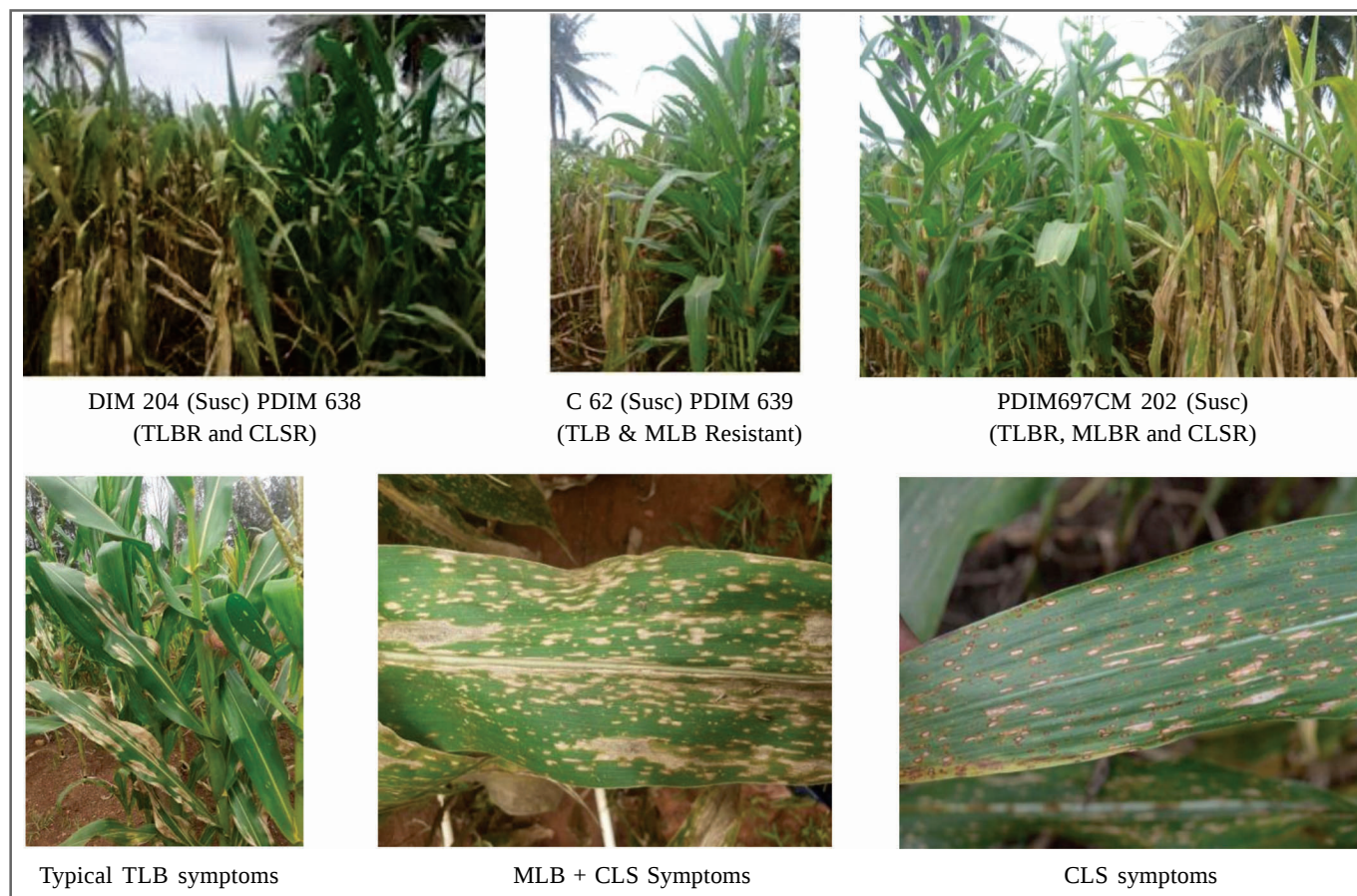


Figure 2. The images of susceptible and resistant inbreds against TLB, CLS, and MLB and their typical symptoms

Table 9. Summary of screening of maize inbred against foliar diseases

Foliar disease / Reaction	Inbred lines
<i>Turicum leaf blight (TLB)</i>	
Resistant	PDM 4641, PDIM 638, PDIM 639, PDIM 697, PDIM 635
Moderate Resistant	C-79, CDM-1105, CML-582, PDIM 805, LM-14, C-8, C-83
<i>Curvularia leaf spot (CLS)</i>	
Resistant	PDIM 697, LM-14, C-79, CDM-1105, TC-6, PDIM 638, C-78, PDIM 635, PML-85, C-14, TC-12, PDM-10, C-67, JK-1800
Moderate Resistant	PDIM 639, CML-582, JK-1553, BLSB-2 B, JK-370, PDM-59, C-83, PML-18 B, PDM-134, DDM-2313, C-2760, C-25, C-23, D-2282_1, PML-25, DT-2, C-12, PML-50, DT-5_1, C-74, PDM-114-2, C-2765, C-62, DIM-204 B, C-8, DIM-316
<i>Maydis leaf blight (MLB)</i>	
Resistant	C-79, CDM-1105, PDM-10, C-83, PDM-134, C-2765, PDIM 697, JK-370, PML-18 B, C-2760, C-25, C-23, DT-5_1, DIM-316, PDIM 635, PML-85, JK-1800, PDM-59, PML-25, C-12, PML-50, C-74, PML-102_1, TC-6, C-78, C-67, JK-1553, DIM-204 B, LM-14, TC-12, DDM-2313, DT-2, BGD-48Y, PDIM 639, PDIM 638
Moderate Resistant	PDM-114-2, PDM 4641, CML-582, C-14, D-2282_1, C-8, PDIM 805
<i>Common Rust (CR)</i>	
Resistant	C-79, CM 202, PDIM 635, PDIM 805, PDIM 697, PML-50, C-67
Moderate Resistant	C-74, PDM-134, JK-1553, C-2765, C-62, C-8, DT-2, BGD-48Y, C-14, JK-1800, C-2760, C-78, DDM-2313, PDM-10, PML-18 B, TC-12, TC-6, C-12, PDM-59, PML-102_1, PML-25
<i>TLB, CLS, MLB, and CR</i>	The remaining inbreds for each foliar disease were either moderately susceptible or susceptible

resistance against two of the four diseases studied. This multiple disease resistance and its possible genetic linkage were also noted in Figure 1. Such multiple resistances have previously been reported in crop plants including maize. Multiple disease resistance (MDR) loci, are defined as “loci that confer resistance to two or more diseases” (Wiesner-Hanks and Nelson 2016). This multiple disease resistance might be due to the presence of resistance genes against different diseases on the same chromosome or different chromosomes in the genotypes. Previously, colocalization of QTLs for resistance to southern leaf blight, northern leaf blight, and gray leaf spot diseases has been reported in maize (Balint-Kurti *et al.*, 2010; Wissner *et al.*, 2011; Li *et al.*, 2018). It was also reported that a maize caffeoyl-CoA O-methyltransferase encoded by *ZmCCoAOMT2* gene confers quantitative resistance to multiple pathogens (Yang *et al.*, 2017).

Further genetic enhancement in foliar disease resistance is possible

The knowledge of heritability and genetic advance of the trait of interest is required to guide the breeder to employ a suitable breeding strategy. Genetic variability together with heritability estimates would give a better idea of the genetic gain expected out of selection (Burton, 1952) and

the magnitude of heritable variability is the most important aspect (Panse, 1961). Heritability estimates along with genetic advance are normally more helpful in predicting gain under selection than heritability estimates alone as it is not sufficiently informative about the existence of gene action (additive/non-additive) and the involvement of other factors in the expression of traits (Johnson *et al.*, 1955). In the present study, the GCV, PCV, heritability (bs), and GAM were high for all the traits studied indicating the amenability of this pool of inbreds for the selection of desirable genotypes and improvement in these traits through population improvement approaches. As the distribution of inbreds and the earlier reports suggest the possible role of quantitative trait loci in controlling the traits, recurrent selection procedures might be appropriate in breeding for foliar disease resistance and higher yield and that also may result in genetic enhancement of multiple disease resistance.

The results of the present study indicated the possibility of further genetic enhancement in resistance against foliar diseases, grain yield, and flowering traits.

Conclusion

The study could identify resistance sources (inbreds) against all four foliar diseases. Few inbreds displayed

multiple disease resistance (MDR) coupled with higher grain yield. The genetic variability noted in the pool of inbreds suggested to go for selection of best resistant inbreds to develop hybrids through heterosis breeding in the immediate future and to breed for lines with higher resistance and grain yield through recurrent selection approaches as the PCV, GCV heritability and GAM in this pool of inbreds is high.

Author's contribution

JSB: Conceptualization of the study and manuscript preparation; GM: Analysis of data and manuscript editing; SB, PS, VK, RS, RT: Disease screening and data recording of foliar diseases; KI: Disease scoring and photography; RNG: Critical inputs and manuscript editing.

Conflicts of interest

Authors declare that there are no conflicts of interest that exist.

Acknowledgment

Authors are grateful to the Director, IARI, and Dharwad for facilitating the conduct of the experiment.

References

- Balint-Kurti, P. J., Yang, J., Van Esbroeck, G., Jung, J. & Smith, M. E. (2010). Use of maize advanced intercross line for mapping of QTL for Northern leaf blight resistance and multiple disease resistance. *Crop Science*, **50**: 458–466. <https://doi.org/10.2135/cropsci2009.02.0066>.
- Barakat, M. N., Shafei, A. A. E. & Al-Doss, A. A. (2009). Identification of molecular markers linked to northern corn leaf blight resistance in yellow population of maize. *Genes, Genomes and Genomics*, **16**: 24–29.
- Bindhu, K. G., Pandurangegowda, K. T., Lohithaswa, H. C., Madhuri, R. & Mallikarjuna, N. (2017). Genetics of resistance to turicum leaf blight caused by *Exserohilum turcicum* (Pass.) Leonard and Suggs in maize (*Zea mays* L.). *International Journal of Current Microbiology and Applied Sciences*, **6**(11): 964–969.
- Burton, G. W. (1952). Quantitative inheritance in grasses. In: *Proceedings of 6th International Grassland Congress*, **1**: 273–283.
- Craven, M. & Fourie, A. P. (2011). Field evaluation of maize inbred lines for resistance to *Exserohilum turcicum*. *South African Journal of Plant and Soil*, **28**(1): 69–74. doi: 10.1080/02571862.2011.10640015.
- Dutta, R., Anita, N., Chandra, S. & Ngachan, S. V. (2012). Sources of resistance to turicum leaf blight (*Exserohilum turcicum*) of maize for NEH region. *Indian Phytopathology*, **65**(2): 200–202.
- FAOSTAT (2020). <https://www.fao.org/faostat/en/#data/QCL/visualize>.
- Harlapur, S. I., Wali, M. C., Anahosur, K. H. & Muralikrishna, S. (2000). A report on survey and surveillance of maize diseases in northern Karnataka. *Karnataka Journal of Agriculture Sciences*, **13**: 750–751.
- Hooda, K. S., Khokhar, M. K., Shekhar, M., Karjagi, C. G., Kumar, B., Mallikarjuna, N., Devlash, R. K., Chandrashekara, C. & Yadav, O. P. (2017). Turicum leaf blight—sustainable management of a re-emerging maize disease. *Journal of Plant Diseases and Protection*, **124**: 101–113.
- Johnson, H. W., Robinson, H. F. & Comstock, R. E. (1955). Estimates of genetic and environmental variability in soybeans. *Agronomy Journal*, **47**(7): 314–318.
- Kuselan, K., Manivannan, N., Ravikesavan, R. & Paranidharan, V. (2017). Combining ability analysis for yield and its component characters in maize (*Zea mays* L.). *Electronic Journal of Plant Breeding*, **8**(2): 591–600.
- Li, Y. X., Chen, L., Li, C., Li, P., Bradbury, P. J. & Shi, Y. S. (2018). Increased experimental conditions and marker densities identified more genetic loci associated with southern and northern leaf blight resistance in maize. *Scientific Report*, **8**: 1–12. <https://doi.org/10.1038/s41598-018-25304-z>
- Panse, V. G. & Sukhatme, P. V. (1961). *Statistical Methods for Agric. Workers*. 2nd Edition. ICAR, New Delhi, pp 361.
- Reddy, R. V., Sheshagiri, R. A. & Sudarshan, M. R. (2013). Heritability and character association among grain yield and its components in maize (*Zea mays* L.). *Journal of Research ANGRAU*, **40**(2): 45–49.
- Reynolds, M. P. & Ortiz, R. (2010). Adapting crops to climate change: a summary. In: *Climate change and crop production*. (M. P. Reynolds, Ed.), pp. 1–8. CABI, UK.
- Shah, T. R., Prasad, K. & Kumar, P. (2016). Maize—A potential source of human nutrition and health: A review. *Cogent Food & Agriculture, part of the Taylor & Francis Group*, **2**(1): 1166995.
- Sibiya, J., Tongoon, P. & Derera, J. (2013). Combining ability and GGE biplot analyses for resistance to northern leaf blight in tropical and subtropical elite maize inbred lines. *Euphytica*, **191**(2): 245–257.
- Singh, V., Lakshman, D. K., Roberts, D. P., Ismaiel, A., Abhishek, A., Kumar, S. & Hooda, K. S. (2021). Fungal species causing maize leaf blight in different agro-ecologies in India. *Pathogens*, **10**: 1621. <https://doi.org/10.3390/pathogens10121621>.
- Wiesner-Hanks, T. & Nelson, R. (2016). Multiple Disease Resistance in Plants. *Annual Review of Phytopathology*, **54**: 229–252. <https://doi.org/10.1146/annurev-phyto-080615-100037>.
- Wisser, R. J., Balint-Kurti, P. J. & Nelson, R. J. (2006). The genetic architecture of disease resistance in maize: A synthesis of published studies. *Phytopathology*, **96**: 120–129.
- Wisser, R. J., Kolkman J. M., Patzoldt M. E., Holland J. B. & Yu, J. (2011). Multivariate analysis of maize disease resistances suggests a pleiotropic genetic basis and implicates a GST gene. *Proceedings of National Academy of Sciences, USA*, **108**: 7339–7344. <https://doi.org/10.1073/pnas.1011739108>.
- Yang, Q., He, Y. & Kabahuma, M. (2017). A gene encoding maize caffeoyl-CoA O-methyltransferase confers quantitative resistance to multiple pathogens. *Nature Genetics*, **49**: 1364–1372. <https://doi.org/10.1038/ng.3919>.