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Resistance to multiple leaf diseases in popcorn lines with potential for baby corn production

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ABSTRACT. The cultivation of special corns, such as baby corn, has had a positive influence on the economy of the country. Despite its importance, there is still a need for studies aimed at increasing production and planting areas of the crop. Phytosanitary studies are of particular interest, as the cultivation of such crops is susceptible to a series of pathogens, such as *Bipolaris maydis*, *Exserohilum turcicum*, and *Puccinia polysora*. The use of resistant cultivars is the most effective way to prevent the occurrence of these diseases. Thus, the present study aimed to identify popcorn lines that have the potential for baby corn production and are resistant to the main leaf diseases that affect the crop. The experiment was conducted in randomized blocks with four replications of 30 lines in each area, during two planting seasons. The area was located at the Federal Institute of Espírito Santo (IFES) Campus of Alegre, situated in Rive district, Espírito Santo State, Brazil. Using the obtained data, the area under the disease progress curve was obtained. Subsequently, analysis of the joint variance of the data was conducted, and when a significant effect was found, a grouping of means test was conducted. The Mahalanobis distance for each pair of lines was also calculated, and the genetic distance matrix was used to construct a dendrogram using the UPGMA method. Considering the averages obtained for the three diseases (Southern corn leaf blight, Northern corn leaf blight, and Southern rust), lines L61, L63, L65, L683, L684, L685, L691, L694, and L695 were identified as possible donors of resistance alleles for multiple diseases. Multivariate analysis efficiently grouped the lines L61, L63, L684, L685, and L691, which are described as most resistant in the univariate analysis.

Keyword: baby corn; Northern corn leaf blight; Southern corn leaf blight; Southern rust; *Zea mays.*

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Introduction

Corn (*Zea mays* L.) is cultivated throughout Brazil, and is prominent owing to its diverse uses, among which is the cultivation of special corns, such as baby corn. Such cultivation refers to female inflorescences of any type of corn that are harvested after the emission of the stigma-style (Targanski & Tsutsumi, 2017) during the initial development stage, before pollination.

Baby corn is of particular interest as an alternative crop that can be used to diversify production and increase profitability, especially for small producers. The possibility may introduce gains four- to five-fold greater than those produced by corn destined for grain (Ranjan, Ahmed, Das, Ranjan, & Mishra, 2013). In addition, the corn sowing density for this approach can be up to three-fold higher than that of common corn cultivation (Carvalho, Von Pinho, & Pereira Filho, 2002). For the production of this special type of corn, sweet corn and popcorn have been used. The latter has the advantages of a smaller size, early ripening, uniform flowering, and prolificity (Thakur, Sharma, & Pathik, 2000).

However, despite the economic importance of corn, there are still few studies on special corns, notably baby corn (Scapim, Pacheco, Tonet, Braccini, & Pinto, 2010). This highlights the need for studies aiming at increasing production and planting areas of the crop. In particular, the phytosanitary nature of the cultivation needs elucidation, as the culture is susceptible to a series of pathogens, among which *Exserohilum turcicum* (Pass.) K.J. Leonard & E.G. Suggs and *Bipolaris maydis* (Nisik and Miyake) Shoemaker, are the causal agents of Northern corn leaf blight and Southern corn leaf blight, respectively; and *Puccinia polysora* is the causal agent of Southern rust. In general, these leaf diseases reduce the photosynthetic capacity of the plants, resulting in a shortened life cycle, reduction in the productive potential of the crops, diminished leaf area, decreased vigor and weight of the grains, premature aging, and lodging (Brito, Pinho, Sousa Filho, & Altoé, 2008; Costa, Da Silva, & Cota, 2013).

Several strategies have been utilized as control measures for these diseases; among which, the planting of resistant varieties is considered the most effective alternative, as their use does not generate additional costs for the producer and does not have a negative impact on the environment (Santos et al., 2016). For common corn, breeding programs aimed at resistance to leaf diseases have already been established; however, studies on special corns are lacking (Kurosawa et al., 2016; Kurosawa et al., 2017; Kurosawa et al., 2018). Therefore, the objective of the present study was to evaluate the incidence and severity of diseases in popcorn lines that have the potential for baby corn production.

Material and methods

Two competition trials were conducted in experimental areas found at the Espírito Santo Federal Institute (IFES) Campus de Alegre, located in Rive district, Espírito Santo State, Brazil (latitude: 20°45′44″ S; longitude: 41°27′43″ W; altitude: 134 m): the first in the summer growing season (2017/2018) and the second in the winter growing season (2018). The climate of the region is "Aw" type according to the Köppen classification, with a dry season in winter, annual rainfall around 1,200 mm, and an average annual temperature of 23°C (Lima, Silva, Oliveira, Cecílio, & Xavier, 2008). Overall, the annual climate variability is well characterized and is associated with the seasons. During the summer season (2017/2018), an average temperature of approximately 26.12°C was obtained, with an average rainfall of 5.39 mm (Figure 1A and B). In the winter season (2018), an average temperature of 22.33°C was obtained, with an average rainfall of 0.25 mm (Figure 1C and D).

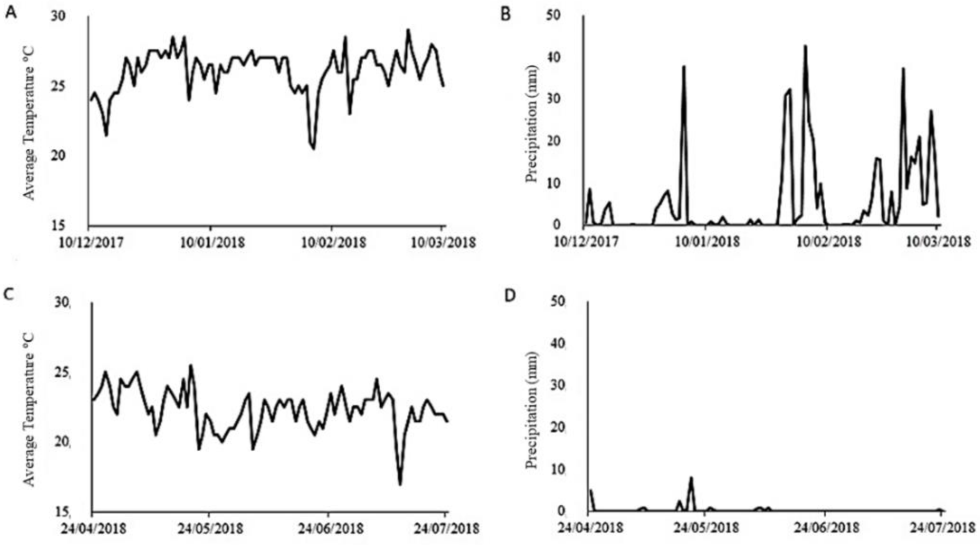

Figure 1. Average temperature and precipitation during popcorn cultivation in Alegre, ES, in two different seasons: December 2017 to March 2018 (A and B); April to July 2018 (C and D).

Thirty popcorn lines (Table 1) with potential for baby corn production were used in the present study, since they were shown to be prolific in previous studies. The experimental design was a randomized complete block design (RCB) with four replicants, totaling 120 experimental plots. Each experimental plot consisted of one line of 2 m in length and line spacing of 0.8 m, using a standard cultivar as a border. The total area of the experimental zone was 384 m^2, with a usable area of 192 m^2.

The soil was prepared by plowing and harrowing. After preparation, a portable sprinkler irrigation system with movable sides was installed in the area of the experiment. For planting, poultry litter was used for organic fertilization at a rate of 6 t ha^{-1} (Pereira, Hafle, Oliveira, Oliveira, & Gomes, 2012). Weed control was performed mechanically as needed. Pathogen infection occurred spontaneously, given the history of the area and planting of corn in areas adjacent to the experiment.

Table 1. Genealogies of evaluated popcorn lines with potential for baby corn production.

Lines	Genealogy	Type	Institution of Origin
L61	BRS-Angela	Open Pollinated Variety	Embrapa
L63	BRS-Angela	Open Pollinated Variety	Embrapa
L65	BRS-Angela	Open Pollinated Variety	Embrapa
L69	BRS-Angela	Open Pollinated Variety	Embrapa
L70	BRS-Angela	Open Pollinated Variety	Embrapa
L203	IAC-125	Hybrid	IAC
L204	IAC-125	Hybrid	IAC
L261	PARA-172	Open Pollinated Variety	CIMMYT
L270	PARA-172	Open Pollinated Variety	CIMMYT
L363	PR-023	Open Pollinated Variety	UEM
L476	SE-023	Open Pollinated Variety	UEM
L477	SE-023	Open Pollinated Variety	UEM
L623	PA-091	Open Pollinated Variety	UEM
L681	UENF-14	Open Pollinated Variety	UENF
L682	UENF-14	Open Pollinated Variety	UENF
L683	UENF-14	Open Pollinated Variety	UENF
L684	UENF-14	Open Pollinated Variety	UENF
L685	UENF-14	Open Pollinated Variety	UENF
L686	UENF-14	Open Pollinated Variety	UENF
L688	UENF-14	Open Pollinated Variety	UENF
L689	UENF-14	Open Pollinated Variety	UENF
L691	UENF-14	Open Pollinated Variety	UENF
L692	UENF-14	Open Pollinated Variety	UENF
L693	UENF-14	Open Pollinated Variety	UENF
L694	UENF-14	Open Pollinated Variety	UENF
L695	UENF-14	Open Pollinated Variety	UENF
L696	UENF-14	Open Pollinated Variety	UENF
P2	CMS-42	Composites	EMBRAPA
P3	CMS-42	Composites	EMBRAPA
P9	IAC-112	Hybrid	IAC

CIMMYT, Centro Internacional para el Mejoramiento de Maíz y Trigo; EMBRAPA, *Empresa Brasileira de Pesquisa Agropecuária*; IAC, *Instituto Agronômico de Campinas*; UEM, *Universidade Estadual de Maringá*; UENF, *Universidade Estadual do Norte Fluminense Darcy Ribeiro*.

The reactions of the lines to the diseases were evaluated by estimating the incidence and severity of symptoms. Four evaluations were performed within 7 days of the male flowering season, taking the five central plants of each plot. To evaluate the incidence of diseases in the whole plant, the scale adopted by Agroceres (1996) was used. For the severity of Southern rust (*P. polysora*) on the first ear leaf, the modified Cobb scale (Chester, 1950) was used. For the severity of Southern corn leaf blight (*B. maydis*), the diagrammatic scale proposed by James (1971) was used. For the severity of Northern corn leaf blight (*E. turcicum*), the diagrammatic scale proposed by Vieira et al. (2013) was used.

Data obtained from long-term evaluations were used to establish the area under the disease progress curve (AUDPC) for each disease, according to the Shaner and Finney (1977) equation. Using the AUDPC data, a joint variance analysis of the data for each variable was conducted considering the two experiments. When a significant effect was found, grouping tests were conducted (Scott-Knott at the 0.05 probability level). Mahalanobis distances were calculated for all line pairs using the AUDPC variables that were determined significant by ANOVA. Based on the genetic distance matrix, a dendrogram was constructed using the unweighted pair group method with arithmetic mean (UPGMA). The fit between the distance matrix and the dendrogram was estimated using the cophenetic correlation coefficient (CCC) developed by Sokal and Rohlf (1962). All data analyses were performed using Genes software (Cruz, 2013).

Results and discussion

Analysis of variance showed significant differences ($p < 0.05$) between lines based on the AUDPC estimated for the incidence and severity of *B. maydis* (Southern corn leaf blight, SCLB), *E. turcicum* (Northern corn leaf blight, NCLB), and *P. polysora* (Southern rust, SR). The existence of a significant difference indicates that when working with the lines evaluated in this study, it is possible to select those with the highest resistance level for each of the three diseases studied. It is believed that the resistance present in the ancestry (Pacheco et al., 1998; Pacheco et al., 2005; Amaral Júnior et al., 2013; Ribeiro et al., 2016; Kurosawa et al., 2016; 2018) was transmitted to inbred lines. This population improvement process has been one of the strategies adopted to obtain lineages and, later, superior hybrids. Based on the results obtained by the joint analysis, it was observed that the line and environmental interaction were significant for all variables. Thus, subsequent analyses were conducted considering each environment in isolation.

In the analyses conducted for each crop season, differences were observed between lines for variables associated with SR resistance only in the experiment conducted during the summer season. In contrast, significant differences between lines for variables associated with SCLB and NCLB resistance were only observed during the winter season. This may be due to environmental conditions of the summer season favoring SR and disadvantaging the incidence of NCLB and SCLB. During the winter season, the opposite occurred, and the incidence of SR was disadvantaged.

In the present study, it was observed that the summer season was the best for distinguishing genotypes for resistance to SR. To determine resistance to NCLB and SCLB, the winter season was when genotypes were better differentiated. These results are believed to be due to environmental conditions that favor the development of the different diseases during each season (Figure 1). High humidity and temperatures between 25 and 35°C support the emergence of the pathogen for SR (Godoy et al., 2003), consistent with the findings of the present study, in which the summer growing season favored the development of the disease. The winter growing season favored the emergence of NCLB and SCLB, since temperatures between 18 and 27°C and between 22 and 30°C, respectively, favor the appearance of these diseases (Richard & Stuart, 2005).

According to Melching (1975), at lower temperatures, *P. polysora* requires more time to produce pustules, which may explain the lower SR intensity during the winter season obtained in the present study. The results found in this study are in line with those obtained by Kurosawa et al. (2016), who observed lower SR intensity during winter cultivation, when compared to that during summer cultivation. Cunha, Negreiros, Alves, and Torres (2019) also reported a greater severity of *P. polysora* during summer cultivation. These results demonstrate that summer cultivation favors the occurrence of *P. polysora* and suggest that to evaluate corn resistance to SR, experiments in summer crops should be prioritized. In the Scott-Knott cluster analysis conducted during this season, it was possible to observe the formation of three groups for the area under the disease progress curve for incidence (AUIPC) and the area under the disease progress curve for severity (AUSPC) of SR. The groups of lines that presented the highest values for AUIPC of SR and, therefore, higher susceptibility levels, were formed by L692 and L689, which comprised groups A and B, respectively. The other lines comprised group C and were resistant to the disease, with an average of 22.44 (Table 2). Based on the AUSPC of SR during the summer season, lines L692 and L689 (group A) and L69, L70, L623, L688, and P2 (group B) presented the highest susceptibility levels, with an average of 100.73. The other lines, composing group C, possessed the lowest average rust severity, with an average value of 2.58 (Table 2).

Resistance to SR is governed by a few genes with the greatest resistance effect, and resistance is attributed to incomplete dominant or dominant alleles (Holland, Uhr, Jeffers, & Goodman, 1998, Brewbaker et al., 2011). These favorable genes may be inherited by future generations (Colombo, Vaz-de-Melo, Taubinger, Tavares, & Silva, 2014). Considering the above determination, that is, resistance is ruled by a few genes and expressed in the presence of dominant alleles, lines identified as resistant in the present study can be considered as candidate parental lines that are promising for the incorporation of rust resistance from simple crossings. In terms of breeding, susceptible lines, although not favorable sources of alleles for resistance breeding in hybrids, can be used as testers for the creation of genetic designs aimed to discriminate parents with high resistance levels. According to Borém and Miranda (2013), narrow genetic testers, who are poor in relation to the number of favorable alleles for the character under study, are testers that best discriminate potential parents.

Considering the two crop seasons, as well as the AUDPC values for the incidence and severity of SR, the lines L61, L63, L65, L203, L204, L261, L270, L363, L476, L477 L681, L682, L683, L684, L685, L686, L691, L693, L694, L695, L696, P3, and P9 stood out as most promising for this study. The lines indicated in the group with the highest resistance come from the following genealogies: BRS-Angela, an open-pollinated variety, from six cycles of recurrent selection of CMS-43 (Pacheco et al., 2001), considered to be moderately tolerant to SR (Vieira et al., 2009); the IAC-125 hybrid, which is moderately susceptible to disease (Scapim et al., 2010); PARA-172, an open-pollinated population, originating from CIMMYT; PR-023, an open-pollinated variety from UEM, on which there have been no studies on rust resistance; SE-023, on which there have been no studies on disease resistance; UENF-14, an open-pollinated population that originated from the UNB-1 varietal, and on which there have been no studies on disease resistance; CMS-42, an open-pollinated variety, which was developed by EMBRAPA (Pacheco, Gama, Lopes, & Santos, 1992); and hybrid IAC-112, on which there have also been no studies on SR resistance.

Table 2. Area under the disease progress curve for incidence (AUIPC) and severity (AUSPC) of *Puccinia polysora* (Southern rust, SR) evaluated in popcorn lines with potential for baby corn production.

Lines	Area under the incidence progress curve of Southern rust				Area under the severity progress curve of Southern rust			
	First season		Second season		First season		Second season	
L61	3.94	C*	7.00	A	0.00	C	12.25	A
L63	0.68	C	6.60	A	0.00	C	12.25	A
L65	22.42	C	5.43	A	13.65	C	4.90	A
L69	38.85	C	5.74	A	83.83	B	27.13	A
L70	219.89	C	0.00	A	59.33	B	1.05	A
L203	1.93	C	4.74	A	0.00	C	17.85	A
L204	2.63	C	2.00	A	0.00	C	7.35	A
L261	0.88	C	13.21	A	0.00	C	11.11	A
L270	0.53	C	3.90	A	0.53	C	5.43	A
L363	1.75	C	0.84	A	1.05	C	4.73	A
L476	0.21	C	9.84	A	0.35	C	19.99	A
L477	28.39	C	12.74	A	7.00	C	11.55	A
L623	28.68	C	2.15	A	22.17	B	0.18	A
L681	1.45	C	0.53	A	0.70	C	0.88	A
L682	6.58	C	0.00	A	0.00	C	0.18	A
L683	0.35	C	1.89	A	0.00	C	5.08	A
L684	5.51	C	0.00	A	0.53	C	0.00	A
L685	0.00	C	11.73	A	0.00	C	6.30	A
L686	38.33	C	0.00	A	12.51	C	0.00	A
L688	61.58	C	1.05	A	50.40	B	6.48	A
L689	303.42	B	26.72	A	263.29	A	25.03	A
L691	18.11	C	2.96	A	5.25	C	0.96	A
L692	589.23	A	20.74	A	203.18	A	16.98	A
L693	0.00	C	11.94	A	0.00	C	1.58	A
L694	55.30	C	0.51	A	8.93	C	1.58	A
L695	8.30	C	5.20	A	0.00	C	13.65	A
L696	10.03	C	0.54	A	5.78	C	2.98	A
P2	7.33	C	13.65	A	22.93	B	4.29	A
P3	40.64	C	0.14	A	0.53	C	0.00	A
P9	23.98	C	4.45	A	1.66	C	11.20	A

*Averages followed by the same letter constitute a homogeneous group by the Scott-Knott cluster test at 0.05 probability.

A significant effect was only observed for NCBL-related variables evaluated during the winter season. During the summer season, for areas under the disease progress curve for incidence (AUIPC) and severity (AUSPC) of NCLB, the treatments did not differ statistically from each other. For this disease, the mean AUIPC was 36.22 and the mean AUSPC was 20.08. Similar results were found by Julliati and Souza (2005), who evaluated corn hybrids and found no differences for the variable AUDPC, calculated based on the severity of NCLB. According to Fancelli and Dourado Neto (2000), the highest severity of NCLB occurs during the sowing and planting seasons, during which significant effects were observed. In general, the severity during the winter season was higher than that during the summer season. Fernandes and Oliveira (2000) stated that some diseases, such as NCLB, occur more intensely during winter cultivation, causing greater damage when infecting plants during flowering. During the winter season (Figure 1), it can be observed that temperatures were lower than during the summer season, which favored the development of the pathogen for NCLB. Therefore, it is noted that winter cultivation is advantageous for evaluating the resistance of corn genotypes to *E. turcicum*.

The cluster test showed the formation of two groups based on the AUIPC of NCLB, evaluated during the winter season (Table 3). The lines, L623, L695, P3, L689, L691, L692, L693, L684, L685, L686, L61, L63, L65, L69, and L70, were allocated to the group with the lowest averages and, therefore, the highest resistance level. The lines allocated to the highest resistance group were obtained from different genealogies, namely, PA-091, UENF-14, CMS-42, and BRS-Angela. Resistance to *E. turcicum* has already been reported in the populations (genealogies) UENF-14, CMS-42, and BRS-Angela (Pacheco et al., 2001; Scapim et al., 2002; Amaral Júnior et al., 2013; Ribeiro et al., 2016). Therefore, the existence of resistance genes and alleles in these populations has been observed and this information suggests that these lines have inherited the most favorable alleles and best resistance to the studied diseases. The possibility of obtaining superior hybrids can also be inferred, since there are resistant lines from different genealogies, making it possible to explore heterosis. According to Santos et al. (2019), non-additive gene effects are more important for the characteristics related to NCLB resistance; therefore, hybridization is the most suitable option for obtaining productive and resistant genotypes.

The lines that were allocated to the group with the greatest resistance based on the AUIPC also stood out with resistance when analyzing the means of the AUSPC. For this variable, obtained during the winter season, three groups were formed (Table 3). The lowest intensity group was formed by lines L623, P3, L689, L691, L692, L693, L694, L695, L683, L684, L695, L686, L61, L63, L65, L69, and L70. Of these, only lines L683 and L694 were not also allocated to the lowest AUIPC group of NCLB. This indicates a possible correlation between these two characteristics.

Table 3. Area under the disease progress curve for incidence (AUIPC) and severity (AUSPC) of *Exserohilum turcicum* (Northern corn leaf blight, NCLB) evaluated in popcorn lines with potential for baby corn production.

Lines	Area under the incidence progress curve of NCLB				Area under the severity progress curve of NCLB			
	First season		Second season		First season		Second season	
L61	14.91	A*	62.09	B	21.00	A	25.11	C
L63	8.10	A	35.58	B	2.59	A	6.42	C
L65	53.64	A	4.97	B	27.55	A	2.99	C
L69	43.56	A	53.06	B	35.70	A	7.25	C
L70	138.97	A	86.84	B	63.47	A	23.84	C
L203	8.79	A	187.64	A	4.52	A	108.10	B
L204	37.01	A	218.77	A	17.34	A	154.02	A
L261	6.74	A	153.67	A	4.24	A	118.14	B
L270	35.67	A	135.08	A	58.45	A	96.09	B
L363	14.21	A	221.41	A	13.48	A	139.44	B
L476	2.26	A	233.89	A	5.02	A	241.32	A
L477	34.41	A	155.51	A	23.59	A	98.98	B
L623	6.66	A	39.87	B	37.21	A	14.95	C
L681	33.93	A	162.26	A	19.18	A	93.49	B
L682	19.27	A	230.53	A	6.83	A	110.32	B
L683	24.33	A	107.03	A	1.89	A	52.10	C
L684	94.90	A	27.62	B	46.53	A	19.93	C
L685	15.47	A	9.40	B	8.07	A	3.42	C
L686	12.41	A	39.57	B	2.52	A	17.90	C
L688	15.63	A	98.47	A	2.59	A	98.79	B
L689	27.30	A	39.88	B	7.00	A	16.28	C
L691	1.26	A	22.45	B	0.56	A	3.54	C
L692	81.08	A	45.22	B	41.06	A	21.23	C
L693	8.93	A	32.95	B	0.00	A	3.06	C
L694	34.00	A	132.60	A	17.99	A	41.79	C
L695	23.40	A	15.24	B	7.35	A	16.26	C
L696	18.18	A	227.89	A	3.76	A	110.18	B
P2	111.13	A	336.23	A	36.49	A	229.58	A
P3	43.79	A	16.01	B	46.76	A	10.38	C
P9	116.67	A	161.39	A	39.67	A	62.88	B

*Averages followed by the same letter constitute a homogeneous group by the Scott-Knott cluster test at 0.05 probability.

Similar to the findings observed for resistance to *E. turcicum* (NCLB), when analyzing the resistance characteristics for *B. maydis* (SCLB), no significant effect was observed for lines during the summer season. During the winter season, based on the AUIPC to SCLB resistance, three groups were formed (Table 4). The lowest average group was composed of the lines L69, L691, L694, P2, P9, L681, L682, L683, L684, L685, L204, L261, L270, L363, L61, and L63. These lines are from the following genealogies: BRS-Angela, UENF 14, CMS-42, IAC 112, IAC 125, and PARA 172. From these populations, Kurosawa et al. (2017) reported that PARA-172 is considered promising for resistance to NCLB and SCLB. The authors also reported the potential for resistance to SCLB in strains L61, L63, and P2. SCLB has not been extensively studied in popcorn, there are limited evaluations of scarce genotypes (Kurosawa et al., 2017; 2020; Saluci et al., 2019). Therefore, the present study aimed to identify resistance to *B. maydis* (SCLB) in popcorn lines.

When analyzing AUSPC, three groups were formed. The lines L61, L63, L65, L69, L204, L261, L270, L363, L476, L623, L681, L682, L683, L684, L685, L689, L691, L694, L695, P2, and P9 were distinguished for their resistance to SCLB in this study. The group of lines with the lowest averages was developed from the genealogies CMS-42, IAC 112, UENF-14, IAC 125, PARA 172, PR-023, SE-023, and BRS-Angela. Few studies have investigated the resistance of popcorn to SCLB (Kurosawa et al., 2017; 2020; Saluci et al., 2019). Among the aforementioned studies, only Kurosawa et al. (2017) studied the resistance of strains and populations to *B. maydis* and indicated that populations ARZM-05083, ARZM-07049, and PARA-172 are a source of resistance to SCLB. However, there is a need for further studies to evaluate popcorn populations for resistance to *B. maydis*. When selecting a population with SCLB resistance characteristics, it may be improved by the addition of resistance and productivity genes, for later extraction of lines and hybrid production.

Table 4. Area under the disease progress curve for incidence (AUIPC) and severity (AUSPC) of *Bipolaris maydis* (Southern corn leaf blight, SCLB) evaluated in popcorn lines with potential for baby corn production.

Lines	Area under the incidence progress curve of SCLB				Area under the severity progress curve of SCLB			
	First season		Second season		First season		Second season	
L61	28.89	A*	71.33	C	11.64	A	21.98	C
L63	2.42	A	31.68	C	0.88	A	27.21	C
L65	10.50	A	166.99	B	5.78	A	45.33	C
L69	32.18	A	78.33	C	26.78	A	39.20	C
L70	19.57	A	166.90	B	45.50	A	77.35	B
L203	0.44	A	209.06	B	0.00	A	85.58	B
L204	30.00	A	80.94	C	9.45	A	28.96	C
L261	5.78	A	57.09	C	39.73	A	21.61	C
L270	10.90	A	12.44	C	0.53	A	4.80	C
L363	6.91	A	51.59	C	2.63	A	35.14	C
L476	12.81	A	139.89	B	5.69	A	60.74	C
L477	34.86	A	141.52	B	5.43	A	34.91	C
L623	46.24	A	122.62	B	19.25	A	56.33	C
L681	48.14	A	121.22	C	15.05	A	27.23	C
L682	14.44	A	93.01	C	1.40	A	49.35	C
L683	37.52	A	89.88	C	1.05	A	20.34	C
L684	8.65	A	28.12	C	4.29	A	14.00	C
L685	0.00	A	46.66	C	0.00	A	17.80	C
L686	93.54	A	230.43	A	33.60	A	81.99	B
L688	55.95	A	292.95	A	5.78	A	104.90	B
L689	1.75	A	148.54	B	2.28	A	56.14	C
L691	28.89	A	108.13	C	2.63	A	34.13	C
L692	37.99	A	269.37	A	19.25	A	158.00	A
L693	0.00	A	294.46	A	0.00	A	82.20	B
L694	65.54	A	134.59	C	15.93	A	35.18	C
L695	9.35	A	198.99	B	0.00	A	54.53	C
L696	79.54	A	260.23	A	109.99	A	109.11	B
P2	42.44	A	45.78	C	50.23	A	30.10	C
P3	27.34	A	318.92	A	11.03	A	206.68	A
P9	20.27	A	57.37	C	16.80	A	19.44	C

*Averages followed by the same letter constitute a homogeneous group by the Scott-Knott cluster test at 0.05 probability.

Santos et al. (2019) found the importance of the genetic effects of dominance in the control of the resistance characteristics against *B. maydis*. This is corroborated by studies performed by Carson, Stuber, and Senior (2004) that observed that resistance to SCLB was most influenced by non-additive effects. Therefore, it is opportune to obtain hybrids by heterosis, since the lines highlighted for resistance come from different genealogies.

In general, considering the area under the disease progress curve obtained for the severity of the three diseases, lines L61, L63, L65, L683, L684, L685, L691, L694, and L695, can be identified as possible allele donors for resistance to multiple diseases. In the dendrogram formed based on the studied variables, it was considered as a cutoff point at a distance of 53%, thus forming five groups (Figure 2). The cophenetic correlation coefficient was 0.89, indicating high consistency of the grouping performed (Cruz & Carneiro, 2003; Araújo et al., 2014).

The largest distances were found between the L691-P3, L61-L691, and L61-L686 lines. Cluster analysis points to genotypes that are most likely to be parental, reducing the number of crosses required in a breeding program beyond the increase of heterosis (Mohammadi & Prasanna, 2003; Rigon, Capuani, & Rigon, 2015). These distances represent the highest degree of dissimilarity between these lines and are, therefore, considered candidates for the generation of superior hybrids. L61, L63, L684, L685, and L691 were identified as the most resistant and formed group 1. The L692 lines, susceptible to SR and SCLB constituted group 2. Group 3 was formed by the L689 line, which is susceptible to SR, and moderately resistant to SCLB. Group 4 was comprised of the lines L476 and P2, which were resistant to SCLB, moderately resistant to SR, and susceptible to NCLB. Group 5 was formed by the P3 line, which was susceptible to SCLB, and moderately resistant to SR and NCLB.

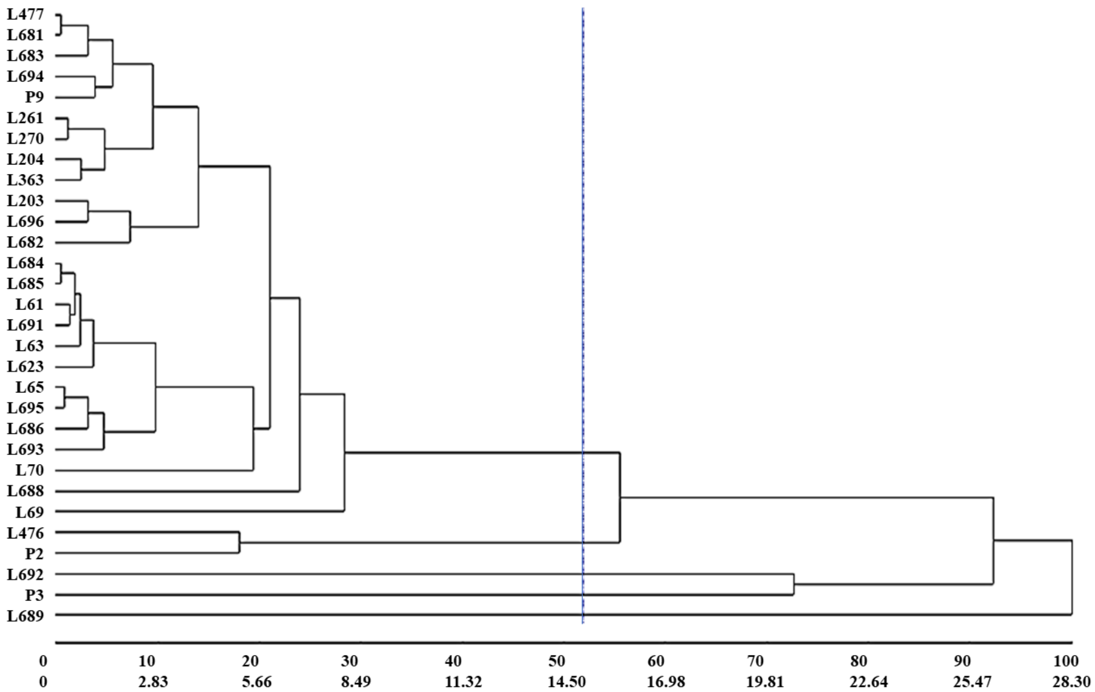

Figure 2. Dendrogram obtained by UPGMA clustering method, from genetic dissimilarity measurements of 30 baby corn lines.

The lines composed of group 1 (L61, L63, L684, L685, and L691) were the most resistant, and possibly have the potential for superior hybrid generation. In previous studies, Mafra et al. (2018) reported the resistance of lines L61 and L63 to SR, which are present in group 1. The lines present in group 1 come from the BRS-Angela and UENF-14 populations that are distinct genealogies, which allows for an increase in heterosis, since it is usually increased along with the genetic distance between parents (Borém & Miranda, 2013).

The populations mentioned above, in addition to serving as sources of resistance to multiple diseases, have the potential for increased productivity (Scapim et al., 2010; Amaral Júnior et al., 2013). Thus, this information is important for aspects, including the extraction of elite strains, which can be used in breeding programs aimed at obtaining resistant and productive genotypes. Another consideration is population improvement, which ensures genetic variability in the populations under study and promotes the displacement of the mean of the trait in the desired direction, through the continuous increase in the frequency of favorable alleles in the population.

Conclusion

The warmest and rainiest season provided the best conditions to distinguish genotypes for resistance to Southern rust, and the coldest and driest season provided the best conditions to distinguish genotypes for resistance to Southern corn leaf blight and Northern corn leaf blight. The L61, L63, L634, L685, and L691 lines are favorable allele sources for resistance to multiple diseases. BRS-Angela and UENF-14 populations may be used to extract lines that show resistance alleles to multiple fungal diseases.

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