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Rodolfo Vargas Castilhos[1](✉), Cirio Parizotto[2], Felipe Bermudez[1], Leandro do Prado Ribeiro[1] and Maria Cristina Canale[1]

[1] Empresa de Pesquisa Agropecuária e Extensão Rural de Santa Catarina – Centro de Pesquisa para Agricultura Familiar, Chapecó, SC.
Email: rodolfocastilhos@epagri.sc.gov.br; felipepereira@epagri.sc.gov.br; leandroribeiro@epagri.sc.gov.br; cristinacanale@epagri.sc.gov.br.

[2] Empresa de Pesquisa Agropecuária e Extensão Rural de Santa Catarina – Estação Experimental de Campos Novos, Campos Novos, SC.
Email: cirio@epagri.sc.gov.br.

✉ Corresponding author

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SEVERITY OF CORN STUNT DISEASE ON MAIZE GENOTYPES IN THE MIDWEST OF THE BRAZILIAN STATE OF SANTA CATARINA

Abstract – In an attempt to provide regionalized information about maize genotypes' response to corn stunt disease complex, this study evaluated the corn stunt disease severity and productivity of conventional (7) and transgenic (11) maize genotypes under natural infestation of its insect vector, *Dalbulus maidis* (Hemiptera: Cicadellidae). The work was carried out in Campos Novos, SC, Brazil, during the 2020/2021 crop season. In a randomized block design, the genotypes were sowed in experimental plots of 14 m^2, with four replicates (plot) per genotype. At 90 days after sowing, the severity of corn stunt disease was analyzed using a visual symptoms scale, while the maize productivity was assessed at physiological maturation. There was variability for response to stunt disease in the genotypes and a negative correlation between severity and grain yield. Among the conventional genotypes, P3456, FS055, SCS154 Fortuna, SCS156 Colorado, and SCS155 Catarina had lower severity of corn stunt disease. For the transgenic genotypes, AS1757 PRO3 and P3551 PWU were more resistant, while B2418 VYHR, AG9025 PRO3, and P1225 VYHR had high corn stunt disease severity. The corn stunt severity varied from 1 (absence of symptoms) in P3551 PWU to 4.8 (more than 75% of leaves with symptoms) in P1225 VYHR, while the lowest and highest yields were obtained for BG7056 (1,253.7 $kg.ha^{-1}$) and P3016 VYHR (9,794.6 $kg.ha^{-1}$), respectively. The genotypes with low corn stunt disease severity are suitable options for sowing in the Midwest region of Santa Catarina, Brazil, in conditions of high population pressure of *D. maidis.*

Keywords: *Zea mays*, spiroplasma, phytoplasma, *Dalbulus maidis*.

SEVERIDADE DE ENFEZAMENTOS EM GENÓTIPOS DE MILHO NO MEIO-OESTE DE SANTA CATARINA, BRAZIL.

Resumo - No intuito de disponibilizar informações acerca da resposta de genótipos de milho às doenças do complexo dos enfezamentos, avaliou-se neste estudo a severidade dos enfezamentos e a produtividade de genótipos de milho convencionais (7) e transgênicos (11), em condição de infestação natural do inseto-vetor *Dalbulus maidis* (Hemiptera: Cicadellidae). O trabalho foi realizado em Campos Novos, SC, Brazil, na safra agrícola 2020/21. Os genótipos foram semeados em parcelas de 14m^2 em delineamento de blocos ao acaso, com quatro repetições (parcela) para cada genótipo. Aos 90 dias após semeadura, a severidade dos enfezamentos foi avaliada utilizando escala visual de notas, enquanto a produtividade foi obtida após maturação fisiológica. A resposta aos enfezamentos variou entre os genótipos, e houve correlação negativa entre a severidade e a produtividade. Entre os genótipos convencionais, P3456, FS055, SCS154 Fortuna, SCS156 Colorado e SCS155 Catarina apresentaram a menor severidade de enfezamentos. Entre os genótipos transgênicos, AS1757 PRO3 e P3551 PWU apresentaram maior resistência, enquanto B2418 VYHR, AG9025 PRO3 e P1225 VYHR expressaram sintomas mais severos. A severidade dos enfezamentos variou de 1 (ausência de sintomas) em P3551 PWU até 4.8 (mais de 75% de folhas com sintomas) em P1225 VYHR, enquanto a menor e maior produtividade foram obtidas para BG7056 (1.253,7 $kg.ha^{-1}$) e P3016 VYHR (9.794,6 $kg.ha^{-1}$), respectivamente. Os cultivares com menor severidade de enfezamentos se constituem em boas opções para semeadura na região do Meio-Oeste Catarinense, Brasil, em condição de alta pressão populacional de *D. maidis*.

Palavras-chave: *Zea mays*, espiroplasma, fitoplasma, *Dalbulus maidis.*

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The mollicutes, *Spiroplasma kunkelii* and "*Candidatus* Phytoplasma asteris", are the causal agents of corn stunt spiroplasma (CSS) and maize bushy stunt phytoplasma (MBSP) diseases, respectively. These pathogens are responsible for the corn stunt complex and are among the most limiting diseases in maize (Sabato et al., 2014). These pathogens are transmitted by the corn leafhopper *Dalbulus maidis* (DeLong & Wolcott) (Hemiptera: Cicadellidae) in a persistent-propagative manner. The incidence of *D. maidis* and corn stunt disease in maize fields of the Brazilian State of Santa Catarina was relatively low until the 2020/21 season. After that, an intense outbreak of this insect and corn stunt disease occurred in the main growing areas of the State, causing estimated losses of more than 800,000 tons (Canale & Ribeiro, 2021).

CSS symptom is mainly characterized by chlorotic strips extended from the base to the apex of leaves; on the other hand, MBSP typical symptom is a reddening that starts from the marginal part and evolves toward the leaf limb. Both diseases in severe stages can cause internodes shortening, reduction in plant size, malformation of ears, and tillering, resulting in drastic yield reduction (Sabato et al., 2014). The management of the vector *D. maidis* is crucial to prevent the occurrence of stunt disease in maize fields; however, due to its high reproduction and migration capacity, the control of this pest with registered insecticides becomes difficult, especially in situations of high infestation (Cota et al., 2018). In this sense, in the face of the low efficacy of chemical control, maize genotypes with resistance to corn stunt may play an essential role in managing this disease in areas with high mollicutes pressure (Oleszczuk et al., 2020).

Many genotypes are recommended for sowing in the Santa Catarina State. However, the difference in their response to corn stunt disease is unclear, as the disease complex has never occurred in such a high incidence before. In this sense, regionalized information about genotype's reaction to the corn stunt disease complex is expected. So, the objective of this study was to evaluate the corn stunt severity and productivity of conventional and transgenic genotypes in the Midwest of Santa Catarina, Brazil, in a season with a high incidence of infective leafhoppers.

The trials with transgenic and conventional corn genotypes were conducted in the 2020/21 agricultural year at Epagri Experimental Station of Campos Novos, SC (27º23'11"S, 51°13'19"W), following the method described by Sabato and Teixeira (2015). It was evaluated eleven transgenic genotypes (P3016 VYHR, P1225 VYHR, B2418 VYHR, AG9025 PRO3, AG8780 PRO3, FS620 PWU, DKB290 PRO3, SYN505 VIP3, SYN422 VIP3, P3551 PWU, and AS1757 PRO3) and seven conventional genotypes (P3456, FS055, P2501, BG7046, SCS154 Fortuna, SCS 155 Catarina, and SCS156 Colorado). The genotypes were sowed in 14 m^2 plots, with row spacing of 0.7 m and plant density of 71.000 plants ha^{-1} on hybrid materials and 57.000 plants ha^{-1} on open-pollinated varieties. Four replicates (experimental plots)

were used in a randomized block design for each genotype. Sowing was carried in November 3rd, 2021. The cultural treatments followed the technical recommendations for maize production in the South of Brazil (Eicholz et al., 2020). At 90 days after sowing, the severity of corn stunt disease was evaluated using a symptom scale proposed by Silva et al. (2003), as follows: 1= absence of symptoms; 2 = less than 25% of leaves with symptoms; 3 = 25 to 50% of leaves with symptoms; 4 = 50 to 75% of leaves with symptoms; 5 = more than 75% of leaves with symptoms; 6 = premature death of plants. At physiological maturation, the two central lines of the plots were harvested to obtain grain yield ($kg.ha^{-1}$). The grain humidity was measured and corrected to 13%.

For data analysis, firstly, the normal distribution of residues was verified by the Shapiro-Wilk test, and Bartlett's test checked the homoscedasticity of variances. Next, the severity and yield data were subjected to ANOVA, and the Scott-Knott test compared means at a 5% probability of error. Finally, the relationship between the corn stunt severity and yield was verified using the parametric Pearson's correlation analysis at 5% probability of error.

The severity of corn stunt disease varied among the genotypes evaluated. For the conventional genotypes, the severity scores ranged from 2 to 3.5 (Figure 1A). The open-pollinated varieties SCS154 Fortuna, SCS156 Colorado, SCS 155 Catarina, and the hybrids P3456 and FS055 were less affected by corn stunt disease, with an average severity score of around 2 (less than 25% of leaves with symptoms). At the same time, P2501 and BG7046 were more susceptible and received a severity score of 3.3 and 3.5, respectively. The highest yields were obtained for P3456 and FS055; SCS154 Fortuna, SCS156 Colorado, and SCS 155 Catarina were in an intermediate yield group, whereas the lowest yields were verified in P2501 and BG7046 (Figure 1A).

The transgenic genotypes P3551 PWU and AS1757 PRO3 were less affected by corn stunt, with a severity score of 1 and 1.5, respectively (Figure 1B). For P3016 VYHR, SYN422 VIP3, AG8780 PRO3, SYN505 VIP3, DKB290 PRO3, and FS620 PWU, the severity score varied from 2 to 2.5. The most affected transgenic genotypes were B2418 VYHR, AG9025 PRO3, and P1225 VYHR, with average corn stunt severity scores of 3.5, 3.8, and 4.8. Significant differences were checked in grain yield, higher in the genotypes with lower corn stunt severity.

The grain yield was negatively correlated with corn stunt severity in conventional and transgenic genotypes (Table 1). Despite the yield potential of a maize genotype being an intrinsic characteristic and influenced by several factors, the corn stunting directly affected grain production since grain yield was lower in genotypes with high severity of corn stunt disease complex. Similar to our study, Cota et al. (2018) and Costa et al. (2019) also verified differences in the resistance level to corn stunt in different maize hybrids, with the tendency to

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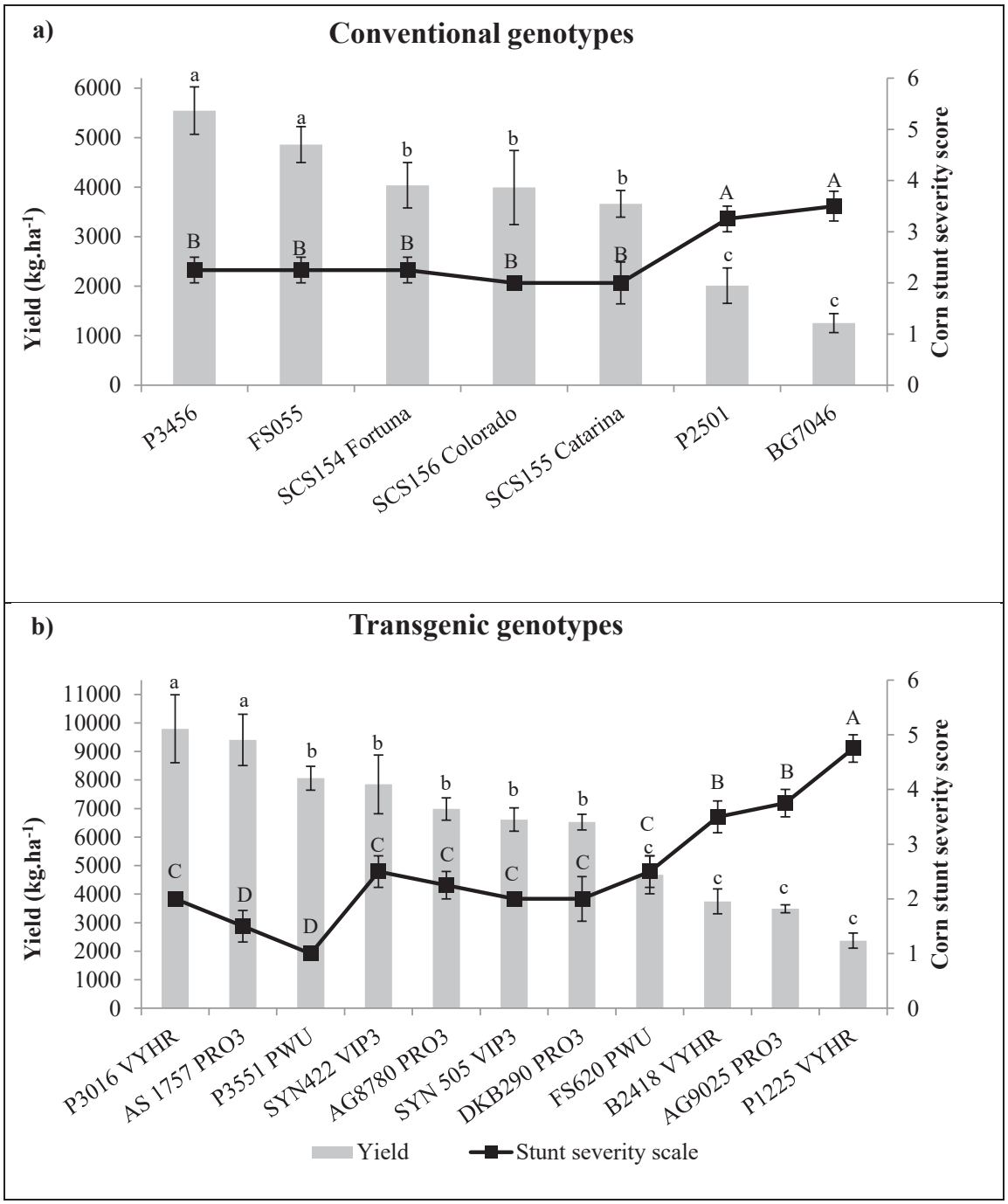

Figure 1. Yield and corn stunt disease severity on conventional (a) and transgenic (b) maize genotypes. Means followed by different letters, lower case for yield and upper case for severity scale, significantly differ by the Scott-Knott test, at 5% probability of error. a) yield: df = 6, 21; F = 11.73; p < 0.0001, severity scale: df = 6, 21; F = 5.25; p = 0.0019; b) yield: df = 10, 33; F = 14.52; p < 0.0001, severity scale: df = 10, 33; F = 18.69; p < 0.0001.

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Table 1. Correlation between the grain yield and corn stunt disease severity in conventional and transgenic maize genotypes.

Correlation	r*	p-value
	Conventional genotypes	
Yield x stunt disease severity	-0.62	0.00046
	Transgenic genotypes	
	-0.73	<0.0001

*Person's coefficient correlation

decrease grain yield with the increase of corn stunt severity and incidence.

Usually, a higher incidence of corn stunt disease is observed in late sowing crops, mainly due to the migration of many infectious leafhoppers from older adjacent crops (Costa et al., 2019). Our study delayed the sowing due to drought conditions in September and October 2020. This decision resulted in a high incidence of leafhoppers in the experimental area along the vegetative stage of the crop. Sabato and Teixeira (2015) stated that the field assessment of corn stunt resistance/tolerance is suitable for evaluating many genotypes. Therefore, late sowing is highly recommended in this kind of study to assure the concentration of *D. maidis* in the area.

Studies that aimed to evaluate the response of maize genotypes were performed in the state of Tocantins by Costa et al. (2019). The authors verified a corn stunt disease incidence of 39.7% in DKB290 PRO3 and obtained a yield of 6.980 $kg.ha^{-1}$, which was close to the same genotype in our study (6.524 $kg.ha^{-1}$). In a similar study carried out in the state of Minas Gerais, Cota et al. (2018) verified the high severity of corn stunting in DK290 PRO3 (severity score between 4 and 5). In our study, lower severity was observed for this genotype, which can be explained by different environmental conditions, especially temperature that can influence the multiplication of mollicutes and expression of symptoms by the plant (Sabato & Teixeira, 2015). To date, little is known about maize resistance mechanisms to stunt disease. Oleszczuk et al. (2020) stated that corn stunt resistance might be due to a reduction in the pathogen movement or multiplication in the plant, leading to low severity levels of the disease, or by an antibiosis or antixenosis effect to the vector *D. maidis*, impairing insect-plant interaction and reducing mollicutes inoculation. According to Faria et al. (2021), morphological factors such as hardness of the leaves and stiffness of the ribs are associated with antixenosis or antibiosis to *D. maidis*, which can lead to a decrease in corn stunt disease incidence.

The open-pollinated varieties SCS154 Fortuna, SCS 155 Catarina, and SCS 156 Colorado usually do not have the same yield potential as conventional hybrids. Nevertheless,

these materials have higher genetic variability and presented less severe corn stunting symptoms and superior yield than the conventional hybrids P2501 and BG7046. In addition, it is known that genotypes with a tropical genetic basis are less susceptible to corn stunting than genotypes with a temperate genetic basis (Oleszczuk et al., 2020). Therefore, this information must be considered in developing new hybrid materials recommended for areas with historical incidence of corn stunt disease.

Regional studies are crucial for obtaining accurate information about genotype x environment interactions and subside local recommendations of cultivars or hybrids. Considering the severity of symptoms and grain yield, the transgenic genotypes P3016 VYHR, AS1757 PRO3, and P3551 PWU and the conventional P3456 and FS055 were less affected by corn stunting. Therefore, they constituted a valuable tool in corn stunt disease management. However, all genotypes evaluated in our study are adapted to the Midwest region of Santa Catarina, with excellent yield potential. Therefore, those with higher symptoms should not be disregarded but appropriately managed to prevent the corn stunt disease incidence. For this purpose, the integrated pest management practices should be intensively disseminated and adopted in a regional context.

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