

Evaluation of Quality Protein Maize Inbred Lines for Turcicum Leaf Blight and Gray Leaf Spot at Bako, Ethiopia

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Abstract. Currently, Ethiopia has the second-highest national average yield reported in Sub-Saharan Africa (SSA), only below South Africa. But maize production in Ethiopia is constantly threatened by the potential outbreak of major foliar diseases such as turcicum leaf blight (TLB) and gray leaf spot (GLS). These diseases are characterized by relatively rapid leaf necrosis and premature death of foliage which eventually reduces grain yield. The diseases become a major problem in all major maize growing areas. Development of host resistance to these diseases can provide an important component of integrated disease management; which is the most effective and practical method of managing maize diseases. The study was conducted to evaluate the reaction of quality Protein maize inbred lines to TLB and GLS in the main cropping season during 2018. The inbred lines were obtained from Bako National Maize Research Center, breeding program, and it was arranged using alpha-lattice design with two replications and the inbred lines were inoculated with TLB and GLS disease inoculum under field condition and the experiments were set in separate field trial in respective disease. Disease severity (1-5 scale) was used to assess at ten days intervals from disease onset until the maize attained senescence. All the inbred lines showed symptoms of both diseases during the season, but the intensity of the diseases differed significantly ($P < 0.05$) among the inbred lines. Accordingly, out of 42 genotypes screened for both TLB and GLS, lines MBRC5BcF108-2-3-1-B-5-2-B-B-#, Obatanpa-5-4-1-1-1-#-#-#, ([[[CML159/[CML159/[MSRXPOOL9]C1F2-205-1,(OSU23i)-5-3-X-X-1-BB]F2-3sx]-8-1-B-B/CML509]F2 1/[GQL5/[GQL5/[MSRXPOOL9]C1F2-205-1(OSU23i)-5-3-X-X-1-BB]F2-4sx]-1-1-3-1-1B*4]-12/CML373IR)-B-8-B-7-2-1-B-#-#-#, (CML176xKULENI(F2)-4-3-1-1-1-#-#,(CUBA/GUADC1F27-4-3-3-B-1-BX[KIiIMAIaTA94A]-30MSV-03-2-10-B-2-B-B)-306-1-B-2-B-B-#), based on a 1–5 rating scale system for disease severity, they were selected as resistant.

Keywords. Diseases, Genotypes, Grey leaf spot, Inbredlines, Resistant, Turcicum leaf blight.

1. Introduction

Maize (*Zea mays* L.) is a major cereal crop in many regions of the world, including Ethiopia [1]. After rice and wheat, maize is the most important cereal crop worldwide and is produced extensively throughout Ethiopia's lowland to highland agro-ecologies [2]. Currently, Ethiopia has the second-highest national average yield reported in Sub-Saharan Africa (SSA), only below South Africa [1]. Its overall yearly production and productivity in the 2020 cropping season was 10.02 million tons and 4.24 t ha⁻¹, respectively [3]. Ethiopia's average yield of 4.179 t/ha is still less than the global average

of 5.78 t/ha, despite the fact that maize is an essential commodity for food security [4]. The poor utilization of cultivars resistant or tolerant to biotic and abiotic stresses is mostly responsible for this yield discrepancy [1]. According to Tewabech *et al.* [5] foliar diseases pose the greatest threat to yields of maize in Ethiopia's warm and humid growing zones. Of the several foliar diseases that affect maize, the two most economically significant ones are turicum leaf blight (TLB) and gray leaf spot (GLS), which are caused by *Excerohillum turcicum* and *Cercosporra zae maydis*, respectively [6]. The most economically significant diseases that cause significant yield loss in Ethiopia's mid-altitude sub-humid agro-ecology during the maize cropping season are turicum leaf blight and grey leaf spot, owing to the favorable environmental factors such as relatively higher humidity, moderate to high temperature, and/or warm areas. According to [7], turicum leaf blight can induce leaf necrosis and premature foliage death if it infects a plant during its early stages of development. This diminishes the crop's grain yield. Grey leaf spot, on the other hand, indicates necrotic lesions that are often long-lasting and that may merge, resulting in leaf senescence and a significant reduction in photo-synthetic regions and poor grain filling [8]. According to Wegary *et al.* [9], there was a yield loss of approximately 37% in Ethiopia and 60% in South Africa as a result of GLS [10]. In a comparable manner TLB driven the highest mean grain yield loss of 50% and thousand kernel weight loss of 16.4% on susceptible cultivars, according to [11]. Cultural practices, chemical methods, and host plant resistance are some of the management strategies for TLB and GLS diseases [12]. Uses of fungicides are ineffective because of their cost and environmental inconsistency. Host plant resistance is the most practical and economical way to control these diseases. To increase genetic resistance to various foliar diseases, it makes sense desirable to find resistant inbred lines from a variety of sources in the maize prebreeding program. Early research efforts were directed toward identifying maize germplasm resistant to these diseases and using it for a breeding program; however, in order to gain new and durable resistance, subsequent research efforts should be focused on screening additional sources of maize germplasm under artificial inoculation. This study aimed to choose high-quality protein inbred lines of maize that are resistant or tolerant to TLB and/or GLS by evaluating locally created and adapted inbred lines for use in maize breeding programs.

2. Materials and Methods

2.1. Description of the Study Area

The trials were conducted out in the main 2018 season at the Bako National Maize Research Center (BNMRC), a maize disease nursery area. The mid-altitude sub-humid agro-ecology zone of Ethiopia is represented by Bako, which is situated at 9°06' N and 37°09' E. It receives an annual rainfall of approximately 1237 mm and is 1650 m above sea level. Its average temperature ranges from 15.60C at minimum to 30.70C at maximum. The two studies were evaluated against TLB and GLS in the field under artificial epiphytotic circumstances.

2.2. Description of Experimental Materials and Design

A 6x8 alpha lattice design with three replications was implemented, using 42 QPM inbred lines in total. While BNMRC generated some of the genotypes, CIMMYT provided the remaining genotypes. Inbred lines were developed first for yield and quality protein traits, but resistance level was also crucial. Each inbred line was planted in a plot consisting of two rows of 3.6m long spaced at 25 and 75cm between plants with in rows and rows, respectively. Nitrogen (N₂) and diammonium phosphate (P₂O₅) fertilizers were applied at the recommended rates of 92 kg/ha and 69 kg/ha, respectively. All recommended agronomic management practices were implemented for the area.

2.3. Inoculum Preparation and Inoculation

One year before to trial, an inoculum of *E. turcicum* and *C. zae maydis* was produced by gathering samples from heavily infected maize fields exhibiting typical symptoms of TLB and GLS, respectively. The infected leaves were allowed to dry in the shade, then they were crushed or ground into a texture similar to wheat bran and kept in paper bags at 40C until the inoculation date. In accordance with [13], chopped leaves were then dusted into the plant whorls by adding a small amount

of leaf mill when the plant reached the 6–8 leaf stage in moist conditions. This allowed the leaves to stay in place for a long enough period of time to allow for spore germination. In two separate experimental fields, inoculation and data collection for each disease were carried out independently. In order to make sure good enough infection, a second inoculation took place ten days following the first.

2.4. Assessment of Disease Reaction

Two weeks following artificial inoculation, TLB and GLS were visually evaluated in the field on a plot basis from the rows. The date the disease first appeared itself, its incidence and severity, as well as other agronomic characteristics like plant height (cm) and yield of grain (t/ha), were all recorded in the data. Beginning with the development of the diseases, the severity of TLB and GLS on each inbred line was measured every ten days. Percentage of diseased plants relative to total plants in a plot was used to calculate disease incidence. A 1–5 scoring system [14], was used to rate the severity of the disease: 1 represented no disease symptoms, 2 a moderate lesion below the leaf that was subtending the ear, 3 a heavy damage on and below the leaf that was subtending the ear with few lesions above it, 4 a severe lesion on all leaves except the uppermost ones, which may have a few lesions, and 5 represented all dead leaves. Using a modified version of the 1–5 scale [15], each disease reaction was categorized according to the ratings of disease severity: 1.0–2.0 = Resistant (R); 2.1–2.5 = Moderately Resistant (MR); 2.6–3.0 = Susceptible (S); and >3.0 Highly susceptible (HS).

2.5. Statistical Data Analysis

PROC GLM of SAS version 9.2 was used to analyze the data SAS Institute, [16] Using the LSD-test at the 5% level of significance, mean separation was used to compare treatment means.

3. Results and Discussion

To check for resistance to TLB and GLS, 42 QPM inbred lines in total were evaluated. There was a significant ($P < 0.05$) difference in TLB and GLS resistance among the inbred lines, according to the mean disease severity and yield results (Tables 1 and 2). The severity of the disease varied between 1.6 and 4.1 in TLB and 1.3 to 4.5 in GLS. Inbred lines classified as resistant or tolerant to TLB and GLS were those with mean severity values less than 2. On the other hand, inbred lines where the mean severity value ranged between 2.1 and 2.5 were classified as moderately resistant, 2.6–3.0 as susceptible, and severity values greater than 3 as very susceptible to TLB and GLS (Tables 1 and 2). Thus, (Table 1) shows that 32 inbred lines were resistant or tolerant, 8 inbred lines were somewhat resistant, and 2 were susceptible to TLB. The same categories applied to 7, 6, 3, and 26 inbred lines: resistant/tolerant, moderately resistant, susceptible, and very susceptible to GLS, respectively (Table 2). In maize breeding programs, the best chosen inbred lines could be exploited as a source of resistance for TLB and GLS.

Table 1. Mean TLB severity and yield of 42 QPM inbred lines evaluated under artificial inoculation during 2018 main cropping season at Bako.

S/N	Pedigree	TLB Sev (1-5 scale)	Reaction	Grain yield (t ha ⁻¹)
1	BQ00RC3-#-28-2-1-1-1-1-#-#-#	1.5	R	3.29
2	MBRC5BcF108-2-3-1-B-5-2-B-B-#	1.5	R	2.00
3	Obatanpa-180-2-1-1-2-2-1-#-#-#	1.5	R	4.28
4	([[[CML159/[CML159/[MSRXPOOL9]C1F2-205-1(OSU23i)-5-3-X-X-1-BB]F2-3sx]-8-1-BB/CML509]F2-1/[CML182/[CML182/CML395]F2-3sx]-4-1-B]-3/CML390IR)-BBB-4-1-1-B-#-#-#	2.5	MR	3.51
5	(CML142/144-7-B) (F 2)- 9-2-1-2-2-1-#-#-#	2.3	MR	2.15
6	(CML197-B/[CML144/[CML144/CML395] F2-8sx]-1-2-3-2-B*5) F2-B-46-1-3-B-#-#-#	2.0	R	2.49
7	BQ00RC3-#-356-1-1-2-1-1-1-#-#-#	1.5	R	1.16
8	BQ00RC3-#-216-2-2-1-1-1-#-#-#	2.0	R	1.42

S/N	Pedigree	TLB Sev (1-5 scale)	Reaction	Grain yield (t ha ⁻¹)
9	BQ00RC 3- #55-1-2-1-1-1-1-#-#-#	1.5	R	3.00
10	(CML197-B/[CML144/[CML144/CML395] F2-8sx]-1-2-3-2-B*5) F2-B-46-1-4-B-#-#-#	2.00	R	2.17
11	(CML176/Kuleni) (F2)-3-1-1-2-1-1-1-#-#-#	2.3	MR	0.63
12	CML142 X 144-7-b (F 2)- 9-2-1-2-2-1-#-#-#	2.5	MR	1.51
13	BQ00RC3-#-354-2-1-2-2-1-1-#-#-#	1.8	R	3.07
14	([[[CML159/[CML159/[MSRXPOOL9]C1F2-205-1(OSU23i)-5-3-X-X-1-BB]F2-3sx]-8-1-BB/CML509]F2-1/[GQL5/[GQL5/[MSRXPOOL9]C1F2-205-1(OSU23i)-5-3-X-X-1-BB]F2-4sx]-11-3-1-1-B*4]-12/CML373IR)-B-8-B-7-2-3-B-#-#-#	2.00	R	1.53
15	CML142 Short-#-#-#	1.5	R	1.37
16	CML144/KULENI(F2) 11-2-1-3-1-1-1-#-#-#	2.00	R	2.02
17	Obtanpa-14-6-1-1-1-1-#-#-#	1.5	R	1.51
18	cml142x124-b (113) (f2) x124-b (113) (f2) x124-b (113) (f2))-B-4-1-1-1-#-#-#	1.5	R	3.47
19	CML-144 X CML-159 (F2)-20-1-1-1-2-#-#	1.5	R	2.37
20	CML-144 X CML-159 (F2)-20-1-1-1-1-#-#-#	1.5	R	1.74
21	CML142 X 144-7-b (F 2)- 9-2-2-1 -1-1-1-#-#-#	2.3	MR	2.30
22	([[[CML159/[CML159/[MSRXPOOL9]C1F2-205-1(OSU23i)-5-3-X-X-1-BB]F2-3sx]-8-1-BB/CML509]F2-1/[GQL5/[GQL5/[MSRXPOOL9]C1F2-205-1(OSU23i)-5-3-X-X-1-BB]F2-4sx]-11-3-1-1-B*4]-12/CML373IR)-B-8-B-7-2-4-B-#-#-#	1.8	R	3.69
23	BQ00RC3-#-356-1-1-1-1-#-#-#	1.8	R	4.18
24	Obatanpa-5-4-1-1-1-#-#-#	1.5	R	2.03
25	(CML197-B/[CML144/[CML144/CML395] F2-8sx]-1-2-3-2-B*5) F2-B-46-2-2-B-#-#-#	1.8	R	3.00
26	BQ00RC#32-1-2-2-1-1-1-#-#-#	2.8	S	3.44
27	BQ00RC3-#-331-2-1-1-1-1-1-#-#-#	1.5	R	1.15
28	CML194-#-#	1.5	R	1.65
29	[[CML506/[CML205/CML176]-B-2-1-1-B] F2-1/[CML144/[CML144/CML395] F2-8sx]-1-2-3-2-B*4]-24-B-2-BBB-3-B-B-#-#-#	1.8	R	3.51
30	CML142/144-7-B) (F 2)- 9-1-1-1-1-1-#-#-#	1.5	R	2.04
31	Obatanpa-301-4-3-1-1-#-#-#	2.3	MR	2.71
32	Z97SYNGLS(B)-F2-188-2-1-3-B*8-#-#-#-#	1.5	R	2.34
33	(GH-132-28)-22-1-6-1-1-#-#-#	1.3	R	1.28
34	BK02-Z -311-28(F2) B-1-#-#	1.5	R	1.92
35	CML142-#-#	2.5	MR	4.03
36	([[[CML159/[CML159/[MSRXPOOL9]C1F2-205-1(OSU23i)-5-3-X-X-1-BB]F2-3sx]-8-1-BB/CML509]F2-1/[GQL5/[GQL5/[MSRXPOOL9]C1F2-205-1(OSU23i)-5-3-X-X-1-BB]F2-4sx]-11-3-1-1-B*4]-12/CML373IR)-B-8-B-7-2-1-B-#-#-#	1.5	R	2.75
37	(CML176 x KULENI(F2)-4-3-1-1-1-#-#	1.5	R	2.57
38	CML334-#	3.3	S	2.15
39	Obatanpa -5-4-1-2-1-1-#-#	1.5	R	4.05
40	(CUBA/GUADC1F27-4-3-3-B-1-BX[KHiMAiTA94A]-30MSV-03-2-10-B-2-B-B)-306-1-B-2-B-B-B-#	1.5	R	3.68
41	CML142/144-7-B) (F 2)- 2-2-2-2-1-1-#-#-#	1.8	R	2.69
42	CML-144 X CML-159 (F2)-19-1-1-2-2-#-#-#	2.3	MR	3.31
LSD (5%)		1.1		2.01
CV(%)		29.9		32.10

Sev = severity; LSD = least significant difference; CV = coefficient of variation. 1.0 - 2.0=Resistant (R); 2.1-2.5=Moderately Resistant (MR); 2.6 -3.0= Susceptible (S) [15].

Table 2. Mean GLS severity and yield of 42 QPM inbred lines evaluated under artificial inoculation during 2018 main cropping season at Bako.

Entry No.	Pedigree	GLS Sev (1-5 scale)	Reaction	Grain yield t (ha ⁻¹)
1	BQ00RC3-#-28-2-1-1-1-1-1-#-#-#	3.5	HS	3.36
2	MBRC5BcF108-2-3-1-B-5-2-B-B-#	2.3	MR	2.06
3	Obatanpa-180-2-1-1-2-2-1-#-#-#	3.5	HS	4.26
4	([[[CML159/[CML159/[MSRXPOOL9]C1F2-205-1(OSU23i)-5-3-X-X-1-BB]F2-3sx]-8-1-BB/CML509]F2-1/[CML182/[CML182/CML395]F2-3sx]-4-1-B]-3/CML390IR)-BBB-4-1-1-B-#-#-#	2.3	MR	4.09
5	(CML142/144-7-B) (F 2)- 9-2-1-2-2-1-#-#-#	3.8	HS	2.23
6	(CML197-B/[CML144/[CML144/CML395] F2-8sx]-1-2-3-2-B*5) F2-B-46-1-3-B-#-#-#	4.0	HS	2.52
7	BQ00RC3-#-356-1-1-2-1-1-1-#-#-#	2.0	R	1.28
8	BQ00RC3-#-216-2-2-1-1-1-#-#-#	2.3	MR	1.57
9	BQ00RC 3- #-55-1-2-1-1-1-1-#-#-#	3.5	HS	4.95
10	(CML197-B/[CML144/[CML144/CML395] F2-8sx]-1-2-3-2-B*5) F2-B-46-1-4-B-#-#-#	3.5	HS	2.21
11	(CML176/Kuleni) (F2)-3-1-1-2-1-1-1-#-#-#	3.1	HS	0.97
12	CML142 X 144-7-b (F 2)- 9-2-1-2-2-1-#-#-#	3.8	HS	1.65
13	BQ00RC3-#-354-2-1-2-2-1-1-#-#-#	3.3	HS	3.89
14	([[[CML159/[CML159/[MSRXPOOL9]C1F2-205-1(OSU23i)-5-3-X-X-1-BB]F2-3sx]-8-1-BB/CML509]F2-1/[GQL5/[GQL5/[MSRXPOOL9]C1F2-205-1(OSU23i)-5-3-X-X-1-BB]F2-4sx]-11-3-1-1-B*4]-12/CML373IR)-B-8-B-7-2-3-B-#-#-#	3.5	HS	1.52
15	CML142 Short-#-#-#	3.8	HS	1.45
16	CML144/KULENI(F2) 11-2-1-3-1-1-1-#-#-#	3.3	HS	2.09
17	Obtanpa-14-6-1-1-1-1-#-#-#	1.5 R	R	1.88
18	cml142x124-b (113) (f2) x124-b (113) (f2) x124-b (113) (f2))-B-4-1-1-1-#-#-#	3.3	HS	4.52
19	CML-144 X CML-159 (F2)-20-1-1-1-2-#-#	3.3	HS	2.52
20	CML-144 X CML-159 (F2)-20-1-1-1-1-#-#-#	2.8	S	1.83
21	CML142 X 144-7-b (F 2)- 9-2-2-1 -1-1-1-#-#-#	2.3	MR	2.30
22	([[[CML159/[CML159/[MSRXPOOL9]C1F2-205-1(OSU23i)-5-3-X-X-1-BB]F2-3sx]-8-1-BB/CML509]F2-1/[GQL5/[GQL5/[MSRXPOOL9]C1F2-205-1(OSU23i)-5-3-X-X-1-BB]F2-4sx]-11-3-1-1-B*4]-12/CML373IR)-B-8-B-7-2-4-B-#-#-#	3.8	HS	4.68
23	BQ00RC3-#-356-1-1-1-1-1-#-#-#	3.5	HS	4.23
24	Obatanpa-5-4-1-1-1-1-#-#-#	1.5	R	2.09
25	(CML197-B/[CML144/[CML144/CML395] F2-8sx]-1-2-3-2-B*5) F2-B-46-2-2-B-#-#-#	3.3	HS	3.00
26	BQ00RC#32-1-2-2-1-1-1-#-#-#	3.8	HS	3.56
27	BQ00RC3-#--331-2-1-1-1-1-1-#-#-#	3.5	HS	1.20
28	CML194-#-#	2.5	MR	1.67
29	[[CML506/[CML205/CML176]-B-2-1-1-B] F2-1/[CML144/[CML144/CML395] F2-8sx]-1-2-3-2-B*4]-24-B-2-BBB-3-B-B-#-#-#	1.8	R	3.51
30	CML142/144-7-B) (F 2)- 9-1-1-1-1-1-#-#-#	3.8	HS	2.10
31	Obatanpa-301-4-3-1-1-#-#	4.8	HS	2.69
32	Z97SYNGLS(B)-F2-188-2-1-3-B*8-#-#-#-#	3.0	S	3.03
33	(GH-132-28)-22-1-6-1-1-#-#-#	1.5	R	1.36
34	BK02-Z -311-28(F2) B-1-#-#	3.8	HS	1.94
35	CML142-#-#	4.3	HS	3.08
36	([[[CML159/[CML159/[MSRXPOOL9]C1F2-205-1(OSU23i)-5-3-X-	2.0	R	2.92

Entry No.	Pedigree	GLS Sev (1-5 scale)	Reaction	Grain yield t (ha ⁻¹)
37	X-1-BB]F2-3sx]-8-1-BB/CML509]F2-1/[GQL5/[GQL5/[MSRXPOOL9]C1F2-205-1(OSU23i)-5-3-X-X-1-BB]F2-4sx]-11-3-1-1-B*4]-12/CML373IR)-B-8-B-7-2-1-B-#-#-#	1.5	R	3.41
38	(CML176 x KULENI(F2)-4-3-1-1-1 -#-#	3.5	HS	2.29
39	CML334-#	3.0	S	4.19
40	Obatanpa -5-4-1-2-1-1-#-#	2.0	R	3.72
41	(CUBA/GUADC1F27-4-3-3-B-1-BX[KiiIMAiTA94A]-30MSV-03-2-10-B-2-B-B)-306-1-B-2-B-B-B-#	4.3	HS	2.84
42	CML142/144-7-B) (F 2)- 2-2-2-2-1-1-#-#-#	2.5	MR	3.26
LSD (5%)		1.1		2.05
CV (%)		17.9		30.14

Sev = severity; LSD = least significant difference; CV = coefficient of variation. 1.0–2.0=Resistant (R); 2.1-2.5=Moderately Resistant (MR); 2.6 -3.0= Susceptible (S); 3.1-5.00 = Highly Susceptible

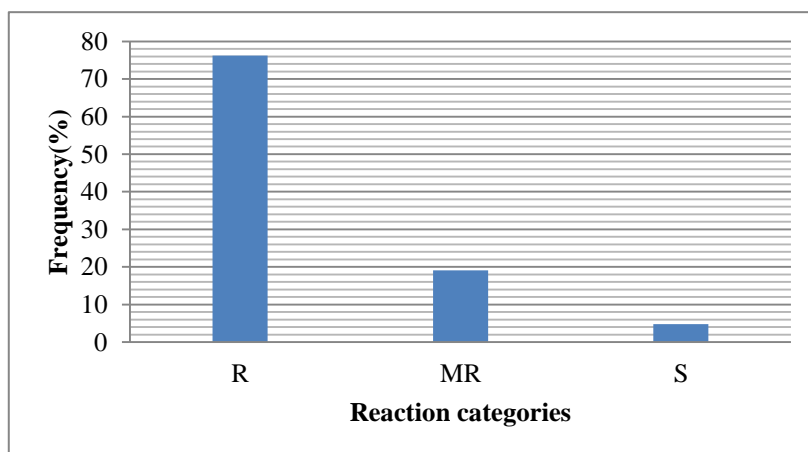


Figure 1. Frequencies of QPM inbred lines with resistant (R), moderately resistant (MR) and susceptible (S) reactions to TLB.

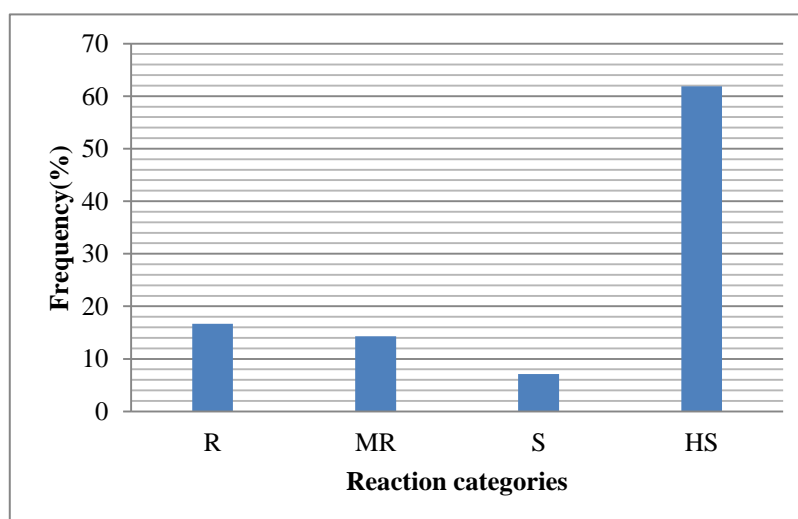


Figure 2. Frequencies of QPM inbred lines with resistant (R), moderately resistant (MR) susceptible (S), and Highly susceptible (HS) reactions to GLS.

Due to artificial inoculation, field screening studies revealed a distinct differential response of inbred lines to TLB and GLS (Figures 1 & 2). This finding was in line with a study by Chandrashekara et al. (2014), which found that maize genotypes that were inoculated with particular diseases differed significantly from one another. Inbred lines evaluated showed resistance/tolerance to TLB in 76.19% and GLS in 16.67% of cases, respectively. Five inbred lines were found to have resistant/tolerant response to both GLS and TLB, out of the total number of evaluated inbred lines that exhibited resistance to both of the diseases. Inbred lines, namely (CUBA/GUADC1F27-4-3-3-B-1-BX[KiiIMAI94A]-30MSV-03-2-10-B-2-BB)-306-1-B-2-B-B-B-#, BQ00RC3-#-356-1-1-2-1-1-1-#-#-#, Obtanpa-14-6-1-1-1- 1-#-#-#, Obatanpa-5-4-1-1-1-#-#-#, (GH-132-28)-22-1-6-1-1-#-#-#, (CML176 x KULENI (F2)-4-3-1-1-1-#-# were showed multiple disease resistance. The more susceptible inbred lines most likely lost their active leaf tissues, which led to a reduction in photosynthetic leaf area. As a result, the plant finally produced few kernels and/or might have contributed to the overall yield loss, demonstrating a negative link with the severity of the disease. Similar research results have been reported by Singh et al. (2014), who found significant variance between 27 populations of maize and 38 inbred lines that were evaluated for resistance to turicum leaf blight. Further evaluation for stability to TLB and GLS across location and years at hotspot locations and/or under controlled conditions should be conducted on the moderately resistant and resistant inbred lines. In the future, the inbred lines that were selected can also be utilized to create hybrids and composites for multiple-disease resistance breeding projects. These results are consistent with research by [17-19], which found that different maize germplasm responded differently to diseases. Inbred maize lines CM-104 and CM-105 showed durable resistance to E. turicum, according to studies conducted by [20]. Moreover, Dagne *et al.* [13], figured out promising sources of resistance to maize disease, identifying 143-5-I and CML-387 as resistant, Gotto LMS5, SC-22, and CML-395 as moderately resistant, and A-7016 and CML-197 as susceptible to GLS.

Conclusion and Recommendation

In general, it was figured out that, in artificial epiphytotic conditions, 32 inbred lines were resistant to TLB and 6 to GLS. The results thus highlight the potential of the selected resistant lines for resistance against TLB and GLS of maize, respectively, caused by E. turicum and C. zea maydis. Maize inbred lines identified as resistant/tolerant in this study should also be screened under controlled environments to properly verify the level of resistance to TLB and GLS. It would be better to use molecular methods to locate the gene (s) involved in the resistance and incorporating them to cultivars having desired agronomic characteristics. Moreover, the promising lines with good yield and other agronomic performance identified through this investigation can be deployed in disease endemic areas for sustainable maize productivity.

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