



Sources of resistance to *Bipolaris maydis* in popcorn lines under field conditions

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Abstract Southern corn leaf blight (SCLB), caused by the pathogen *Bipolaris maydis*, can cause significant damage to popcorn production. However, genetic resistance in maize germplasm offers a viable strategy for disease control. This work investigated the performance of popcorn lines for SCLB resistance and their potential for producing hybrids. Thirty-five lines were evaluated in two environments using a randomized block design with four replicates. Measurements of *Bipolaris* incidence (BI) and severity (BS) were taken 30 days after the beginning of flowering. Grain yield (GY) and popping expansion (PE) were evaluated at grain maturity. The data were analyzed using joint analysis of variance and the Scott-Knott test at a 5% significance level. Significant variation in all four parameters were observed for BI, BS, GY and PE, and the lines were grouped accordingly. Two lines with high

levels of resistance to SCLB (L623 and L624) were identified. Five lines (L509, L204, L683, L292, L70) stand out as having high potential for breeding based on their levels of both popping expansion and SCLB resistance.

Keywords Inbred line · *Zea mays* L. · Genetic resistance · *Bipolaris maydis* · Fungal disease

Introduction

Popcorn (*Z. mays* L.) is widely consumed among Brazilians, particularly as a snack. It influences many sectors of the country's economy and is advantageous for growers because of its profit potential (Freitas Jesus et al., 2013; Paraginski et al., 2016). Although popcorn

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is economically advantageous compared with other corn types, technological improvements are still necessary to increase yield and meet growing demand (Amaral Júnior et al., 2013).

Difficulties related to low yield are present in national varieties, including susceptibility to lodging, a low capacity for grain expansion, and limitations of a phytopathological nature. Research investments are therefore needed to ameliorate these problems (Arnhold, 2008; Sawazaki, 2001). Of these, phytopathological problems, especially leaf diseases, can lead to large losses. Such diseases cause leaf tissue death, reducing the active photosynthetic area and negatively impacting productivity (Nihei & Ferreira, 2012).

Among the leaf diseases, Southern corn leaf blight (SCLB), caused by the fungus *Bipolaris maydis* (Y. Nisikado & C. Miyake) Shoemaker [Basionym: *Helminthosporium maydis* Y. Nisik. & C. Miyake; Obligate synonyms: *Drechslera maydis* (Y. Nisik. & C. Miyake) Subram. & B.L. Jain; Taxon synonyms: *Ophiobolus heterostrophus* Drechsler and *Cochliobolus heterostrophus* (Drechsler) Drechsler], has been the target of research due to its high incidence. Crop infection in the initial stages of cultivation, along with favorable environmental conditions, can lead to yield losses of up to 70% (Huang et al., 2010; Hussain et al., 2016; Kurosawa et al., 2017).

In Brazil, there have been no reports of major epidemics caused by *B. maydis*, such as that observed in the United States in 1970 (Ullstrup, 1972). However, high disease severity has been found in monitored corn crops throughout the country, particularly in states with high grain production, such as Rondônia, Mato Grosso, Goiás and Tocantins (Costa et al., 2014). In corn, three physiological races of the fungus can occur, specifically the races ‘C’, ‘T’, and ‘O’. Globally, the ‘O’ race has the widest distribution, and as the popcorn crop is particularly susceptible to diseases, the spread of this pathogen in crops can reduce production.

SCLB control has been carried out by two main methods, chemical control with the use of pesticides, and genetic control using resistant hybrids (Ye et al., 2012). Genetic control is more frequently studied, since the fungus has acquired resistance to the main fungicide mode of action groups (Raid, 1991; Montesinos, 2003; Ye et al., 2012).

Genetic resistance is one of the most efficient ways to control diseases in plants. The widespread use of resistant varieties is possible in almost all crops and has a low

environmental impact compared with chemical control (Camargo, 2018). The development and evaluation of genotypes with resistance to *B. maydis* has been reported in research groups in Brazil (Arnhold, 2008; Kurosawa et al., 2017; Santos et al., 2019; Amaral Júnior et al., 2019), and worldwide (Belcher et al., 2012; Hussain et al., 2016; Mubeen et al., 2017). However constant monitoring is necessary, as is the continuous search for new genotypes, since variability in the pathogen can result in the breakdown of genetic resistance.

To develop resistant cultivars, one of the first steps is to identify sources of resistance. Once resistance has been identified in popcorn inbred lines, it is possible to use them as parents to develop resistant hybrids from one or just a few crosses. Identification of resistant lines with good agronomic performance and their use as hybrid genitors is therefore extremely useful for popcorn cultivation. This is especially clear when dealing with the resistance to *Bipolaris maydis* due to the additive genetic effects associated with resistance (Hallauer et al., 2010; Kumar et al., 2016; Li et al., 2018; Santos et al., 2019).

The process of selecting the parents is one of the main stages in a plant breeding program (Oliboni et al., 2012). Several methods can be used for this selection, but diallel analysis is the most common genetic design used. However, this method can be impractical when there are many lines to be tested due to the high quantity of resultant crosses (Pena et al., 2016; de Souza Neto et al., 2015).

Other methods, such as top-cross and circulant diallel crosses, can also be used to reduce the total number of crosses (Mafra et al., 2018; Pena et al., 2016; Vivas et al., 2014). However, to obtain results with these methods, pre-breeding is a commonly practiced alternative to increase the success rate in the selection of a small number of promising parent lines. The evaluation of genotypes from different genealogies comprises a pre-breeding strategy that will ideally result in 1) identification of sources of resistance to SCLB; 2) identification of groups of lines with contrasting resistance mechanisms; and 3) identification of promising groups for the development of superior popcorn hybrids.

This research therefore aims to investigate the performance of inbred lines in stage S₇, with regard to their resistance to SCLB, grain yield potential, and popping expansion.

Materials and methods

Thirty-five lines of popcorn in stage S₇ (lines in the seventh generation of self-pollination) obtained from 13 different genealogies (Table 1) were evaluated for resistance to SCLB. A randomized block design with four replicates was used. The experiment was carried out at two sites. At the first evaluation site, the experiment was carried out in November 2017, in the Federal

Institute of Espírito Santo (Instituto Federal do Espírito Santo) – Alegre Campus, in Alegre, in the southern region of the state of Espírito Santo, latitude 20°45', longitude 41°27', at an altitude of 134 m. The overall mean temperature in the region was 23.1 °C, and the average annual precipitation was 1341 mm (Lima et al., 2008). At the second evaluation site, the experiment was carried out in December 2018, at the State Technical School of Agriculture Antônio Sarlo (Colégio Estadual

Table 1 Description of the genealogy, climatic adaptation, and developing institution of the lines used in this study. UEM - Universidade Estadual de Maringá; UENF - Universidade Estadual do Norte Fluminense Darcy Ribeiro

Lines	Genealogy	Climate adaptation	Development Institution
P4	Raças Sul-americanas	Temperate/ Tropical	UEM
P3	Composto CMS-42	Temperate/ Tropical	UEM
P2	Composto CMS-42	Temperate/ Tropical	UEM
L76	Viçosa	Temperate/ Tropical	UENF
L71	BRS-Angela	Tropical	UENF
L70	BRS-Angela	Tropical	UENF
L695	UENF-14	Tropical	UENF
L693	UENF-14	Tropical	UENF
L692	UENF-14	Tropical	UENF
L691	UENF-14	Tropical	UENF
L689	UENF-14	Tropical	UENF
L688	UENF-14	Tropical	UENF
L686	UENF-14	Tropical	UENF
L685	UENF-14	Tropical	UENF
L683	UENF-14	Tropical	UENF
L682	UENF-14	Tropical	UENF
L624	PA 091	Temperate/ Tropical	UENF
L623	PA 091	Temperate/ Tropical	UENF
L55	Beija-flor	Temperate/ Tropical	UENF
L51	Beija-flor	Temperate/ Tropical	UENF
L509	PA 170 Roxo	Temperate/ Tropical	UENF
L477	SE 013	Tropical	UEM
L476	SE 013	Tropical	UEM
L363	PR 023	Tropical	UEM
L294	URUG 298	Temperate	UENF
L293	URUG 298	Temperate	UENF
L292	URUG 298	Temperate	UENF
L270	PARA 172	Temperate	UENF
L266	PARA 172	Temperate	UENF
L265	PARA 172	Temperate	UENF
L263	PARA 172	Temperate	UENF
L262	PARA 172	Temperate	UENF
L261	PARA 172	Temperate	UENF
L204	IAC 125	Temperate/ Tropical	UENF
L203	IAC 125	Temperate/ Tropical	UENF

Agrícola Antônio Sarlo), in Campos dos Goytacazes, in the northern region of the state of Rio de Janeiro, latitude 21° 45', longitude 41° 20', at an altitude of 11 m. The overall mean temperature in the region was 24.4 °C, and the average annual precipitation was 1007.5 mm (INMET, 2020).

The field was prepared with harrowing and furrowing, with fertilization in the sowing furrow in both sites. Each experimental unit consisted of 30 plants arranged in three rows of 2 m in length, with 0.90 m between the rows and 0.2 m between the plants. A plant density of five plants per meter was established. Agricultural practices, such as fertilization (sowing and top-dressing), irrigation, pest, and weed control, followed standard popcorn cultivation requirements.

Each lines' disease resistance was analyzed by estimating the incidence and severity of symptoms in each experimental unit from the five central plants. The evaluation was conducted on the thirtieth day after the start of flowering, under natural infection conditions. The incidence of *Bipolaris* blight in the plant (BI) was evaluated by counting the number of leaves with symptoms relative to the total number of leaves; the results were expressed as a percentage. The severity of *Bipolaris* blight on the leaf (SB) was evaluated visually according to the diagrammatic scale proposed by James (1971). The scale expresses disease severity between 0%, 1%, 5%, 25%, and 50% of the leaf area damaged. Disease severity was evaluated on the leaf attached to the first ear of each plant.

Besides the evaluation of incidence and severity, after harvest other agronomic traits were evaluated. Grain yield in kg.ha⁻¹ (GY) was estimated based on the mass of all plants' harvested grains from all plants within each experimental unit, standardized to 13% humidity. Popping expansion in mL.g⁻¹ (PE) was obtained after popping the grains. To pop the grains, two samples of 30 g of grain were collected from each experimental unit. Each sample was stored separately in paper bags, which were then heated in a microwave oven at 1000 watts for two minutes. The resulting volume obtained was measured in a volumetric cylinder of 1000 mL. The popping expansion was calculated by dividing the expansion volume by the initial grain mass (30 g).

The data were subjected to individual analysis of variance (for each environment). When a significant difference and homogeneity of variance was verified between environments (Hartley's F max test), a joint

analysis of variance was conducted following the randomized block design model in multiple environments (Cruz et al., 2012), according to the statistical model:

$$Y_{ijk} = \mu + B/E_{k(j)} + G_j + E_j + GE_{ij} + e_{ijk}$$

Y_{ijk} is the value observed in the plot corresponding to the i -th genotype allocated in the j -th environment in the k -th block. μ is the general constant, $B/E_{k(j)}$ is the effect of the k -th block in the j -th environment, G_j is the effect of the i -th genotype, E_j the effect of the j -th environment, GE_{ij} is the interactional effect between the i -th genotype with the j -th environment and e_{ijk} is the random error associated with the observation of Y_{ijk} . Anscombe and Tukey's test for the homogeneity of variance and Shapiro-Wilk test for the normality of residuals were used to investigate the assumptions underlying the analysis. The variable BS was transformed with the Box-Cox methodology (Box & Cox, 1964) using an adaptation expressed in the following equation:

$$f(y) = \frac{(1 + \sqrt{y})^\lambda - 1}{\lambda}$$

When a significant difference was found with the F-test, the Scott-Knott test for group means was applied at a p value of 0.05. Additionally, boxplots were made for the BI and BS variables, grouping the values estimated in each experimental unit of lines from the same genealogy to demonstrate the genealogy's potential by their performance.

The following genetic parameters were estimated according to Cruz et al. (2012). CV_g was obtained through the following equation:

$$CV_g = \frac{\sqrt{\phi g}}{Mean} \times 100$$

In this expression: CV_g is the coefficient of genetic variation, and ϕg is the genotype square component obtained through the following equation:

$$\phi g = \frac{MSG - MSR}{er}$$

where MSG is the mean square of genotype, MSR is the mean square of error, e is the number of environments, and r the number of replicates.

The following equation was used to estimate the coefficient of genotypic determination:

$$H^2 = \frac{\phi g}{MSG/er}$$

The relative variation coefficient was obtained by the relation between the coefficient of genetic variation and the coefficient of experimental variation. All analyses were performed using the R software (R Core Team, 2019).

Results

The individual analyses showed differences between the lines in all variables analyzed. Homogeneity of variance between environments permitted the joint analysis of the data from the two sites. The genotype x environment interaction was significant, indicating different responses of the lines in each environment (Table 2).

It was possible to visualize each genealogy's resistance to Southern corn leaf blight through boxplot analysis. For BI, the mean for each experimental unit varied between 16.07 and 97.14%, with an overall mean of 50.99% in environment 1 (Alegre-ES), and between 0 and 88.10%, with an overall mean of 39.23% in environment 2 (Campos dos Goytacazes-RJ). These values grouped by genealogy (Fig. 1). The populations Viçosa, Sul-americanas, SE-013, PR-023, PA-170-Roxo, PA-091, CMS-42, and Beija-flor contain more than 50% of the lines with means below the overall mean in

environment 1. For environment 2, the same was observed for UENF-14, Sul-americanas, SE-013, PR-023, Para-172, CMS-42, BRS-Angela, Beija-flor (Fig. 1). Five genealogies stood out in both environments: Sul-americanas, SE-013, PR-023, CMS-42, and Beija-flor.

BS levels ranged between 0 and 8.5% in environment 1, with a mean of 0.68%, and between 0 and 5.16% in environment 2, with an overall mean of 0.27% (Fig. 2). Sul-americanas, PA-170-Roxo, and PA-091 stood out, having a lower BS level than the overall mean in both environments (Fig. 2).

The joint analysis for each variable demonstrated a significant genotype x environment interaction. Thus, the groups of lines evaluated had a different response in each environment. This is confirmed by observing the group means (Figs. 3, 4, and 5). The results of BI and BS indicate that it is possible to identify groups with contrasting resistance to Southern corn leaf blight, and similarly for GY and PE.

The estimated genetic parameters H^2 , CV_g and CV_r , were high for all variables. The values larger than 1 for the relative coefficient of variation (CV_r) reflects the possibility of reaching gains with genetic breeding (Vencovsky & Barriga, 1992). Additionally, values close to 1 for H^2 demonstrate greater genetic variability. This fact implies higher reliability to distinguish contrasting genotypes due to the low environmental influence perceived in the experiments, as the variance found was mainly caused by genetic factors (Table 2).

Table 2 Summary of joint analysis of variance and estimates of genetic parameters for incidence and severity of Southern corn leaf blight (SCLB), grain yield (GY), and popping expansion (PE)

Source of variation	Degrees of freedom	Mean square			
		Incidence of SCLB	Severity of SCLB	GY	PE
Block/Environment	6	619.8**	0.03633**	397222***	31.9**
Genotypes (G)	34	1622.5**	0.07724**	3429569**	210.2**
Environments (E)	1	9681**	0.59274**	30818497**	52.3*
G x E	34	407.8**	0.01128**	336655**	47.7**
Error	204	115.4	0.000476	80,083	8.78
Overall Mean		45.108	0.26 (0.48) ^m	1064	15.81
CVe		23.82	26.83	26.6	18.74
H^2		0.93	0.99	0.98	0.95
CVg		89.3	106.8	60.81	91.7
CVr		3.7	3.9	2.28	4.9

*Significant at 5% by the F test; ** Significant at 1% by the F test; Overall Mean = Overall mean of the variable; ^m = Original average; CVe = Coefficient of experimental variation; H^2 = Coefficient of genotypic determination; CVg = Coefficient of genetic variation; CVr = Coefficient of relative variation

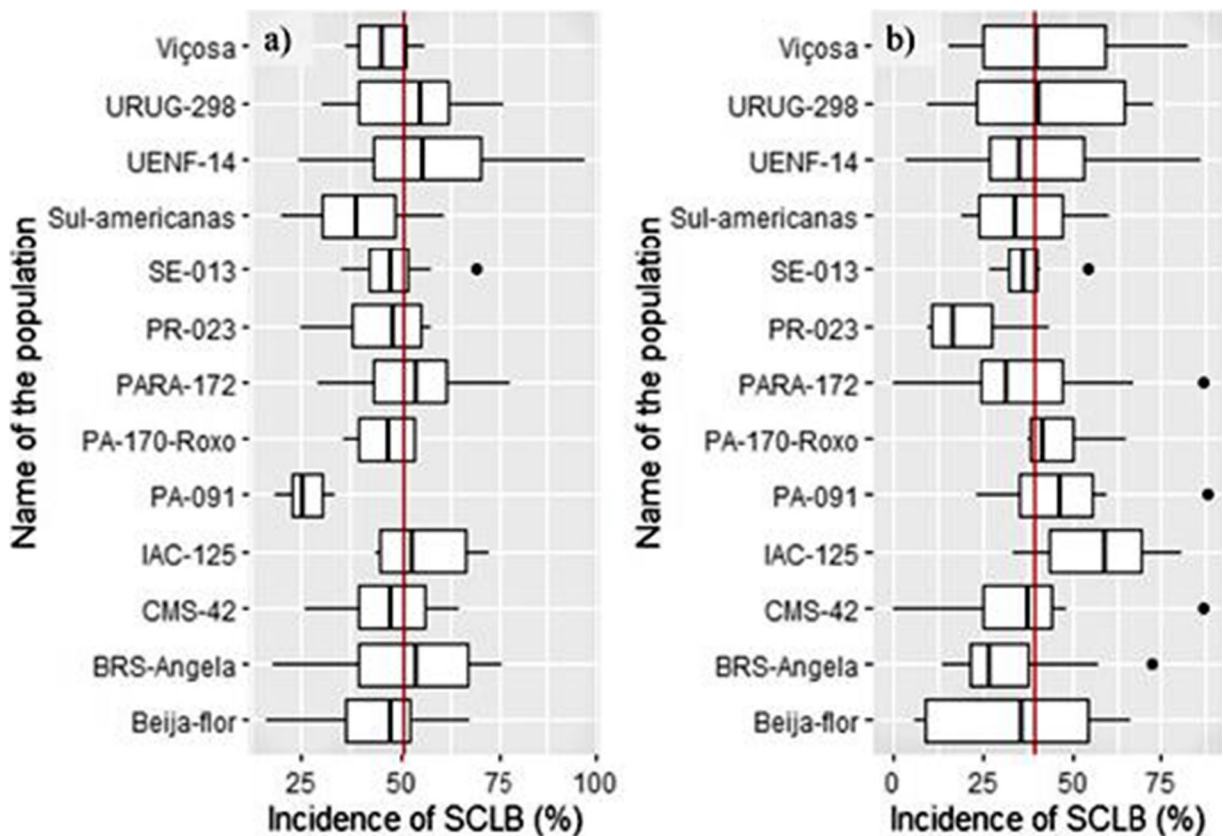


Fig. 1 Distribution of popcorn genealogies according to the response of their respective lines regarding the incidence of Southern corn leaf blight (SCLB). **a** Environment 1 (Alegre-ES) and **b** Environment 2 (Campos dos Goytacazes-RJ). Red line indicates the overall mean

Based on the BI means, the Scott-Knott test showed that four groups could be distinguished in both environments (Fig. 3). Lines L623, L624 and L55 (mean of 28.40%) had lower incidences in environment 1, while L623, L624, L262, L263, L265 and L270 (mean of 14.40%) had lower incidences in environment 2 (Fig. 3).

Comparing the two environments, line L693 was present in the group with the highest incidence, while L624 and L623 were in the group with the lowest incidence. The correlation between environments for BI was 0.65.

For BS, the clustering of means by the Scott-Knott test resulted in four groups for each environment (Fig. 4). In environment 1, lines L685, L624 and L623 showed lower disease severity (average of 0.48%), whereas in environment 2 (Fig. 4), lines P4, L624, L623, L270, L265, and L204 had the lowest severity (mean of 0.013%). Lines L693 and L51 had higher severity in both environments, and L624 and L623 had lower severity. The correlation between environments for BS was 0.62.

For both traits, the clustering of means by the Scott-Knott statistical test separated the 35 lines into five groups for GY and seven groups for PE respectively in environment 1. The minimum and maximum values observed were of 176.85 kg.ha⁻¹ and 3933.69 kg.ha⁻¹ with a mean of 1395.76 kg.ha⁻¹ for GY, and 4 ml.g⁻¹ and 33 ml.g⁻¹ with a mean of 15 ml.g⁻¹ for PE, respectively (Fig. 5 a).

Six lines had the highest PE: L294, L688, L71, L689, L204 and L686 (mean of 23.86 ml.g⁻¹). For GY, only line L261 had a high average value. Line P3 had the second highest grain yield. The lines with the greatest potential for SCLB resistance are those in the two groups with low BI and BS in each environment (Figs. 3 and 4). Three of these lines were present in the group with the highest PE performance; they are L688, L689 and L204 (mean of 24.5 ml.g⁻¹ for PE; 48.2 for BI and 0.27 for BS). Seven lines were in the group with the second highest PE: L685, L509, L76, L683, L55, L292 and L70 (mean of 24.5 ml.g⁻¹ for PE; 48.2 for BI and 0.27 for BS) (Fig. 5 a). None of the lines with the

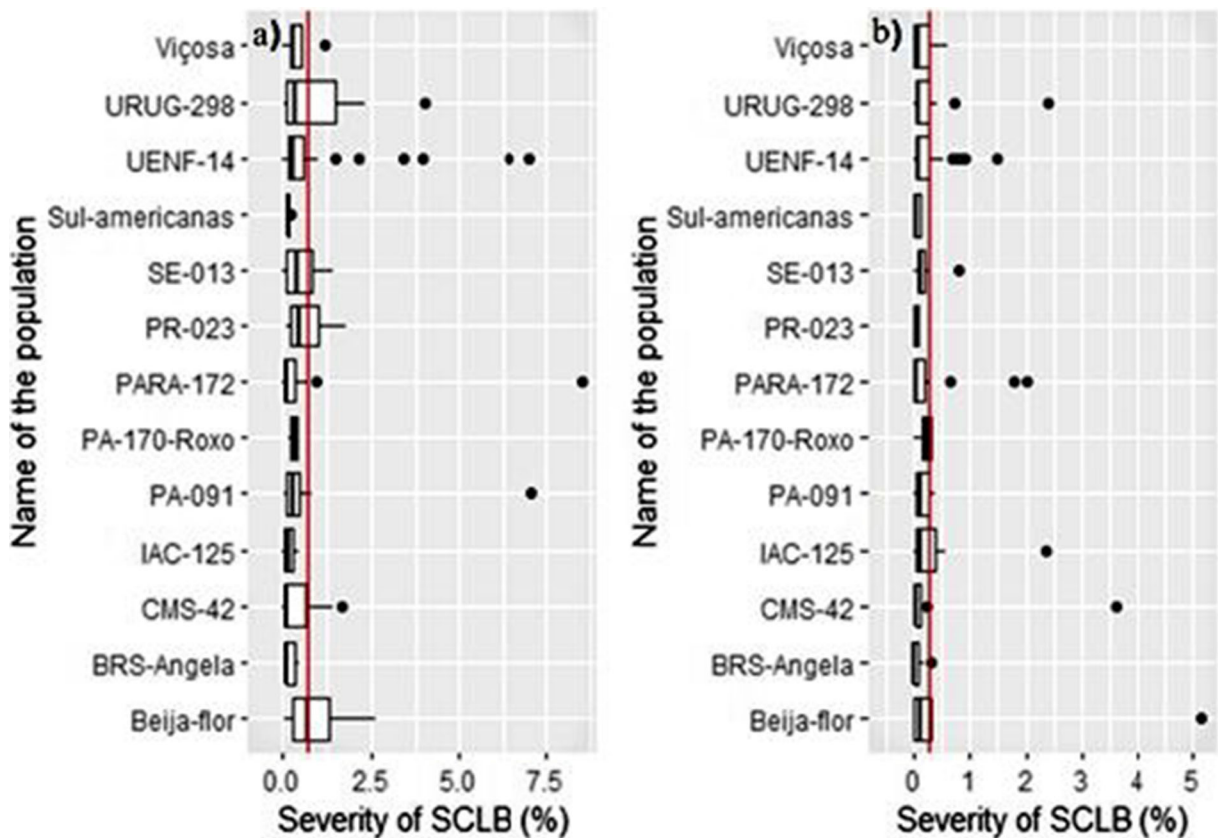


Fig. 2 Distribution of popcorn genealogies according to the response of their respective lines regarding the severity of Southern corn leaf blight (SCLB). **a** Environment 1 (Alegre-ES) and **b** Environment 2 (Campos dos Goytacazes-RJ). Red line indicates the overall mean

potential for resistance were present in the GY group with the highest value (Fig. 5 a).

In Environment 2, the 35 lines were classified in four groups for PE and five groups for GY by the Scott-Knott statistic test. The minimum and maximum values were 34.46 kg.ha⁻¹ and 2863.93 kg.ha⁻¹ with an average of 627.85 kg.ha⁻¹ for GY, and 5 ml.g⁻¹ and 26 ml.g⁻¹ with a mean value of 15 ml.g⁻¹ for PE, respectively (Fig. 5 b). The lines with the highest PE were L689, L70, L71, L509, L688, L292, L683, and L204 (mean of 23.11 g.mL⁻¹). For GY, only the P4 line formed the group with the highest grain yield. The groups with the lowest GY included the highest number of genotypes. Thirteen lines of the total with resistance potential were in both groups with high PE potential. The lines L204, L292, L509, L683, and L70 (mean 22.7 ml.g⁻¹ for PE; 29.4 for BI and 0.06 for BS) were in the group with the highest PE value, and the lines L263, L270, P3, L691, L266, P4, L477, and P2 (mean 18 ml.g⁻¹ for PE; 26.6 for BI and 0.05 for BS) had in the second highest PE value (Fig. 5 b).

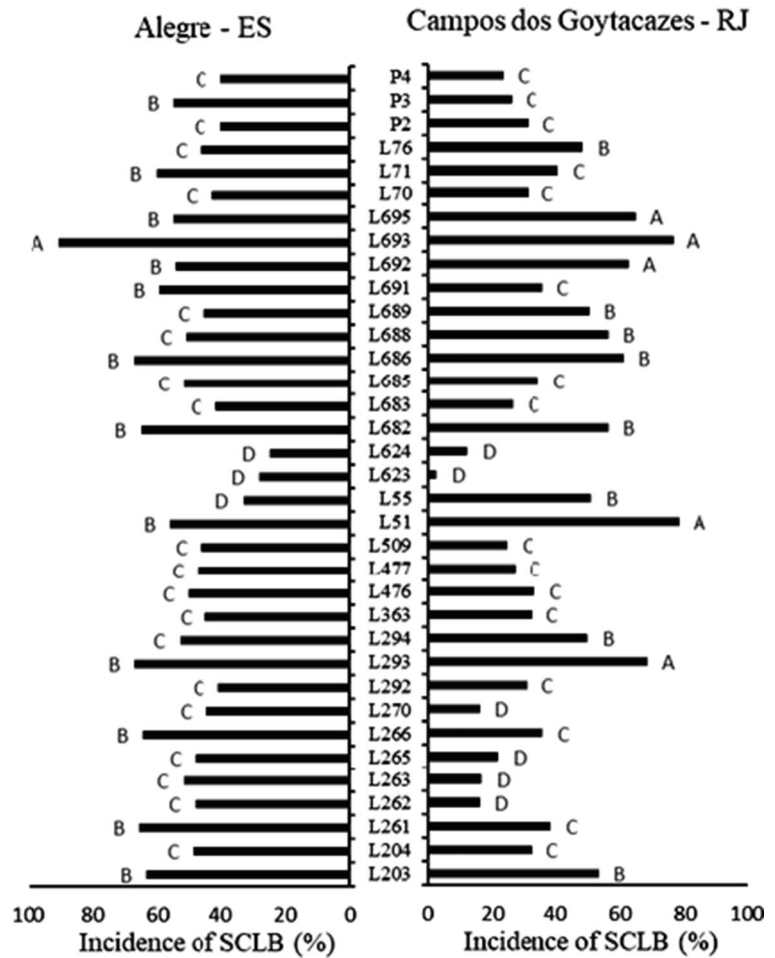
Discussion

Based on the results, it was possible to identify lines that are possible candidate sources of resistance for Southern corn leaf blight. It was also possible to identify lines with higher and lower levels of resistance. This identification may help future research in plant breeding, such as genetic inheritance studies and a pre-selection of promising genotypes for hybrids development.

In all variables with significant F-test effects, distinct groups were observed when comparing group means. This indicated variability between the lines for BI, BS, PE and GY (Table 2), allowing the selection of desirable lines. The different responses between the lines for BI and BS likely reflect genetic variability in resistance. The high values also reinforce the genetic response for CVg and H² as does the value above one for CVr, which expresses higher variation due to genetic effects (Vencovsky, 1987).

Genetic variability for SCLB and other leaf diseases has also been detected in popcorn germplasm (Arnhold,

Fig. 3 Distribution of popcorn lines concerning the incidence of Southern Corn Leaf Blight. Means followed by the same letters represent a statistically homogenous group according to the Scott-Knott algorithm



2008), most recently in a group of lines of the germplasm bank of the State University of Northern Rio de Janeiro (Universidade Estadual do Norte Fluminense – UENF) (Amaral Júnior et al., 2019; Kurosawa et al., 2018). It is worth noting that some of the lines evaluated in this research were obtained from populations evaluated and identified with resistance to Southern corn leaf blight by Kurosawa et al. (2018). Additionally, in this research, the lines were evaluated in two distinct geographic regions, a different approach from previous studies.

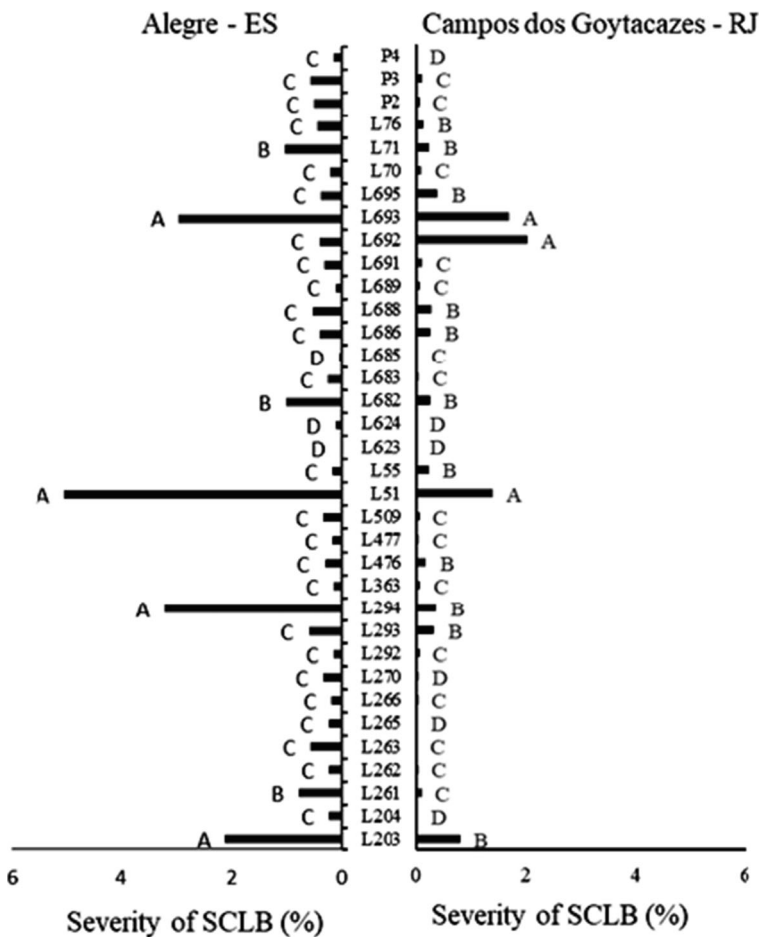
The natural occurrence level of the disease in both of the two environments did not affect the detection of promising material, because SCLB was observed in all treatments, indicating its occurrence in all experimental areas. Also, research carried out by Kurosawa et al. (2018), Santos et al. (2019) and Amaral Júnior et al. (2019) has previously demonstrated the natural occurrence of SCLB in these experimental areas.

Srivastava et al. (2017) stated that screening sources of resistance could be done with a high number of genotypes in field conditions with a disease's natural occurrence. Following this procedure should eliminate more susceptible material and uncover the small number of genotypes with high resistance potential.

Considering both environments, the following lines were in the two groups with higher resistance: P4, P2; L70; L685; L683; L624; L623; L509; L477; L363; L292; L270; L265; L263; L262; and L204. These 16 lines represented 45.72% of the total evaluated.

Considering the results, we highlight lines L624 and L623 which have high potential as gene donors for resistance to Southern corn leaf blight. These lines descend from the population PA – 091, formed from advanced generations of a commercial North-American hybrid. Since it originated in commercial material, it is believed that these lines may have inherited genetic resistance to Southern corn leaf blight,

Fig. 4 Distribution of popcorn lines concerning the severity of Southern Corn Leaf Blight. Means followed by the same letters represent a statistically homogenous group according to the Scott-Knott algorithm



as this disease occurs yearly in corn crops of North America (Bruns, 2017).

The remaining lines selected with resistance potential were from: Sul Americanas (P4); CMS-42 (P2), a

population that was selected for its resistance to leaf diseases (Pacheco et al., 1998); BRS-Angela (L70), an enhanced and registered variety selected for resistance to leaf diseases (Pacheco et al., 2005); UENF-14 (L685

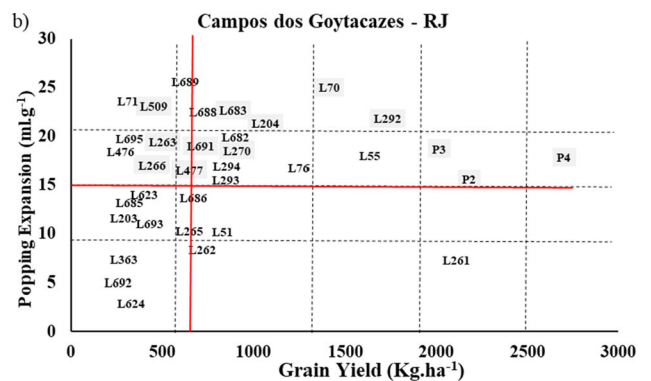
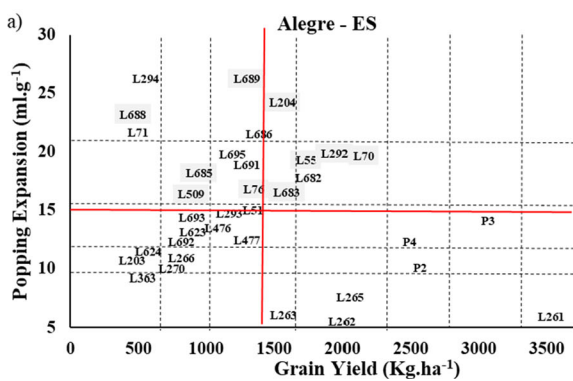


Fig. 5 Distribution of popcorn lines for the grain yield (GY) on the x-axis and popping expansion (PE) on the y-axis. Horizontal lines delimit the limit of similar groups for PE and vertical lines for GY formed by the Scott-Knott algorithm. Outstanding lines are

part of the upper groups for SCLB incidence and severity, simultaneously. **a** Environment 1 (Alegre-ES) and **b** Environment 2 (Campos dos Goytacazes-RJ). Red line indicates the overall mean

and L683), an enhanced and registered variety submitted to recurrent selection cycles (Amaral Júnior et al., 2013); PA-170-Roxo (L509); SE013 (L447); PR-023 (L363); URUG-298 (L292); PARA-172 (L270, L265, L263, L262, and L204). This last genealogy was identified by Kurosawa et al. (2018) for its resistance to *B. maydis*. More recently, Saluci et al. (2020) also showed its resistance in a group of partially endogamic lines from this genealogy. Finally, the genealogy IAC-125 (L204) is a population obtained from the commercial hybrid IAC-125.

Studies identifying resistance genes in corn generally use material from germplasm banks. For instance, some studies aiming to identify resistant sources to canker on corn culm (Nicoli et al., 2016), Southern corn rust (Kurosawa et al., 2016), white spot, and Southern corn rust (Teixeira et al., 2017), ear rot (Kurosawa et al., 2017), Southern and turcicum leaf blights (Kurosawa et al., 2018) use such germplasm bank material.

The results show contrasting levels of disease in the lines L624 and L623 (Resistant) and L693 (Susceptible). From our findings, we suggest the crosses L624 x L693 and L623 x L693 for future research there crosses can also be used as positive and negative controls for disease occurrence in experimental sites. This permits a better characterization and evaluation of genotypes regarding disease occurrence.

Among the most important agronomic traits for the popcorn crop are GY and PE. Other important traits such as plant height, ear height, ear weight, and 100-grain weight are positively related to GY and thus can be selected indirectly (Nardino et al., 2016). A major complexity when selecting genotypes for breeding is the negative correlation between GY and PE (Cabral et al., 2016; Nardino et al., 2016).

Figure 5 presents the cartesian coordinates of each line for each environment concerning GY and PE. In these graphs, we see that some genotypes in the group with a high PE were also present in the group with high resistance to Southern corn leaf blight. Based on Fig. 5, we indicate 18 lines as the most promising for combining PE and resistance: L204 (IAC 125); L263, L266, L270, L292 (PARA 172); L477 (SE 013); L509 (PA-170-Roxo); L55 (Beija-flor); L691, L683, L688, L689, L685 (UENF-14); L76 (Viçosa); L70 (BRS-Angela); P2, P3 (Compound CMS-42), and P4 (Raças Sul Americanas). This group contains representatives from ten of the studied genealogies. The performance of its lines can be traced to the history of their genealogies. For

instance, IAC 125, Beija-flor, UENF-14, Viçosa, BRS-Angela, Compound CMS-42, and Sul Americanas are genealogies with a history of selection and enhancement (Amaral Júnior et al., 2013; Miranda et al., 2003; Pacheco et al., 1998; Pacheco et al., 2005). Such history influences the high number of favorable genes for the main traits of popcorn cultivation, which leads to a good performance of these lines in our research.

Within this group, we identify a group composed of five lines, all with a desirable phenotype in both environments, lines L509, L204, L683, L292, and L70. This group of genotypes contains lines with good performance for PE as well as resistance, that are distributed in different groups of GY.

Popping expansion has a predominantly additive genetic control (Dofing et al., 1991; Pereira & Amaral Júnior, 2001). Thus, it is in the interest of breeders to test crosses for this trait. Some studies have demonstrated that the hybrid resistance performance depends on progenitor lines' resistance. The results of Kumar et al. (2016) suggest that hybrids from crosses of lines that are susceptible to Southern corn leaf blight are also susceptible. Crosses with lines that contrast in their resistance are usually moderately resistant. These results are associated with predominantly additive effects in the genetic control of resistance to Southern corn leaf blight (Kumar et al., 2016; Li et al., 2018; Santos et al., 2019). Conversely, GY normally presents high gain in crosses due to heterosis (Barreto et al., 2012; Pereira & Amaral Júnior, 2001).

Conclusions

In this study we demonstrated that pre-selection of lines from different genealogies made it possible to identify L623 and L624 as a promising source of resistance to SCLB. Lines L623 and L624 (R) and L693 (S) were identified as contrasting in terms of their reaction to SCLB, and could be used in studies exploring the inheritance of SCLB resistance. Lines L509, L204, L683, L292 and L70 formed a group with greater potential to obtain hybrids, having superior performance for both popping expansion and resistance to SCLB.

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Declarations

Ethics approval Not applicable.

Consent to participate The authors agree to participate.

Consent for publication All authors have approved the manuscript and agreed on its submission to the European Journal of Plant Pathology.

Conflict of interest The authors declare no conflict of interest.

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