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Full Length Research Paper

Combining abilities of maize inbred lines for grey leaf spot (GLS), grain yield and selected agronomic traits in Kenya

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The genetics of resistance to grey leaf spot (GLS) disease, grain yield and selected agronomic traits was studied in 42 F_1 progenies from a full diallel cross among seven maize inbred lines. These 42 F_1 progenies and seven parents were evaluated at three locations; Kenya Agricultural Research Institute (KARI), Kiboko, KARI Kakamega and University of Nairobi (Field station) during the period June 2006 to April 2008. The experiments were laid out in a randomized complete block design with three replicates. Combining ability analyses were conducted on the across site data of grey leaf spot disease, grain yield and selected agronomic traits using Griffing's method one, model one in the SAS program. Additive gene action played a greater role than non-additive gene action in the inheritance of resistance to grey leaf spot disease whereas the non additive effects were more important in the inheritance of grain yield. Reciprocal effects were not significant for GLS disease resistance and grain yield indicating absence of maternal effects for these traits. The inbred lines, CML 384 and CML 373 were the best combiners for grain yield with general combining ability (GCA) effects of 0.79 and 0.56 respectively while TZMI 711 and CML 373 were the best combiners for GLS resistance with highest negative values for GCA of -0.51 and -0.398, respectively. The local maize breeders could now incorporate the genes for GLS resistance in CML 373 and TZMI 711 and the grain yield genes in CML 384 into elite lines using recurrent and backcross methods, respectively in order to increase maize production and productivity in Kenya.

Key words: Maize, *Zea mays*, grey leaf spot, grain yield, combining ability.

INTRODUCTION

Maize is an important staple crop providing 50, 30 and 15% of calories in diets in Southern Africa; East Africa and Western and Central Africa, respectively (Beyene et al., 2012). However, the maize crop incurs high yield losses during growth and postharvest stages due to grey leaf spot (GLS), caused by *Cercospora zeae-maydis* (Tehon and Daniels, 1925). GLS is recognized as one of the most yield-limiting diseases of maize with yield losses ranging from 10 to 70% and with intense epidemics, 90 to100% yield losses have been reported (Sibiya et al., 2012; Danson et al., 2008). The GLS disease shows necrotic lesions which after coalescing lead to leaf senescence greatly reducing the photosynthetic area leading to poor grain filling, stalk lodging and low maize yields (Derera et al., 2008; Menkir and Ayodele, 2005). This poses an imminent threat to food security in Kenya where 90% of its population depends on maize as a staple food crop (Kinyua et al., 2010; Vivek et al., 2001). The cultivation of susceptible cultivars coupled with maize monoculture have further led to increased GLS incidence and severity (Okori et al., 2004).

The GLS disease could be managed using various methods. Some of the commonly used strategies include

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cultural control (disposal of plant debris), chemical control (application of pesticides) and host plant resistance, Cultural and chemical control methods are uneconomical in combating the disease especially among the resource constrained small scale farmers. Thus, host plant resistance remains the most viable option for managing the GLS disease pressure. More sources of GLS resistance should be identified to improve the inbred lines which are high yielding but are susceptible to GLS. More maize germplasm should also be characterized and their combining ability established. The combining ability could help to provide inference in the selection of elite inbred lines (Legesse et al., 2009a) in order to establish the type of gene action which control the grey leaf spot resistance (Legesse et al., 2009b). Combining ability comprises both general combining ability (GCA) and specific combining ability (SCA). Previous studies have identified significant GCA and SCA effects for GLS resistance implying that resistance was conditioned by both additive and non additive gene actions (Menkir and Ayodele, 2005; Vivek et al., 2010; Danson et al., 2008). The significant GCA implies that breeders can possibly exploit the available genetic variability while identifying elite materials with desirable traits whereas significant SCA effects suggest that promising single cross combinations could be identified. However, for an effective breeding program, the genotypes tested should exhibit sufficient genetic diversity (Betran et al., 2003). Combining ability studies have also been used to study the yield characters and heterotic groups for inbred lines with the aim of developing new hybrids with good quality, high yields and multiple disease tolerance (Xingming et al., 2001). High GCA and SCA variances for grain yield have also been observed (Derera et al., 2008). Further on, the identification of single crosses with high and positive general combining ability (GCA) effects for grain yield suggested that potential parents could be exploited in the development of various hybrids, including three-way, double-cross and double top cross hybrids. Usually, most high general combiners produce genotypes with high SCA. However, in cases where this is not true, the parents involved are considered to be genetically diverse (Bhatnagar and Mehrotra, 1980). Thus, many genotypes should be evaluated in order to select suitable parents with desirable genotypes.

Another important genetic and statistical methodology is diallel analysis. It helps in explaining the genetic control of important plant traits while enhancing breeding and selection of promising parents. The diallel crosses enable breeders to predict progeny performance from parental performance (Iken and Olakojo, 2002; Ojulong et al., 1996). Pairs of parental lines that yield heterotic crosses identified have been pivotal in the development of appropriate hybrids (Vega and Chapman, 2006). This study was undertaken to (a) to estimate GCA effects for grain yield and grey leaf spot among the inbred lines and (b) to estimate SCA effects and identify best hybrid combinations among the inbred lines.

MATERIALS AND METHODS

Experimental locations

The experiments were conducted at three locations; Kenya Agricultural Research Institute (KARI), Kiboko, KARI Kakamega and University of Nairobi (Field Station). Important characteristics of these locations are presented in Table 1.

Maize genotypes

Seven inbred lines namely, CML 204, CML 312, CML 373 and CML 384 from CIMMYT, TZMI 102, TZMI 711 and TZMI 712 from IITA were sourced for this study. The inbred lines were grown at KARI-Kiboko and cross-pollinated in a full diallel fashion (including reciprocals) to develop forty two single cross hybrids. The 42 single cross hybrids and seven parents were evaluated for GLS resistance and grain yield performance at three locations; KARI-Kiboko, KARI-Kakamega and University of Nairobi (Field station) between June 2006 and April 2008. Each genotype was sown in three five-metre long rows with inter- and intra-row spacing of 75 cm and 30 cm and laid out in a randomized complete block design with three replicates.

Data collection

GLS severity scores were measured according to Saghai Maroof et al. (1993) method where; 1 = no symptoms, 2 = moderate lesion below leaves subtending the ear, 3 = heavy lesion development on and below the leaf subtending the ear with a few lesions above it, 4 = severe lesion development on all but uppermost leaves may have few lesions and 5 = all leaves dead. The GLS scores were made at the period when the disease was fully expressed on the susceptible inbred lines.

Data on grain yield was obtained by harvesting all the ears per plot. The ears were weighed and this was recorded as the field weight. The moisture content of a seed sample from 10 randomly selected cobs was then determined. The weight of grains from the harvested cobs was then adjusted to 13% moisture content while assuming an 80% shelling percentage.

Data analysis

Analysis of variance was carried out for individual and combined environments. The genotypes were considered as fixed effects whereas the environments were considered as random effects. Mean plot GLS scores at full disease development were used for analysis because the lesions were readily observable. Combining ability analyses were conducted using Griffing's (1956) method I (parents, F1's and reciprocals) model I to obtain the estimates of the GCA and SCA effects using the ProcGLM model of the SAS program (SAS, 1996).

RESULTS AND DISCUSSION

Analysis of variance

The analysis of variance showed highly significant mean squares at $P<0.05$ for GLS, grain yield and other agronomic traits due to the genotype, environment and genotype by environment interaction (Table 2). However, the performance of the genotypes varied across

Table 1. Agro-climatic description of the three experimental sites used in the study.

Site	Longitude	Latitude	Elevation (masl)	Rainfall (mm)	Temperature (0°C)		Soil texture	Characteristic/ Remarks
					Min	Max		
Kiboko	37°75 E	2°15'S	975	530	14.3	35.1	Sandy clay	It was used to identify potential losses from the GLS disease. Conditions unfavourable for GLS disease infection and development
Kakamega	34°45 E	0°16 'N	1585	1916	12.8	28.6	Sandy loam	It is a hot spot for most foliar diseases. Hot spot for GLS *Cercospora zeae maydis* infection and spread
University of Nairobi, Field station	36°44 E	I°15' S	1820					It was also used to identify potential losses from GLS. Prone to GLS

masl: Metres above sea level.

Table 2. ANOVA for GLS, grain yield and selected agronomic traits recorded across sites.

Source of variation	Df	GLS	DTFF	Ear height	Grain yield	Plant height	Root lodge	DTMF
Genotype	48	2.05***	77.94***	1782.64***	43.66***	4961.9***	18.79***	71.79***
Environment	2	77.43***	5408.49***	14010.56***	3275.95***	30161.8***	32.62***	6200.27***
G X E	96	0.59***	10.95	130.21***	10.93***	304***	10.19***	11.713**
GCA	6	13.4**	162.27**	6341.96**	34.6**	15611.9**	7.9**	147.9**
SCA	21	0.78**	125.39**	2180.09**	89.1**	6720.8**	39.92**	112.04**
GCA/SCA ratio		17.2	1.294	2.9	0.388	2.3	5.05	1.32
GCA X E	6	4.4**	14.82	76.05	17.84**	190.97	14.8**	16.97*
SCA X E	21	0.52**	3.8	153.15**	13.81**	349.4**	24.15**	4.32
MAT	5	0.1061	7.95	75.77	0.3188	200.67	0.3464	15.15
Error	146	0.14	8.44	54.6	2.85	114.4	1.11	7.461
Total	293							

***Significance at p<0.001; **significance at p<0.05; GLS, grey leaf spot; DTMF, days to male flowering; DTFF, days to female flowering; GCA, general combining ability; SCA, specific combining ability; GCA/SCA ratio, baker's ratio; MAT, maternal effects.

environments and that GXE interaction was small in comparison to the genotype effect.

Highly significant differences were noted for GCA values of all the traits studied across the sites (Table 2). The significant GCA indicated the evidence of additive gene action. With reference to SCA, all the traits showed significant SCA effects. This implies that the difference noted among the hybrids were due to both GCA and SCA effects. Other researchers have reported that additive gene action was important in the inheritance of GLS resistance (Legesse et al., 2009a; Menkir and Ayodele, 2005; Verma, 2001). The relative importance of general and specific combining ability on progeny performance gene action was important in the inheritance of GLS resistance (Legesse et al., 2009a; Menkir and Ayodele, 2005; Verma, 2001). The relative importance of general and specific combining ability on progeny performance was estimated as the ratio of the variances of GCA to that of SCA referred to as Baker's Ratio (1978). The Baker's ratio (Table 2) showed the predominance of additive gene effects in the inheritance of all traits except grain yield. Thus, the response of hybrids to these agronomic traits could be predicted based on the GCA of the parents (Munthali et al., 2003).

The GCA by environment interaction was significantly different for GLS, grain yield and days to maturity among the genotypes. Thus, the different parental lines for hybrids could be selected at specific environment. It also

implies that the GCA effects of the parents were influenced by the environmental variability (Bhatnagar et al., 2004). From this study, the maternal effects for all traits were not significant and this implies that there is no cytoplasmic effect in the conditioning the inheritance of the various traits.

Mean performance of the genotype across sites

The inbred line CML 384 was the highest yielding parent with 2.9 t ha^{-1} followed by CML 373 with 2.5 t ha^{-1} while CML 312 and CML 204 had the lowest grain yields of 1.6 and 1.7 t ha^{-1}, respectively (Table 3). This implies that CML 384 and CML 373 had high frequencies of yield favouring alleles as opposed to the other inbred lines.The inbred line CML 373 (GLS score of 1) was immune to GLS while TZMI 711 was highly resistant to GLS with score of 1.6. Thus, CML 373 could be an excellent source of both grain yield and GLS resistance genes while CML 384 could be an excellent source of grain yield genes. The parental means of these inbred lines also revealed the breeding potential for the characters involved and which could easily be used to discriminate poor lines in future breeding efforts.

The highest yielding hybrid across sites was CML 312 / CML 204 with 11.3 t ha^{-1} and a GLS score of 2.1 (Table 3). This hybrid had early flowering and longer grain filling period making it escape severe GLS attack and this could have led to its high yields across sites. Saghai Maroof et al (1993) also reported that late maturing lines showed high GLS resistance and this was associated with QTL 4 which also has genes for stay green trait in maize. Other hybrids that showed superior yield performance and GLS resistance were CML 384 /CML 373, CML 373 / CML 384, TZMI 711/ CML 384 and CML 384/ TZMI 711 (Table 3). In this study, CML 384 was a common parent in all these good crosses and this supports the fact that CML 384 has a high frequency of yield improving alleles. These superior hybrids also had either CML 373 and / or TZMI 711 as one of the parent further confirming that these two inbred lines are good sources of GLS resistance genes. These good hybrids were also among the late maturing entries since they took more than 80 days to flower. This supports the statement by Verma (2001) that late maturing maize lines are usually more resistant to GLS than early maturing lines. In addition, TZMI 711 produced crosses highly resistant hybrids with GLS scores ranging from 1.3 to 1.9 even with the susceptible parents (CML 204 and TZMI 102). Thus, in TZMI 711, the GLS resistance could be conditioned by both additive and dominant gene actions (Beyene et al., 2011). It was also noted that the TZMI 711 plants stayed green longer in the field and further work is imperative to determine the interrelationship between stay green and the GLS resistance. However, GLS resistant lines have been reported to possess the stay green trait (Saghai Maroof et al., 1993).

Combining ability

The parents, CML 384 and CML 373 had the highest positive GCA effects for grain yield of 0.79 and 0.56 respectively. TZMI 711 and CML 373 had the highest negative GCA values for GLS of -0.51 and -0.398 respectively while the most susceptible inbred lines were CML 204 and TZMI 102 with GCA values of 0.40 and 0.549 respectively across sites (Table 4). The single cross hybrids which expressed high GLS resistance across the sites comprised CML 204 / TZMI 712 (SCA for GLS of -0.42), CML 373 / CML 384 (-0.36), TZMI 711/TZMI 712 (-0.32) and TZMI 102/ TZMI 711 (-0.30). Most of these promising hybrids were crosses between good combiners for grain yield and / or grey leaf spot resistance. Thus, the additive gene action in the inbred lines for grain yield and GLS and the non additive gene action in the good crosses complement each other to favour GLS resistance and improve yields (Solanki and Gupta, 2001). These promising hybrids could be suitable heterozygous testers in recurrent selection for SCA to produce high yielding and GLS resistant synthetics. TZMI 711 when crossed with the susceptible inbred line TZMI 102 produced a cross TZMI 102/ TZMI 711 with significantly high GLS resistance of -0.30. This suggests the presence of both additive and non additive gene action in conditioning the inheritance of GLS resistance of TZMI 711 (Table 5). The poor combiners for GLS, TZMI 102 and CML 204 produced GLS resistant hybrids when crossed to TZMI 712 (good combiner for GLS resistance with GCA for GLS of -0.22). However, the parents CML 373 and TZMI 711, which had good combining ability for GLS resistance, produced a cross CML373 / TZMI 711 with low SCA for GLS resistance of 0.2 signifying the genetic diversity of these inbred lines. Thus, efficient breeding methods should first accumulate favourable genes in homozygous state while breaking the linkage blocks and this will greatly help reduce the grain yield losses associated with GLS. Additionally, with the presence of significant non additive gene action, this population should be maintained in heterozygous state.

Nevertheless, across the sites, no parent had high GCA for all the characters measured thus the parents involved were genetically diverse. The genetic diversity revealed in these breeding materials is imperative for breeders and farmers in the adaptation of varieties with GLS disease resistance and which can be grown in different agro ecological zones. Furthermore, the GXE interpretations could be based on the GCA effects enabling breeders to select stable inbred parents across environments. Thus, these breeding materials may be developed further for release in Kenya to avoid risks associated with GLS epidemics and general crop failure.

CONCLUSION AND IMPLICATIONS

The elite sources of GLS resistance identified in this work

Table 3. Means for grain yield, grey leaf spot and selected agronomic traits among seven maize inbred lines and 42 single cross hybrids across sites.

Cross	Grain yield (t ha^{-1})	Grey leaf spot (1-5)	[a]DTMF (days)	[b]DTFF (days)	Plant height (cm)	Ear height (cm)	Root lodge (counts)
CML373	2.5	1.0	90	93	163.4	72.6	5
CML373/TZMI 711	8.5	1.3	82	84	194.4	98.7	0
TZMI 712/CML373	7.9	1.3	86	87	189.6	87.6	0
TZMI 712/TZMI 711	6.6	1.3	85	88	159.0	104.4	0
TZMI 711/TZMI 712	6.2	1.3	87	89	152.2	73.8	0
TZMI 711	1.9	1.4	91	93	97.8	49.5	3
CML373/TZMI 712	8.2	1.4	84	87	186.4	90.9	0
TZMI 711/CML373	8.3	1.4	83	87	186.7	90.3	0
CML384/CML373	11.3	1.5	84	86	200.6	98.5	0
TZMI 711/CML384	10.6	1.5	84	86	191.7	100.0	0
TZMI 711/CML312	9.3	1.5	80	82	199.2	97.6	0
CML373/CML384	10.7	1.6	83	84	203.7	99.7	0
CML373/CML312	9.6	1.6	79	81	202.9	93.3	0
CML312/CML373	9.2	1.6	79	81	159.0	94.0	0
CML312/TZMI 711	9.5	1.7	80	82	203.0	97.3	0
CML312/TZMI 712	8.6	1.7	81	82	200.1	93.6	0
TZMI 712/CML312	8.2	1.7	82	83	207.6	98.3	0
TZMI 712/CML204	7.7	1.8	85	86	212.7	78.9	0
TZMI 102/TZMI 711	8.1	1.8	82	85	193.2	98.9	1
CML384/TZMI 711	10.1	1.8	81	83	196.0	99.1	0
CML204/TZMI 711	8.6	1.8	84	86	207.1	112.3	0
TZMI 711/TZMI 102	8.0	1.8	83	86	191.2	102.8	0
TZMI 711/CML204	9.1	1.9	86	86	204.8	110.8	0
TZMI 712/TZMI 102	7.0	1.9	86	87	179.3	78.3	0
CML204/TZMI 712	8.7	1.9	82	84	214.4	103.8	0
CML204/CML373	9.6	2.2	82	84	216.3	108.3	0
CML384/CML312	9.4	2.2	81	81	213.1	106.8	0
TZMI 102/TZMI 712	7.0	2.2	84	85	176.7	83.3	2
CML204/CML312	10.9	2.3	80	81	238.5	125.9	0
TZMI 712/CML384	9.9	2.3	83	84	197.5	93.5	0
CML312	1.6	2.3	88	90	176.1	70.4	3
CML384/TZMI 712	9.6	2.3	85	85	187.0	90.5	0
CML373/CML204	10.1	2.3	81	83	220.1	116.0	0
CML 384	3.0	2.4	93	93	147.2	77.6	6
CML312/CML384	9.5	2.4	81	82	210.9	101.8	1
CML373/TZMI 102	9.6	2.5	81	84	198.1	103.0	0
CML312/TZMI 102	10.1	2.5	78	80	214.9	104.7	0
CML312/CML204	11.3	2.5	80	81	235.9	125.3	0
TZMI 712	1.8	2.5	91	94	119.4	53.0	4
TZMI 102/CML373	10.7	2.6	80	83	209.3	102.4	0
CML204/CML384	10.2	2.8	82	84	231.7	128.5	0
TZMI 102/CML312	9.6	2.8	78	79	228.8	111.2	0
CML204/TZMI 102	8.2	2.9	83	84	230.3	120.4	0
TZMI 102/CML204	8.7	3.0	81	85	229.8	122.4	0
CML384/CML204	9.7	3.0	85	86	214.6	113.0	0
TZMI 102/CML384	9.3	3.0	82	82	222.0	114.3	1
CML384/TZMI 102	9.4	3.1	81	82	210.8	109.5	3
CML204	1.6	3.2	89	92	162.0	86.2	7
TZMI 102	2.2	3.3	87	89	148.5	73.4	6

Table 3. Contd.

Least significant differences	3.1	0.7	5	6	21.1	14.6	2

[a]DTMF, Days to male flowering; [b]DTFF, days to female flowering.

Table 4. GCA Estimates for GLS, grain yield and selected agronomic traits across sites.

Parent	Grain yield	Grey leaf spot	[a]DTMF	[b]DTFF	Plant height	Ear height	Root lodge
CML 204	0.13	0.40**	0.18	0.24	17.30**	14.398**	0.12
CML 373	0.56**	-0.398**	-0.19	0.45	0.25	-2.44**	-0.095
CML 312	0.33*	-0.03	-2.31**	-2.54**	12.55**	2.06**	-0.36**
CML 384	0.79**	0.21**	0.69*	-0.07	2.57*	3.48**	0.32**
TZMI 102	-0.35*	0.549**	-0.94**	-0.93**	3.11**	2.58**	0.45**
TZMI 711	-0.46**	-0.51**	0.83**	1.32**	-18.86**	-7.297**	-0.29**
TZMI 712	-1.03**	-0.22**	1.76**	1.51**	-16.9**	-12.79**	-0.15

Significance levels, **,P<0.01 and *,P<0.05; GCA, general combining ability; [#]GLS, grey leaf spot where severity scores were measured according to Saghai Maroof et al. (1993) method where; 1 = no symptoms, 2 = moderate lesion below leaves subtending the ear, 3 = heavy lesion development on and below the leaf subtending the ear with a few lesions above it, 4 = severe lesion development on all but uppermost leaves may have few lesions and 5 = all leaves dead. [a]DTMF, days to male flowering; [b]DTFF, days to female flowering.

Table 5. SCA estimates GLS, yield and selected agronomic traits across sites.

Cross	Grain yield	Grey leaf spot	[a]DTMF	[b]DTFF	Plant height	Ear height	Root lodge
CML204/CML373	1.05**	0.16	-1.94**	-2.11**	5.07	2.95	-0.90*
CML204/CML312	2.62**	-0.09	-1.15	-1.70*	11.77**	11.84**	-0.56*
CML204/CML384	0.79*	0.18**	-0.73	-0.34	7.74**	5.58**	-1.15**
CML204/TZMI 102	0.35	-0.05	-0.27	0.02	14.08**	7.149**	-1.37**
CML204/TZMI 711	1.004**	-0.10	0.46	-0.31	11.93**	7.18**	-0.63*
CML373/CML312	0.33	-0.07	-1.87**	-1.75*	-3.57	-3.27	-0.35
CML373/CML384	1.58**	-0.36**	-0.70	-0.72	3.73	0.77	-1.02**
CML373/TZMI 102	1.82**	0.29	-1.40*	-1.19	4.78	5.26**	-1.07**
CML373/TZMI 711	0.20	0.21*	-1.51*	-1.28	13.58**	6.96**	-0.50
CML312/CML384	0.13	0.03	-0.58	-1.39	1.31	1.50	-0.59*
CML312/TZMI 102	1.60**	0.01	-2.12**	-2.04**	10.59**	6.03**	-0.98**
CML312/TZMI 711	1.57**	0.06	-2.14**	-1.79*	11.85**	5.44**	-0.24
CML384/TZMI 102	0.54	0.23**	-1.69**	-2.00**	15.18**	8.58**	0.26
CML384/TZMI 711	1.98**	-0.12	-2.14**	-1.84*	14.55**	6.09**	-0.92**
TZMI 102/TZMI711	0.73	-0.30 **	-0.51	-0.14	12.40**	8.32**	-0.46
CML204/TZMI712	0.96*	-0.42**	-2.06**	-1.84*	17.58**	5.20**	-0.76**
CML373/TZMI 712	0.42	-0.12	0.31	-0.30	9.09**	7.16**	-0.63*
CML312/TZMI 712	1.01**	-0.17	-1.48*	-1.48*	12.62**	9.44**	-0.29
CML384/TZMI 712	1.74**	0.19*	-1.98**	-2.11**	11.03**	4.07*	-1.05**
TZMI 102/TZMI712	0.33	-0.32**	0.73	-0.09	-3.75	-6.29**	-0.43
TZMI 711/TZMI712	-4.35**	0.85**	4.19**	5.72**	-42.36**	-18.73**	3.43**

Significance levels, **, P<0.01; *, P<0.05; GLS, grey leaf spot where severity scores were measured according to Saghai Maroof et al. (1993) method where; 1 = no symptoms, 2 = moderate lesion below leaves subtending the ear, 3 = heavy lesion development on and below the leaf subtending the ear with a few lesions above it, 4 = severe lesion development on all but uppermost leaves may have few lesions and 5 = all leaves dead; [a]DTMF, days to male flowering, [b]DTFF= days to female flowering.

should be evaluated in more hybrid combination at more locations to confirm the stability of this resistance. CML 204 and TZMI 102 which were the most susceptible inbred lines could be used as suitable checks and / or disease spreaders in further GLS breeding programs aimed at the local evaluation of the presence of the grey leaf spot

disease in Kenya for quick attention. Finally, the lines CML 312, CML 384, CML 373 and TZMI 711 that had more favourable alleles for most traits could be used to initiate a breeding program. This will eventually help to avert further GLS related yield losses in Kenya and ensure food security.

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