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ORIGINAL ARTICLE

Resistance and tolerance to *Exserohilum turcicum* in landrace sweet corn varieties from a diversity microcenter in Southern Brazil

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Abstract
Northern corn leaf blight (NCLB) is a major disease affecting maize worldwide. Understanding resistance and tolerance mechanisms is crucial for developing effective control strategies. This study evaluated genetic variability in landraces, the seed from the Far West of Santa Catarina (FWSC), known for their diverse traits, to assess their potential for resistance and tolerance to NCLB. Two experiments were conducted during the 2019/2020 season using a randomized block design with four replications. One experiment included inoculation with *Exserohilum turcicum* (2×10^3 spores mL^{-1}) without chemical control, while the other utilized fungicide (difenoconazole) to suppress the disease. Key traits assessed were incubation period (IP), latency period (LP), lesion type (LT), severity measured by the area under the disease progress curve (AUDPC), and corn ear productivity (Yield). Significant differences ($p \leq 0.001$) were observed among genotypes for LP and Yield in the absence of chemical control, highlighting the performance of landrace 2029A and the commercial variety BR401. Joint analyses for variables common to both experiments Yield and AUDPC revealed significant differences ($p \leq 0.005$) between treatments, allowing tolerance evaluation based on yield losses and disease severity increments. This is the first report of qualitative resistance genes in landraces in southern Brazil. These findings underscore the potential of landraces for germplasm conservation and breeding programs aimed at enhancing NCLB resistance and tolerance. The use of fungicide provided a baseline for comparing tolerance, demonstrating its relevance for assessing productivity under pathogen pressure.

Keywords The northern corn leaf blight · Landrace · Genetic Improvement · *Zea mays*

Introduction

Northern Corn Leaf Blight (NCLB), caused by the fungus *Exserohilum turcicum* (Pass.) KJ Leonard & Suggs (teleomorph *Setosphaeria turcica*), is considered one of the most limiting diseases in corn production. It affects various types of corn, including sweet corn, and occurs worldwide, with regions experiencing temperatures between 20 to 28 °C and high humidity being (Hooda et al. 2017; Thatcher et al. 2023). The lesions on affected leaves enlarge as the disease progresses, eventually resulting in severely damaged plants in susceptible varieties (Galiano-Carneiro and Miedaner 2017). Records show yield reductions due to NCLB ranging from 10% to over 50% (De Rossi et al. 2022), with the greatest losses occurring when the plant is attacked before tasseling. The percentage of productivity loss is attributed to reduced photosynthesis in the lesioned leaves.

Plants have developed two defense strategies, tolerance and resistance, against pathogens. The main difference lies in that tolerance reduces the negative impact of infection on the host's without affecting pathogen growth, whereas resistance directly inhibits pathogen growth (Mikaberidze and McDonald 2020). Understanding the effectiveness of these strategies in the presence and absence of fungicide applications is critical (Ceresini et al. 2024). This dual approach allows us to determine how well these landrace varieties can contribute to integrated disease management strategies (Thanopoulos et al. 2024). By assessing their performance under fungicide treatment, we can identify varieties that enhance resistance even when chemical control is employed, acknowledging that fungicides alone are often insufficient. Conversely, evaluating these varieties without fungicide provides insight into their potential for sustainable cultivation practices that rely on natural resistance mechanisms.

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The use of resistant varieties in combination with fungicide application and cultural management is the primary mode of NCLB control, with a predominant reliance on resistant varieties due to their cost-effectiveness and environmental sustainability (Galiano-Carneiro and Miedaner 2017). Qualitative resistance conferred by single genes or qualitative resistance conferred by multiple genes has been extensively documented. The first identified qualitative resistance gene for NCLB control was *Ht*1 in the 1960 s (Hooker 1963). Other characterized resistance genes, both dominant and recessive, include *Ht*2, *Ht*3, *ht*4, *HtM*, *HtP*, *HtNB*, *Htn*1, and *rt* (Welz and Geiger 2000; Ogliari et al. 2005; Galiano-Carneiro and Miedaner 2017; Navarro et al. 2020; Yang et al. 2021). The qualitative resistance genes present chlorotic-necrotic lesions or total resistance, as well as assist in quantitative resistance.. *Htn*1 gene which confers quantitative and partial resistance to NCLB by delaying the onset of lesion formation. However, reliance on varieties harboring these genes may lead to pathogen race selection, resulting in resistance breakdown. Therefore, it is imperative to have diverse sources of resistance genes available for maize breeding programs (Dinglasan et al. 2022; Thatcher et al. 2023).

Plants can tolerate pathogen infection in various ways, primarily through increased activities or processes, including leaf chlorophyll concentration, new leaf size, the number of new shoots, the duration infected leaves remain attached to the plant, and nutrient uptake – all processes directly related to productivity (Rios et al. 2017). Tolerance is often represented by the slope of a regression between host fitness and pathogen load (Pagán and García-Arenal 2018); the steeper the slope, the lower the tolerance of the evaluated genotypes (Little et al. 2010; Råberg 2014).

To ensure success in breeding programs aimed at resistance and tolerance, it is essential to identify varieties with these defense strategies, as well as effective sources of resistance. Locations with high disease pressure such as China, India, East and South Africa, and Latin America are ideal sites for disease development (Galiano-Carneiro and Miedaner 2017). Study identified different sources of resistance and their origins, with Colombia and Mexico being the only Latin American countries with registered sources (Hooda et al. 2017; Rashid et al. 2020).

In the Microcenter of Diversity in the Far West of Santa Catarina (FWSC), 1,513 landrace maize populations conserved in situ – *on farm* by farmers in this region were found (Costa et al. 2017). These populations may possess characteristics that aid in genetic improvement programs due to their remarkable adaptability to biotic and abiotic factors (Begna et al. 2022). Thus, they emerge as a promising alternative for safeguarding maize varieties, aiming to increase productivity and reduce dependence on agrochemicals. The objective of this study was to evaluate resistance and/or tolerance to *E. turcicum* in three landrace sweet corn varieties from the municipalities of Anchieta and Guaracha (FWSC), one access from BAG-Maize, and one commercial variety from EMBRAPA, and their relationship with and without fungicide management in sweet corn production. Exploring their relationship under both conditions is crucial because it allows us to assess the effectiveness of fungicide applications evaluated resistance and/or tolerance. This dual-condition approach can reveal the potential of landrace varieties to maintain productivity under low-input sustainable agricultural practices, reducing reliance on chemical treatments.

Materials and methods

Study location

The study included two experimental conditions: one with pathogen inoculation and no chemical control (experiment I), and another without pathogen inoculation but with fungicide application of difenoconazole (experiment II). Both experiments were conducted starting in (Summer-Fall/2020) at the Ressacada Experimental Farm of the Federal University of Santa Catarina (UFSC) in Florianopolis, SC, Brazil. According to the Köppen climate classification, the region falls under the'Cfa'climatic category. Specifically, it belongs to a sub-region characterized by a consistently humid subtropical climate, devoid of a dry season and with hot summers. During the experimental period (January 20 to May 30), During the experimental period, daily data on maximum temperature (Tmax), minimum temperature (Tmim), relative humidity (Ur) and precipitation were collected, by measurement of the meteorological station located at the Ressacada experimental farm.

Material vegetal and experimental design

Three landrace sweet corn varieties exhibiting the (*su*) allele, identified by Costa et al (2017) as conferring the sweet phenotype, originating from the municipalities of Anchieta (2255 A* and 2029 A*) and Guaraciaba (319 A*) in the state of FWSC, were included. In addition to these, two control varieties with the same genotype were included: the BR401 variety, developed by the Brazilian Agricultural Research Corporation—EMBRAPA, and a Cubano accession from the Germplasm Active Bank of Maize of the same institution.

A randomized complete block design was used for both experimental conditions, consisting of five treatments and four replications. The experimental plots were set up with three rows, each 3.0 m long, with a spacing of 0.8 m between rows. The seeding density was maintained at five seeds per linear meter, resulting in an experimental plot of 7.2 m^2**.** The experiment unit was the central plot, evaluating 13 plants, where the first and last plants were considered as borders**.** Fertilization was carried out in accordance with the Fertilization and Liming Manual for the States of Rio Grande do Sul and Santa Catarina (2004), based on the results of the analysis of soil.

Top dressing was carried out 40 days after sowing, when the plants were at the V7 and V9 stages. The control *Spodoptera frugiperda*, an insecticide based on spinosad-spinosyn, was applied. Manual weeding was done according to need.

Collection, storage, and inoculation of *E. turcicum*

Pathogenic *E. turcicum* was isolated from leaf tissue samples of infected maize collected from the Catarina variety at the Agricultural Research and Rural Extension Company of Santa Catarina in the Center for Agricultural Sciences, Florianópolis—SC. The infected tissue was kept in a moist chamber on Petri dishes at room temperature for 24 h. Fungal reproductive structures were then collected from parts of the leaf with higher sporulation, using a platinum loop. For the generation of monosporic cultures, conidia were carefully extracted using a histological needle, observed under a microscope, and transferred to plates containing potato dextrose agar culture medium, leaving one spore per plate (De Rossi et al. 2015).

Subsequently, monosporic cultures were maintained in a growth chamber (BOD, with a photoperiod and alternating temperature—Electrolux) at 25 °C and a 12-h photoperiod for fifteen days. Isolates were stored using the filter paper method at −20 °C. Inoculum production involved the inoculation of sterile sorghum seeds previously soaked in water (25 g of seeds; 40 ml of distilled water) with the isolate. The inoculated seeds were then incubated in the dark at 24 °C for three weeks. To complete grain colonization, the inoculated seeds were placed in a tray containing two damp paper towels, covered with plastic wrap, and kept in a moist chamber for seven days, maintaining the same temperature and photoperiod conditions. The inoculum suspension was prepared by adding 100 mL of sterile distilled water, followed by agitation, and the spore concentration was quantified (2×10^3 spores mL^{-1}) using a Neubauer chamber (De Rossi et al. 2015; Oliveira et al. 2022).

Preparation and application of treatments

The first experimental condition (experimental I) with inoculation was performed, a spore concentration of (2×10^3 spores mL^{-1}) 39 days after sowing, during the V_4 to V_6 vegetative stages. Inoculation involved the uniform distribution of the spore suspension, of spores were atomized over whole plants, carried out in the late afternoon under low light intensity and in the absence of precipitation (De Rossi et al. 2015; Oliveira et al. 2022). This experiment was conducted without chemical control.

In contrast, the second experimental condition (experimental II) did not include pathogen inoculation and was managed with a difenoconazole-based fungicide. Commercial fungicide formulated emulsible concentrate (EC). Was used, following the manufacturer's recommended dosage and spray volume. The selection of difenoconazole was based on its registration with the Ministério da Agricultura, Pecuária e Abastecimento for this specific crop and pathogen. Applications began 38 days after sowing, and the second application was performed when disease symptoms began to manifest. Notably, a third fungicide application proved unnecessary, as symptoms in this experiment appeared during the R_3 vegetative stage, close to the sweet corn harvest time. All applications were carried out using a portable commercial sprayer, with the applied volume adjusted according to the crop's developmental stage to ensure full coverage.

Epidemiological components and plant assessment

Plant assessments were conducted daily, starting after the inoculation of *E. turcicum*. The following epidemiological components were evaluated in both experiments (experimental I and II): disease severity through the area under the disease progress curve (AUDPC) and corn ear productivity (YIELD).

Assessments were conducted only in experiment I. Regarding lesion type (LT), plants were evaluated 14 days after inoculation, following the scale proposed and adapted by Ogliari et al. (2005). Plants were classified as resistant if they exhibited chlorotic-necrotic lesions or remained asymptomatic, and as susceptible if they displayed olive-green necrotic lesions. The incubation period (PI) was defined as the number of days between inoculation and lesion sporulation. The latency period (LP) was determined as the number of days between inoculation and the onset of the first disease symptoms (Ferreira et al. 2017). Disease severity (SEV) was assessed using the diagrammatic scale for the assessment of northern corn leaf blight (Vieira et al. 2014), with values ranging from 1 (no visible symptoms) to 9 (> 50% of leaves covered by lesions), and the data were used to calculate the area below of the disease progression curve (AUDPC). based on severity data obtained at each evaluation and applied to formula of Campbell and Madden (1990): $AUDPC = \sum(Yi + 1 + Yi)\ (Ti + 1 + Ti)/2$. yield was assessed during the milky grain stage when the grain has 70 to 80% moisture content. Where:

Yi severity of disease at time of evaluation,

Ti time of evaluation i;

ti + 1 time of evaluation i + 1 e;

n total number of observations.

Statistical analysis

Data were analyzed using analysis of variance (ANOVA), the collected data underwent verification of the assumptions of analysis of variance, and the Hartley Cochran C test, Hartley, Bartlett test was applied to assess variance homogeneity using the GENES program (Cruz 2016). Individual variance analyses were conducted for each environment, employing the fixed statistical-mathematical model: Yij = μ + Tj + Bi + Ɛij. Here, Yij represents the observation of the i-th treatment (i = 1, 2,…,9) within the j-th block (j = 1, 2, 3, 4), where μ denotes the overall mean, Tj signifies the effect of the i-th treatment, Bi represents the effect of the j-th block, and Ɛij represents the impact of experimental error.

For the joint analysis of the experiments, a random statistical-mathematical model was considered: Yijk = μ + Ti + Pj + TPij + Bjk + Ɛijk. In this model, Yijk represents the observation of the i-th treatment (i = 1, 2, …, 9) within the j-th block (j = 1, 2, 3, 4) and k-th environment (k = 1, 2, 3, 4); μ represents the overall mean; Ti signifies the treatment effect, k represents the environment effect, Taij denotes the treatment-environment interaction effect, bj (k) represents the block effect within the environments, and Ɛijk indicates the effect of experimental error.

Individual and joint statistical analyses were conducted using the GENES software (Cruz 2016). Variables showing significant differences among treatments at a significance level of 5% probability ($p \leq 0.05$) based on the F-test were subjected to the Tukey test at the same significance level.

Results and discussion

The maximum temperature and minimum temperature were 27.51 °C and 22.68 °C respectively, an average temperature of 25.68 °C, the average relative humidity was 71.48% and the precipitation accumulation was 329 mm. (Fig. 1). The amplitudes, in maximum and minimum temperatures as well as in humidity, present favorable conditions for the development of the pathogen *E. turcicum*. thus, allowing evaluations of the resistance and tolerance of sweet corn landraces and controls.

Experiment I

Individual analyses of the *E. turcicum* isolate used in the experiment revealed the presence of both resistant (chlorotic-necrotic lesions) and susceptible (necrotic lesions) types. landrace varieties 2255 A and 319 A, along with the commercial variety BR401, exhibited resistant reactions, suggesting the presence of at least one gene with a significant phenotypic effect. In contrast, landrace variety 2029 A and Cubano the BAG-Maize variety did not show these distinctive characteristics, indicating their susceptibility.

Individual variance analyses of the conducted experiments, according to the F-test, showed significant differences ($p < 0.001$) among the treatments evaluated regarding the latency period and productivity when treated with fungicide (Table 1). Regarding LP, the BR401 variety exhibited the highest value at 18.5 days, indistinguishable from the 319 A variety, which recorded a value of 17 days. The latter, in turn, did not show differences compared to the other varieties, with values of 16.8, 16.3, and 16.0 for the 2255 A, Cubano, and 2029 A varieties, respectively. Concerning corn ear productivity in the experiment managed with fungicide, the 2029 A variety showed the highest productivity at 9.9 t/ha^{-1}, with no significant difference from the Cubano (8.2 t/ha^{-1}). The 319 A (7.5 t/ha^{-1}) and BR401(6,5 t/ha^{-1}) varieties, with no significant difference from the Cubano and 2255 A varieties, exhibited yields of 6.0 t/ha^{-1}.

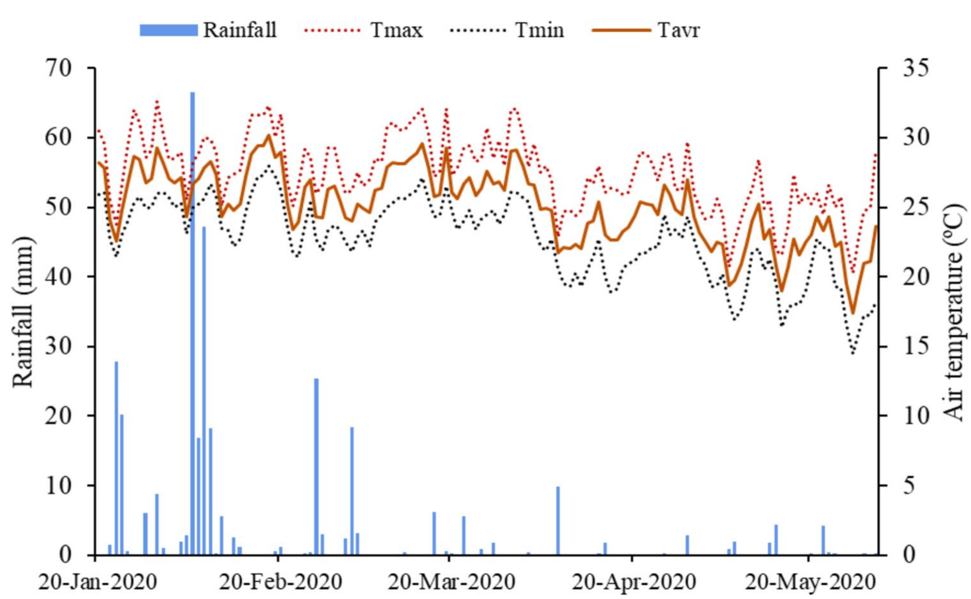

Fig. 1 Minimum temperatures (Tmin, °C), maximum temperatures (Tmax, °C), average air temperature (Tavr, °C) and precipitation (rainfall, mm) for two experiments evaluating landrace sweet corn during the experimental period in the 2020/2021 crop season in Florianopolis, Santa Catarina, Brazil

Table 1 Results of individual and joint variance analyses of two experiments evaluating landrace sweet corn for quantitative resistance to Northern Corn Leaf Blight and ear yield under two *Exserohilum turcicum* management systems during the 2020/2021 crop season in Florianopolis, Santa Catarina, Brazil

GENOTYPE[1]	Exp I[2]		Exp I		Exp I		Exp II[3]		MEA[6]		Exp I	Exp II		MEA		L.T[7]
	INCU		LATE		AUDPC[4]		AUDPC				YIELD[5] (t. ha^{-1})	YIELD (t. ha^{-1})				
2029 A	13.5		16.0	B	438.1		26.6		232.3		7. 3	9.9	a	8.6	A	S
2255 A	14.2		16.8	B	432.7		27.0		229.9		5. 5	6.0	c	5.8	B	R
319 A	15.0		17.0	AB	431.2		24.3		227.7		6. 5	7.5	bc	7.0	AB	R
BR 401	14.2		18.5	A	439.7		18.9		229.3		6. 0	6.5	bc	6.3	B	R
Cubano	14.0		16.3	B	449.8		21.6		235.7		8.1	8.2	ab	8.2	A	S
MEAN[8]	14.2		16.93		438.3	B	23.7	A			6.73	7.66				
Probability F-test [9]	27.64	ns	6.69	**	100		100				11.31	10.29	**			
VCe % (individual analysis)[10]	6.33		4.37		0.80		0.08				23.69	12.91				
VCe % (joint analysis) [11]									0.78					17.54		
Probability F-test G[12]									100	ns				0.26	**	
Probability F-test E[13]									0.005	**				11.07	ns	
Probability F-test Interaction G x E[14]									100	ns				34.05	ns	

[1] landrace sweet corn varieties from the westernmost region of Santa Catarina (2029 A. 2255 A. and 319 A) and two controls (BR401 and Cubano) from EMBRAPA; [2] Experiment inoculated with *E. turcicum* isolate from Florianopolis-SC. managed without chemical disease control; [3] Experiments conducted with chemical control of the pathogen; [4] Area under the disease progress curve (AUDPC). as a percentage of the affected area; estimated from four replications; [5] Ear Productivity (YIELD). in t. ha^{-1}. estimated from four replications; [6] Experiment mean; [7] Lesion type (S: susceptible—R: resistant); [8] Mean treatment of two experiments; [9] Probability of F-test (%) associated with differences between treatments of individual experiments; [10] Coefficient of variation (individual analyses); [11] Coefficient of variation (joint analyses); [12] Prob. F-test (%) associated with differences between genotypes; [13] Prob. F-test (%) associated with differences between experiments; and [14] Prob. F-test (%) associated with genotype x experiment interaction. Means followed by the same uppercase letters. in the rows and columns of joint analysis. do not differ by Tukey's test at 5% probability. Means followed by the same lowercase letters. in the columns of individual variance analyses per experiment. do not differ by Tukey's test at 5% probability. ** Significant at 1% by F-test; * Significant at 5% by F-test; ns not significant

AUDPC and yield in both experiments

The joint data analysis revealed a difference ($p \leq 0.001$) in the management of the experiments regarding the variable AUDPC. NCLB blight is a widely distributed disease across all corn-producing regions. Therefore, it was necessary to apply a fungicide in Experiment Two (with control) to keep the plants free from the pathogen and thus allow us to identify plants with resistance and/or tolerance to the northern corn leaf blight..

The experiment I showed a mean of 438.3, while the experiment II had a mean of 23.7 for the same variable (Table 1). Experiment I showed a mean 18.5 times higher than the overall mean of experiment II for the AUDPC evaluation. Regarding the variable YIELD, the varieties in the experiment II showed a difference ($p \leq 0.001$). The 2029 A variety had the highest yield at 9.9 t/ha^{-1}, with no significant difference compared to the Cubano varieties, with a mean of 8.2 t/ha^{-1}, and 319 A, with a mean of 7.5 t/ha^{-1}. These, in turn, showed no significant difference compared to the BR401 variety, with a mean of 6.5 t/ha^{-1}, and the 2255 A variety, which had an average yield of 6.0 t/ha^{-1}.

A comparative analysis of severity and yield variables was conducted at the R_3 phenological stage, comparing experiments I and II. Using these two variables, the average percentage reduction in ear yield was estimated for each genotype, considering the average percentage increase in Northern Corn Leaf Blight severity between experiments with the lowest (Exp. II) and highest (Exp. I) disease levels (Table 2).

Variety 2029 A exhibited the highest rate (1.87) of yield reduction for each unit increase in disease severity. Variety 319 A was ranked as the second treatment with one of the highest rates (0.91) of ear yield loss for each unit increase in disease severity, positioning itself close to the threshold between tolerant and intolerant categories (Table 2). Varieties 2255 A and BR 401 showed intermediate tolerance to the disease, with yield reduction rates of 0.41 and 0.45 per unit increase in leaf severity, respectively. On the other hand, the Cubano variety, despite exhibiting a leaf severity increase of over 22.8% from Exp. II to Exp. I practically showed no yield reduction (0.25%), demonstrating a significant capacity to tolerate the disease (rate of 0.01) without substantial yield losses.

The study of the genetic basis of resistance can be analyzed based on the type of lesion exhibited by the varieties in relation to the evaluated isolate of *E. turcicum*, given that the pathosystem studied fits into the gene-for-gene model proposed by Flor (1971). Thus, the presence of chlorotic-necrotic lesions in the varieties, the time elapsed from inoculation to lesion appearance, the low or even inhibition of sporulation, or even the absence of lesions (Camera et al. 2020). This phenotypic effect response present in the evaluated varieties is in accordance with the results presented in the literature for the *Ht*1 gene, which expresses necrosis and chlorosis (Bentolila et al. 1991). In the *Ht*2 gene, it presents chlorosis and small lesions, in the *Ht*3 gene, it reports chlorotic spots, and the *Ht*P gene can present complete resistance or chlorotic-necrotic lesions (Ogliari et al. 2005), depending on the plant's genetic background and pathogen race. Other dominant genes show specific defense reactions to infection, such as the *HtM* gene, which shows complete resistance (Robbins and Warren 1993). The *HtNB* and *Htn*1 genes, which are expressed by the decrease in the number of lesions (Wang et al. 2012; Navarro et al. 2020), as well as a lower number of lesions during the incubation period. Additionally, the only two recessive genes described in the literature may exhibit chlorotic rings (*ht*4 gene) and complete resistance or lesions with chlorotic halo (*rt* gene) (Ogliari et al. 2005).

Table 2 Severity (%) analysis of Northern Corn Leaf Blight and ear yield (t ha^{-1}) in landrace sweet corn varieties subjected to various management conditions for the fungal pathogen *Exserohilum turcicum* during the 2020/2021 season in Florianopolis, Santa Catarina, Brazil

Gen [1]	Experiment Management [2]	SEV (%) [3]	INCR SEV (%) [4]	Yield (t. ha^{-1}) [5]	Redution Yield (%) [6]	Tax [7]	Tolerance
2029 A	Exp I	19.60	13.7	7.38	25.6 7	1.87	More intolerant
	Exp II	5.90		9.93			
319 A	Exp I	20.45	15.02	6.51	13.89	0.91	close to the limit between tolerant and intolerant
	Exp II	5.40		7.56			
2255 A	Exp I	19.60	13.6	5.54	5.59	0.41	Intermediate tolerant
	Exp II	6.00		6.06			
BR 401	Exp I	21.05	16.85	6.05	7.64	0.45	Intermediate tolerant
	Exp II	4.20		6.55			
Cubano	Exp I	27.50	22.85	8.19	0.25	0.01	More tolerant
	Exp II	4.65		8.21			

[1] landrace sweet corn varieties from the westernmost region of Santa Catarina (2029 A. 2255 A. and 319 A) and two controls (BR401 and Cubano) provided by EMBRAPA; [2] Experiment management type (Experiment I—without chemical disease control and Experiment II—with chemical pathogen control); [3] Severity (SEV)—percentage of leaf area with lesions assessed at the R_3 phenological stage; [4] Increase Severity; [5] Ear Yield (PROD). in t. ha^{-1}. evaluated as green corn; [6] YIELD reduction rate for each unit increase in disease severity; [7] Reduction tax

Studies conducted at CIMMYT have shown improved lines for resistance to NCLB presenting highly resistant materials with medians of 14.23, 22.34, and 24.95, along with highly susceptible lines, with values of 84.91, 100.66, and 49.17 for the AUDPC trait (Ding et al. 2015). These findings are consistent with the results of the experiment with chemical control but differ in the results of the inoculated experiment, which showed higher values, the severity and progression of NCLB can be affected by the plant's development when it is hit by the fungus. Thus, maize plants can exhibit NCLB symptoms from the early stages of development (Ding et al. 2015).

The presence of the gene in the BR 401, 2255 A, and 319 A varieties did not allow differentiating the genotypes regarding the degree of resistance quantified by AUDPC, possibly because the pathogen affected the genotypes very early (Oliveira Jr. et al. 2006; Mayara Cazadini et al. 2022). Jamann et al. (2014) suggest that the gene of significant phenotypic effect may contribute to quantitative resistance even after the first has been overcome by the pathogen. Studies have found quantitative resistance QTL´s in the same region as the *Ht*2 gene or closely linked to its function (Dingerdissen et al. 1996; Chung et al. 2010). Welz and Geiger (2000), evaluating the incubation period and AACPD as important quantitative resistance components, identified QTLs and *Ht*1 and *Ht*2 genes, suggesting the presence of a group of major and minor genes closely related to plant resistance.

Based on the individualized analysis of variance by experiment, the genotypes differed significantly for ear productivity ($p \leq 0.05$) only in the chemically controlled experiment (Table 1). Reported yield reductions ranging from 10.5% to 50% in India. with the cultivation of susceptible hybrids (De Rossi et al. 2022).

Records of grain yield losses ranging from 10 to 30% were documented in studies conducted in Germany and from 15 to 30% in South Africa. Yield losses were much lower when plants were affected shortly after tasseling. Stated that sweet corn needs to be productive to meet industry and fresh consumption production needs, sweet corn production in Brazil is close to 13 t/ha^{-1}. being a very low production compared to similar conditions for the production of this type of corn (De Rossi et al. 2022). However, the results were very similar to those obtained in other studies, such as the one conducted by Oliveira Jr. et al. (2006) in the state of MG, which reported a yield of 6.91 t ha^{-1}.

The results of this study suggest a greater tendency for some treatments to exhibit tolerance mechanisms to the phytopathogen *E. turcicum*. (Argentel-Martínez et al. 2016) assessed wheat tolerance and recorded a decrease of less than 1.3 t ha^{-1} for tolerant and moderately tolerant varieties. In this study, four varieties (2255 A; 314 A; BR401, and Cubano) showed decreases lower than those reported in that study, with reductions of 0.5 t ha^{-1} in varieties 2255 A and BR 401, 1.0 t ha^{-1} in variety 319 A, and 0.1 t ha^{-1} in variety Cubano. indicating that it is necessary to know the mechanisms that these plants have that allow tolerance to the disease.

Conclusion

The landrace varieties 2255 A, 319 A, and the commercial variety BR401 from EMBRAPA exhibited lesions of the chlorotic-necrotic type, indicating the presence of qualitative resistance to the *E. turcicum* race used, being the first record of this type of gene, in landrace varieties in southern Brazil. The correlation between green corn productivity and severity indicates the inherent potential for resistance and/or tolerance of the sweet corn varieties 2255 A, Cubano, and BR401. This study highlights the potential of sweet corn landrace varieties as an alternative for *E. turcicum* control, exhibiting qualitative and/or quantitative resistance characteristics that provide an alternative for corn producers in the far west of Santa Catarina, as well as for conservation activities and genetic improvement programs.

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Author's contribution All authors whose names appear on the submission:

1) made substantial contributions to the conception or design of the work; or the acquisition, analysis, or interpretation of data; or the creation of new software used in the work; 2) drafted the work or revised it critically for important intellectual content; 3) approved the version to be published; and 4) agree to be accountable for all aspects of the work in ensuring that questions related to the accuracy or integrity of any part of the work are appropriately investigated and resolved.

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Data Availability Data will be made available on reasonable request.

Declarations

Conflict of interest On behalf of all authors, the corresponding author states that there is no conflict of interest.

Dataset The datasets generated during and/or analyses during the current study are available from the corresponding author on reasonable request.

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