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Research Article

Development of *R. solani* and yield response in herbicide-tolerant irrigated rice genotypes in Southern Tocantins, Brazil

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ABSTRACT

Rice (*Oryza sativa* L.) is a staple crop of global importance, but its productivity is often constrained by diseases and weeds, which lead to significant reductions in rice yield and quality. The technology of Clearfield enables the effective use of imidazolinone herbicides in rice with a resistant genotype. Nonetheless, besides the presence of weeds, diseases like the sheath blight, which is caused by the *Rhizoctonia solani*, are another limitation to irrigated rice farming. Clearfield genotypes have not been extensively studied for their resistance to sheath blight, and this disease has been on the rise in recent years, especially in the State of Tocantins, Brazil. The objective of this study was to determine the resistance of herbicide-resistant genotypes of irrigated rice to sheath blight at floodplain conditions in southern Tocantins. This was tested in 2019/20 and 2020/21 with a randomized block design (4 replications) in naturally infested commercial fields where sheath blight has previously occurred. The treatments consisted of advanced breeding lines and commercial cultivars. The temporal dynamics of sheath blight in the two years were best represented by the monomolecular model. Genotypes AB191132-RH and AB191122-RH exhibited the lowest disease severity and area under the disease progress curve (AUDPC) values without compromising yield, indicating partial resistance to sheath blight. Disease severity and yield loss were also minimized by the preventive use of fungicides. These results indicate that resistant Clearfield(r) rice genotypes and fungicide management are promising methods of sheath blight control in irrigated rice systems as integrated approaches.

Keywords: Sheath blight; *Oryza sativa*; fungicides; weeds; clearfield ® technology.

INTRODUCTION

Rice (*Oryza sativa* L.) is one of the most important staple foods worldwide, cultivated and consumed on all continents. Brazil ranks ninth in global rice production, with irrigated systems accounting for more than 90% of the national output (Conab, 2022). Tocantins is the third-largest producer of irrigated rice in Brazil, where cultivation is concentrated in floodplain areas of the southeast region of the state (Fragoso, 2019). Over the years, advances in genotype development, fertilization practices, and weed and disease management have contributed to increased

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productivity (Awlachew & Mengistie, 2022). However, phytosanitary problems remain a major constraint, especially fungal diseases that significantly reduce grain yield and quality (Chen et al., 2023). More than 70 pathogens can infect rice at different growth stages, causing substantial yield losses (Zhang, 2019).

Rice sheath blight, caused by the necrotrophic fungus *Rhizoctonia solani* Kuhn, is among the most destructive diseases of irrigated rice worldwide (Jia, 2012; Wang, 2021). The disease occurs in both tropical and subtropical production systems, as well as in upland areas, and can severely reduce rice yield and grain quality. Characteristic symptoms include water-soaked lesions with brown margins on sheaths and culms, which may progress to large necrotic areas (Mishra Rajput, 2020). In Tocantins, sheath blight has become increasingly important due to crop rotations with susceptible hosts such as soybean, watermelon, and beans, which maintain inoculum levels in floodplain areas (Molla et al., 2020; Singh, 2019). Recent genomic studies also highlight the high genetic diversity of *R. solani*, which contributes to the difficulty of achieving durable resistance (Nizamani, 2025).

In addition to disease management, effective weed control is critical in irrigated rice systems, as it directly impacts production costs and yield potential. Among the most problematic weeds, red rice (*Oryza sativa* L. weedy form) is particularly damaging due to its competitive ability and genetic similarity to cultivated rice, which complicates control (Xavier, 2022). In Tocantins, infestations of red rice have expanded across major floodplain production areas, threatening the economic viability of rice farming. The introduction of Clearfield(r) technology, which combines herbicide-resistant cultivars with the application of imidazolinone herbicides, has revolutionized weed management in irrigated rice systems (Rangel et al., 2022). In Brazil, the herbicides Only® (imazapic + imazethapyr) and Kifix® (imazapic + imazapyr) are recommended for use with this system (Andre, 2017; Germani., 2022).

Given the scarcity of information on the relationship between Clearfield® rice and sheath blight resistance, studies that integrate genotype performance with epidemiological analyses are essential. Therefore, this study aimed to evaluate the resistance of herbicide-resistant rice genotypes to sheath blight in floodplain areas of southern Tocantins, to identify promising materials that combine effective weed control and tolerance to disease.

MATERIALS AND METHODS

Study location

To strengthen the environmental context of disease progression, additional climatic details are provided for both sites. Formoso do Araguaia has a humid tropical climate characterized by mean daily temperatures of 24–28 °C and consistently high relative humidity (74–88%) during the evaluation period. These conditions are well recognized as favorable for the development of *Rhizoctonia solani*, particularly when combined with flood-irrigated production.

In contrast, Lagoa da Confusão experiences similar seasonal temperature and rainfall patterns, with high nighttime humidity typical of lowland rice environments. Although real-time weather data could not be recorded due to lack of equipment, growers commonly report comparable microclimatic conditions to Formoso do Araguaia, which also support sheath blight development. These climatic backgrounds help contextualize disease pressure observed across both sites.

Experimental units

At both sites, a four-replication random complete block design (RCBD) was used. In October 2019 and 2020, the experiments were set up, and the following February, the samples were harvested. Over the course of the 2019–20 season, 17 genotypes were studied, comprising additional cultivars and 15 herbicide-resistant lines coming from BRS Pampeira (Appendix 1). During the 2020–21 season, 12 genotypes—eight lines and four varieties were evaluated (Appendix 2).

These trials were part of the Value for Cultivation and Use (VCU) tests, the final stage of breeding that assesses broad agronomic and commercially relevant traits. The evaluation forms a component of the EMBRAPA Rice and Beans irrigated rice breeding program and is mandatory for new cultivars to be certified in Brazil.

Crop management

The fungicides applied in Lagoa da Confusão were selected based on their known efficacy against fungal pathogens that share similar infection biology with R. solani, even though none are officially registered for sheath blight control in Brazil. Azoxystrobin and picoxystrobin (QoI fungicides) were included because of their preventive activity and their ability to suppress early infection events. Tricyclazole- and tricyclazole + tebuconazole–based products were added due to their systemic properties and their widespread use by growers for managing blast and other canopy diseases, which indirectly reduces overall disease pressure.

Application timing followed a preventive schedule aligned with the critical infection window of sheath blight (late vegetative to early reproductive stages). This timing was chosen to minimize initial inoculum establishment and to reflect realistic farmer practices for integrated disease management in irrigated rice systems.

Disease severity assessment

Formoso do Araguaia (without fungicides), sheath blight severity was scored weekly using the CIAT (Works, 1923) diagrammatic scale, adapted as follows:0 (healthy) 1 (1% of sheath tissue affected), 3 (1 to 5% of tissue affected) 5 (6–25% of tissue affected) ,7 =(26–50% of tissue affected) , 9 =(>50%. of tissue affected). A total of five assessments were carried out in each season, based on symptoms observed mainly on sheaths of plants within the usable plot area.The fungicides applied were Priori Xtra® (azoxystrobin + cyproconazole), Opera® (pyraclostrobin + epoxiconazole), and Nativo® (trifloxystrobin + tebuconazole).

Pathogen identification

Plants showing typical sheath blight symptoms were collected from the field. The pathogen was isolated on potato dextrose agar (PDA) and identified as *Rhizoctonia solani* based on standard morphological characteristics observed under a microscope, including right-angle branching of hyphae, constriction at the branching point, and the presence of septa. Plants showing typical sheath blight symptoms were collected from the field. The pathogen was isolated on potato dextrose agar (PDA). Pathogenicity was confirmed by fulfilling Koch's postulates. Mycelial plugs from pure cultures were used to inoculate healthy pot-grown rice plants of a susceptible cultivar, which subsequently developed characteristic sheath blight lesions. The fungus was re-isolated from these lesions, confirming its identity as *Rhizoctonia solani* based on morphological characteristics observed under a microscope.

Yield assessment

Harvesting each plot's two middle rows (a useful area), eliminating the border rows, enabled a calculation of grain yield. The yield of grain (kg ha^{-1}) was calculated by weighing the cereal grains once they had been cleaned and dried to 13% moisture.

Area under the disease progress curve (AUDPC)

The area under the disease progress curve (AUDPC) was employed to quantify disease development over time, with lower values indicating slower disease progression. The AUDPC was calculated using the formula:

$$AUDPC = \Sigma [((Y_i + Y_{i+1})/2) \times (t_{i+1} - t_i)]$$

Temporal progress of herbicide-resistant rice sheath blight

The midpoint of each severity score was used to convert it to the percentage of diseased leaf area in order to fit epidemiological models and create disease progress curves (Campbell & Madden, 1990). Three models were subjected to the test.Monomolecular: $y = 1 - (1 - y0)\exp(-rt)$, Gompertz: $y=\exp(\ln(y0)\exp(-rt))$ and Logistics ($y=1/1(1+((1-y0)-1) \exp((- rt))$ Where y= disease intensity, y0 initial inoculum, r = disease progression rate, and t=epidemic duration evaluated according to the adjusted coefficient of determination (R^{*2}), obtained between the values of the actual disease progress curve (dependent variable) and the curve predicted by the model (AMORIM, 2016; Gustavo Castilho Beruski, 1990).The adjusted coefficient of determination (R^2) for each model was calculated, and the model with the highest R^2 value was selected as the best fit for the disease progress curve of each genotype.

In vitro screening of bacteria isolates

The bacteria were isolated in rhizosphere of the healthy rice plants planted in the same experimental field. These isolates were filtered out on their potential biocontrol agent against. The bacterial growth was quantified in the 96-well plates measuring optical density 600 nm (OD600) after 48 hours using a spectrophotometer. A promising Bacillus sp. isolate has been shown to have a growth curve.

Statistical analysis

Analysis of variance (ANOVA) was carried out on data on yield, maximum sheath blight degree, and AUDPC. The Scott-Knott test was employed to compare means at $p < 0.05$. Graphs were generated using Sigma Plot version 10 (Systat Software, 2014).

RESULTS AND DISCUSSION

Disease progression, severity, and yield - 2019/20 season

Herbicide-resistant irrigated rice genotypes productivity and resistance to sheath blight in a Floodplain Area in Southern Tocantins Figure 1 shows the temperature (°C), relative humidity (%), and precipitation (mm) in Formoso do Araguaia during the assessment periods. Climate data could not be recorded in Lagoa da Confusão due to a lack of equipment. During the investigation, the temperature varied between 24°C and 28°C, and the relative humidity ranged from 74% to 88%. Because flood conditions were used in the trials, rain was not a controlling problem. The growth of *R. solani*, which is the cause of rice sheath blight, was facilitated by the climate caused by these external variables.

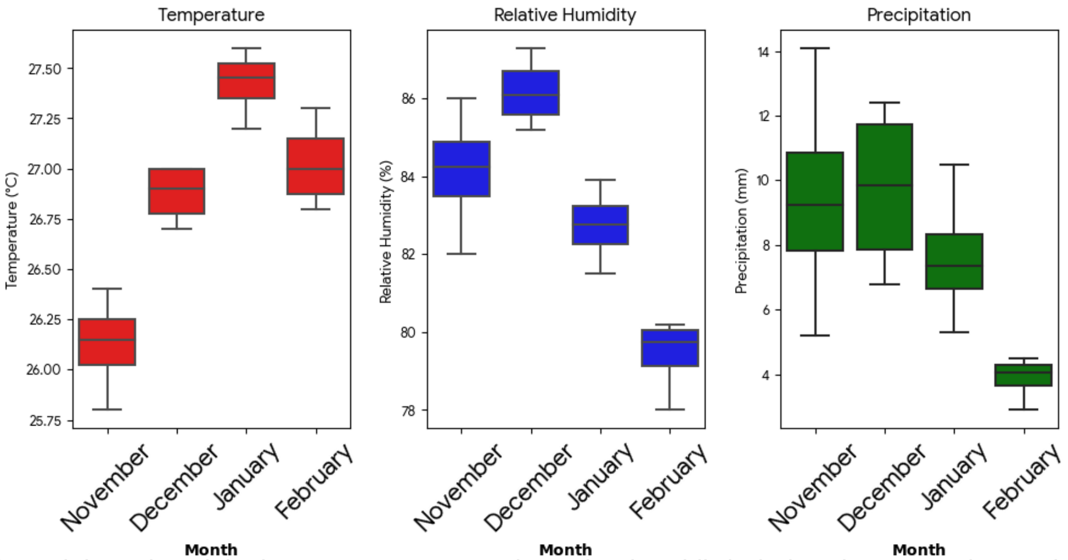

Figure 1. Climatic variables (precipitation, temperature, and relative humidity) during the evaluation periods of the 2019/20 and 2020/21 experiments in Formoso do Araguaia, Tocantins.

A correlation analysis between AUDPC and yield revealed distinct patterns among genotypes (Table 1). Based on the magnitude of the correlation coefficient ($|r| > 0.70$ considered strong), only AB191122-RH showed a strong negative correlation ($r = -0.707$), indicating that higher disease levels were associated with lower yields in this genotype. Conversely, genotypes BRS Pampeira ($r = 0.743$), AB191131-RH ($r = 0.807$), AB191125-RH ($r = 0.905$), and AB191133-RH ($r = 0.949$) exhibited strong positive correlations. Importantly, all these correlations were statistically significant ($p < 0.05$), as confirmed by a t-test for correlation coefficients. These positive relationships suggest potential tolerance mechanisms, where yield was maintained or even appeared positively associated with higher recorded disease levels in these specific materials

Significant differences were observed among genotypes for AUDPC in the 2019/20 season ($p < 0.01$). Genotypes AB101124-RH, AB191134-RH, AB191122-RH, and AB191128-RH recorded the lowest AUDPC values, indicating slower disease progression. In contrast, AB191126-RH, AB191125-RH, and AB191131-RH exhibited the highest AUDPC values, confirming greater susceptibility. Maximum sheath blight severity also varied significantly among genotypes ($p < 0.01$). The least affected materials (15.5%) included BRS Pampeira, AB191123-RH, AB101124-RH, AB191127-RH, AB191129-RH, AB191130-RH, AB191132-RH, AB191133-RH, and AB191134-RH, whereas IRGA 424-RI, AB191121-RH, and AB191125-RH showed the highest severity (38.0%). Although grain yield did not differ significantly ($p \geq 0.05$), numerical differences were evident, with AB191128-RH achieving the highest yield (5,622 kg ha^{-1}) and IRGA 424-RI the lowest (3,711 kg ha^{-1}). Several correlations between AUDPC and yield were statistically significant ($|r| > 0.7$, $p < 0.05$). Notably, AB191122-RH showed a significant negative correlation, indicating that yield decreased with increasing disease. In contrast, BRS Pampeira, AB191131-RH, AB191125-RH, and AB191133-RH showed significant positive correlations, suggesting possible tolerance mechanisms. To evaluate the effects of preventing disease on productivity, fungicides were applied to all genotypes in Lagoa da Confusão in both seasons (Table 1). Disease pressure reduced yields in contrast with Formosa do Araguaia, where fungicides were not applied Formoso da Aragauia, Brazil, where fungicides were not applied. Fungicide use, on the other hand, increased yields in Lagoa da Confusão; however, genotype-to-genotype productivity changes were not statistically significant.

When comparing the genotypes with and without fungicide application, productivity losses were observed, ranging from 171.2 kg ha-1 (AB191121-RH) to 2,257.2 kg ha-1 (IRGA424 RI). This reduction corresponded to 3.11% and 38.8% when compared to their productivities using fungicides. Other genotypes showed reductions within this range, emphasizing the importance of using preventive fungicides. In R. solani-endemic surroundings, variable associations between AUDPC and productivity were found by correlation analysis, indicate how dependent the two variables are on each other and how strongly they are associated with each other. The higher this value (positive or negative), the stronger the association. A correlation coefficient above 0.7 and -0.7 is considered strong. Coefficients between -0.7

and 0.0 indicate moderate to weak correlation and are not significant. A positive correlation (r>0) indicates that as x increases, so does y, and a negative correlation (r<0) indicates the opposite: as x increases, y decreases.

Only AB191122-RH showed a substantial negative correlation, indicating that lower yields were related to higher AUDPC values. On the other hand, BRS Pampeira, AB191131-RH, AB191125-RH, and AB191133-RH showed significant beneficial relationships, with increases in AUDPC being directly proportionate to yield.

Table 1. Area Under the Disease Progress Curve (AADPC). Maximum severity of Sheath Blight (%). Productivity without fungicide application (without control). Productivity with fungicide application (with control). Correlation coefficient between productivity and (AADPC) in the 2019/20 year.

Genotypes	AACPD	Maximum severity (%)	Uncontrolled productivity	Productivity with control	Correlation coefficient
BRS Pampeira	354.5 b	15.5 c	5089.9 a	6078.0 a	0.743
IRGA 424 RI	332.5 b	38.0 a	3711.7 a	5969.0 a	0.000
AB191121-RH	341.2 b	38.0 a	5328.7 a	5500.0 a	0.408
AB191122-RH	249.4 c	26.7 b	5292.0 a	5813.0 a	-0.707
AB191123-RH	354.4 b	15.5 c	5181.7 a	5813.0 a	0.549
AB101124-RH	166.2 c	15.5 c	4961.2 a	5625.0 a	0.700
AB191125-RH	455.0 a	38.0 a	3858.7 a	5297.0 a	0.905
AB191126-RH	507.5 a	26.7 b	4042.5 a	5047.0 a	-0.633
AB191127-RH	354.4 b	15.5 c	4814.2 a	5156.0 a	-0.038
AB191128-RH	249.4 c	26.7 b	5622.7 a	5141.0 a	-0.612
AB191129-RH	310.6 b	15.5 c	4851.00 a	5516.0 a	0.291
AB191130-RH	310.6 b	15.5 c	5586.00 a	5406.0 a	0.640
AB191131-RH	393.7 a	26.7 b	4005.7 a	5156.0 a	0.807
AB191132-RH	354.4 b	15.5 c	4832.6 a	5391.0 a	-0.430
AB191133-RH	306.2 b	15.5 c	4263.0 a	5328.0 a	0.949
AB191134-RH	166.2 c	15.5 c	5439.0 a	6063.0 a	-0.236
AB191135-RH	293.1 b	26.7 b	4557.0 a	5750.0 a	0.266
Calculated F	4.74**	6.14**	2.40ns	0.62ns	-
CV(%)	25.05	13.69	11.87	15.04	-

C.V: Coefficient of Variation**: significant at 1% probability level ($p<0.01$); *: significant at 5% probability level ($0.01 \leq p<0.05$); ns: not significant ($p \geq 0.05$) by F test.

Significant variations between the tested genotypes were also visible in the AUDPC values in the following year of the trial (Table 2). The BRS A706 CL, IRGA 424 RI, AB191122-RH, and AB191124-RH (105.0) genotypes had the lowest statistical values. On the other hand, the BRS strain Pampa CL had the highest AUDPC value (458.5), which was 336.6% higher than the most resistant genotypes. For the maximum severity parameter observed in the evaluated genotypes, three of them stood out negatively: BRS Pampeira, BRS Pampa CL, and AB191126, with a value of 56.5% of diseased tissue affected by sheath blight. The maximum severity scores varied among the other genotypes. However, those with the lowest percentages of diseased tissue were BRS A706 CL, IRGA 424 RI, AB191122-RH, AB191124-RH, and AB191129-RH, with a value of 15.5%, representing a difference of 41% between the most and least affected. BRS Pampa CL was the genotype that presented the highest simultaneous AUDPC values and maximum sheath blight severity. In the second year of trial, there were also significant between-genotype variations in grain yield (Table 2). Although it did not have the low AUDPC or severity values, AB191121-RH (9,411.7 kg ha^{-1}) produced the best yield and showed good productivity, indicating some resistance to sheath blight. After this AB191122-RH (8,284.2 kg ha^{-1}). The lowest yield, however, was observed by BRS Pampeira (3,774.5 kg ha^{-1}), which was 5,637.2 kg ha^{-1} (about 60%) below that of AB191121-RH. Likewise, low yields were reported by AB191127-RH, AB191129-RH, and AB191134-RH (3,970.6, 4,411.7, and 4,705.8 kg ha^{-1}, respectively). According to the productivity data from the trial with fungicide application in the 2020/21 year, it is noted that the genotypes presented statistical differences in productivity. The most productive genotype was IRGA 424 RI, with a productivity of 8,627.4 kg ha-1. This genotype simultaneously presented the lowest AUDPC values (105.0) and maximum observed severity (15.5%). The least productive was the genotype BRS A706 RH (4,950.9 kg ha-1), a difference of 3,676.5 kg ha-1 in relation to IRGA 424 RI. When comparing its productivity with fungicide application, it was lower than without application, indicating that external factors influenced the result. A significant positive relationship between AUDPC and productivity was identified

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by correlation analysis in AB191122-RH, AB191124-RH, and AB191134-RH, indicating that higher disease levels were directly linked to better yields in these genotypes. On the contrary hand, there were statistically significant negative correlations between AB191121-RH and BRS A706 CL, suggesting that yield reductions were related to increases in AUDPC.

Table 2. Maximum severity value of Sheath Blight (%). Productivity without fungicide application (without control). Productivity with fungicide application (with control). Correlation coefficient between productivity and AUDPC in the 2020/21 year.

Cultivars	AACPD	Maximum severity (%)	Uncontrolled productivity	Productivity with control	Correlation coefficient
BRS Pampeira	336.0 b	56.5 to	3774.5 c	6801.4 c	0.184
BRS Pampa CL	458.5 a	56.5 to	6470.5 b	6813.7 c	-0.345
BRS A706 RH	105.0 c	15.5 c	6323.5 b	4950.9 c	-0.852
IRGA 424 RI	105.0 c	15.5 c	6213.2 b	8627.4 a	-0.033
AB191121-RH	293.1 b	38 b	9411.7 a	6066.1 c	-0.816
AB191122-RH	105.0 c	15.5 c	8284.2 a	6911.7 c	0.840
AB191123-RH	231.9 c	26.8 c	5245.1 c	6813.7 c	-0.094
AB191124-RH	105.0 c	15.5 c	6580.8 b	6617.6	0.904
AB191126-RH	344.8 b	56.5 to	6213.2 b	6066.1 c	-0.354
AB191127-RH	144.4 c	26.8 c	3970.6 c	6617.6 c	0.465
AB191129-RH	201.3 c	15.5 c	4411.7 c	6911.7 c	0.383
AB191134-RH	288.8 b	38.0 b	4705.8 c	7463.2 b	0.930
Calculated F	9.35**	9.11**	14.89**	5.34**	-
CV(%)	34.23	14.62	14.68	11.51	-

C.V: Coefficient of Variation**: significant at the 1% probability level ($p<0.01$); *: significant at the 5% probability level ($0.01 \leq p<0.05$); ns: not significant ($p \geq 0.05$) by F-test. Maximum severity (%) obtained with the means of the four replicates of the last evaluation of each genotype.

Temporal progress of herbicide-resistant sheath blight in irrigated rice

To determine the best fit for sheath blight in both test years, three epidemiological models of periodic disease development Logistic, Monomolecular, and Gompertz have been investigated based on field severity scores collected over the evaluation period. Regression analysis between observed several levels (dependent variables) and the values predicted by each model (independent variables) produced the adjusted coefficient of determination (R*2), which served as the criterion of evaluating the model (Beruski et al., 1990). The model that best represented the development of the disease was believed to possess the highest R^2 coefficient R2 value. Significant coefficients of dependence were obtained from the evaluation of the data and equations supplied by the Monomolecular model, and the observed level of severity closely matched this model. This suggests that during both evaluation years, the monomolecular model produced the best description of the sheath blight temporal progression in herbicide-resistant rice genotypes. Annex 1 and 2 shows the disease progression rates for both tests. Field-observed severity data modified for the model were linearly regressed to produce these values $y=(\ln(1/1-y)$ as a function of time. Genotype AB191122-RH exhibited a strong and significant negative correlation between AUDPC and yield ($r = -0.707$, $p < 0.05$), indicating that increased disease progression directly led to yield loss (Table 1)

The genotypes BRS A706 RH, IRGA 424 RI, AB191122-RH, and AB191124-RH (0.0038) had the lowest infection rates in the second year (Annex 2), Reduced maximum severity and AUDPC values were associated with these low infection rates (Table 2). Furthermore, AB191124-RH consistently demonstrated one of the lowest rates of infection in both years, indicating that it may be resistant to sheath blight.

According to Annex 2, the genotypes having the smallest rates of infection in the second year included BRS A706 RH, IRGA 424 RI, AB191122-RH, and AB191124-RH (0.0038). These low infection rates were linked to lower AUDPC levels and maximum severity (Table 2). Additionally, in both years, AB191124-RH consistently showed one of the lowest infection rates, further supporting its classification as a genotype with partial resistance to sheath blight.

Among the mathematical models evaluated, the Monomolecular model best adjusted to the temporal progress of the burning of the Sheaths, because it presented the highest adjusted coefficients of determination (R*2), in the two years of evaluation (Annexes 1 and 2). The analysis of disease progression graphs against time (days) enabled an assessment of observed and Monomolecular predicted by the model severity (Figure 2). Three genotype groups have been identified: susceptible (IRGA 424 RI, BRS Pampeira), moderately resistant (AB191128-RH, AB191121-RH), and resistant (AB191134-RH, AB191122-RH). The grouping of resistance was determined by combining the evaluation of production and intensity.

The resistant genotypes AB191134-RH and AB191122-RH showed the lowest predicted maximum severity values, close to 18% and 16%, respectively. An inverse relationship between severity and resistance was observed: as the percentage of affected tissue increased, resistance decreased. The moderately resistant genotype AB191128-RH reached predicted maximum severity levels of approximately 32%, while AB191121-RH reached about 45%. The susceptible genotypes exhibited the highest severity values, with IRGA 424 RI reaching ~50% in the first year and BRS Pampeira ~70% in the second year, according to predictions from the Monomolecular model. Overall, predicted severity levels were higher in the second year compared with the first. In contrast, BRS Pampeira showed a strong positive correlation (r = 0.743, p < 0.05), suggesting a potential tolerance mechanism where yield was maintained despite higher disease levels.

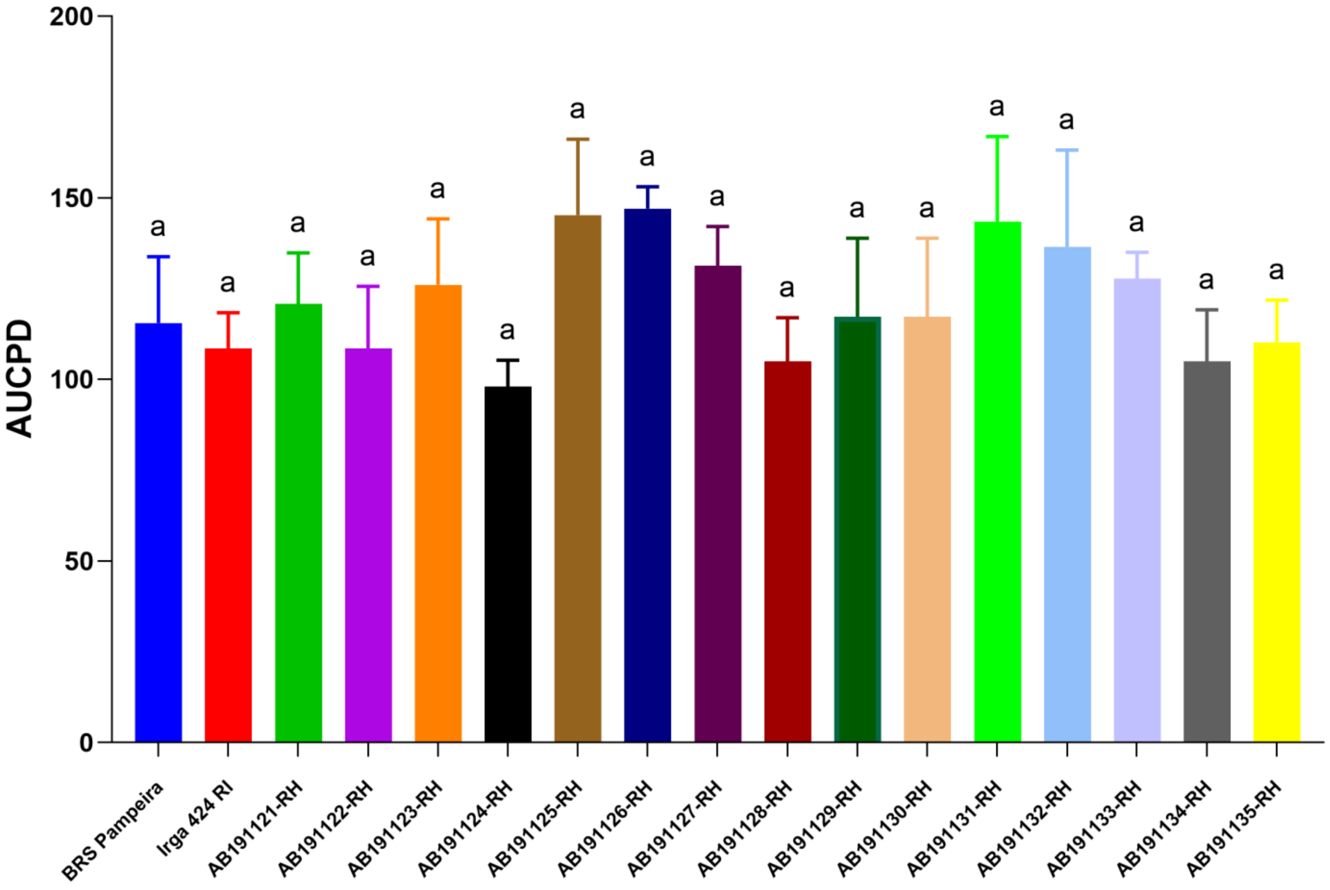

Figure 2. Disease progress curves for selected herbicide-resistant rice genotypes representing resistant (AB191122-RH, AB191134-RH), moderately resistant (AB191128-RH, AB191 121-RH), and susceptible (IRGA 424 RI, BRS Pampeira) categories, as predicted by the Monomolecular model in Formoso do Araguaia during the 2020/21 season (2020/2021).

The findings of this research established that sheath blight, caused by *Rhizoctonia solani,* is one of the primary limitations to irrigated rice production in floodplain environments in Tocantins. The genotypes under analysis exhibited disease symptoms with varying levels of severity, indicating that none of the genotypes was entirely resistant. The disease progression curves (Figure 2) visually confirm the categorization of genotypes into resistant, moderately resistant, and susceptible groups, with the monomolecular model providing an excellent fit to the observed data, particularly for the slower-progressing resistant lines. The result is in line with the existing reports that neither conventional nor herbicide-resistant varieties of rice have vertical or total resistance to sheath blight (Bhaskar Rao et al., 2020; Chen et al., 2023). Rather, the resistance is quantitative and depends on several genes and is affected by plant structures and environmental factors (Yinggen, 2017; Willocquet, & Savary, 2011). AB191132-RH, AB191122-

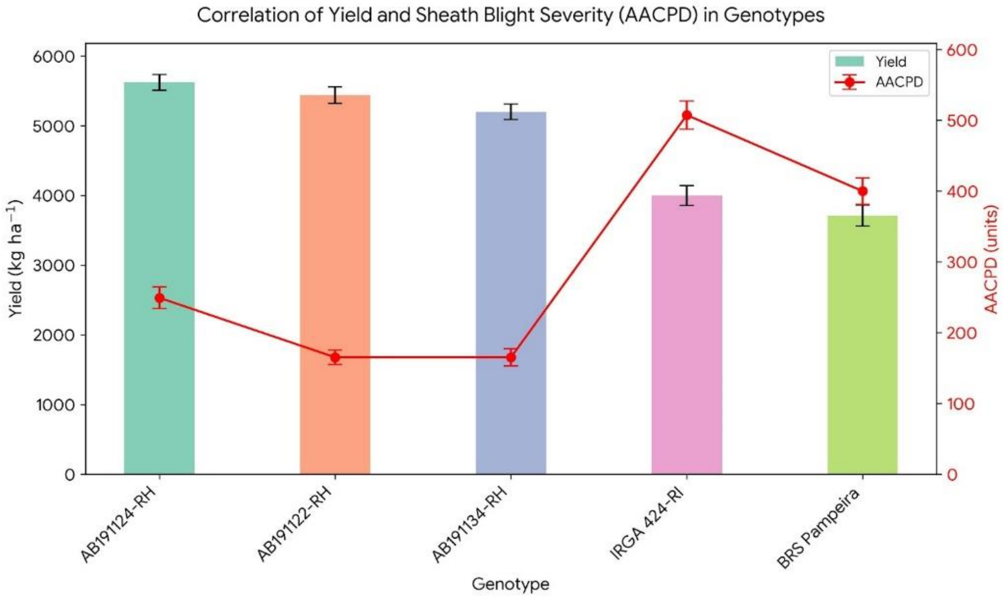

Figure 3. is a dual-axis plot showing the mean Area Under the Disease Progress Curve (AACPD) and the mean Yield (Productivity) for the selected herbicide-resistant genotypes, with error bars representing the standard error (SE).

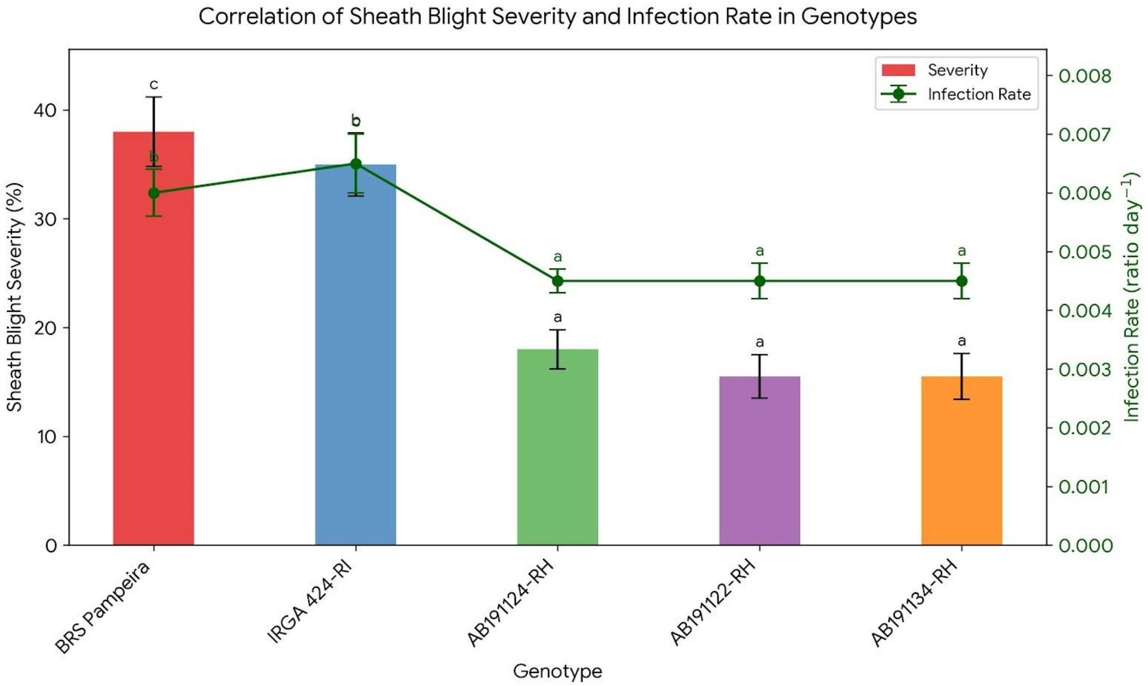

Figure 4. shows this figure allows for the visual comparison of the disease's final damage (Severity) and the speed at which it progressed (Infection Rate) across the genotypes, with the genotypes sorted by descending severity.

RH, and AB191124-RH were consistently associated with lower AUDPC values, reduced maximum severity, and competitive yield performance, indicating partial resistance to the disease. These findings support previous studies that some breeding lines may be a source of resistance alleles to enhance the sheath blight (Molla et al., 2020; Singh et al., 2018). The reliability of AB19124-RH during two growing seasons is another indicator that it has a future in breeding programs as a reliable source of resistance. Although the present study demonstrates that Clearfield® genotypes such as AB191122-RH, AB191124-RH, and AB191134-RH exhibit partial resistance to sheath blight, these findings align with and expand on previous research. Earlier evaluations of Clearfield® materials have generally reported moderate or variable resistance levels, rather than complete resistance, due to the quantitative nature of sheath blight resistance (Molla et al., 2020; Singh, 2019). Studies conducted in Brazil and Asia have similarly shown

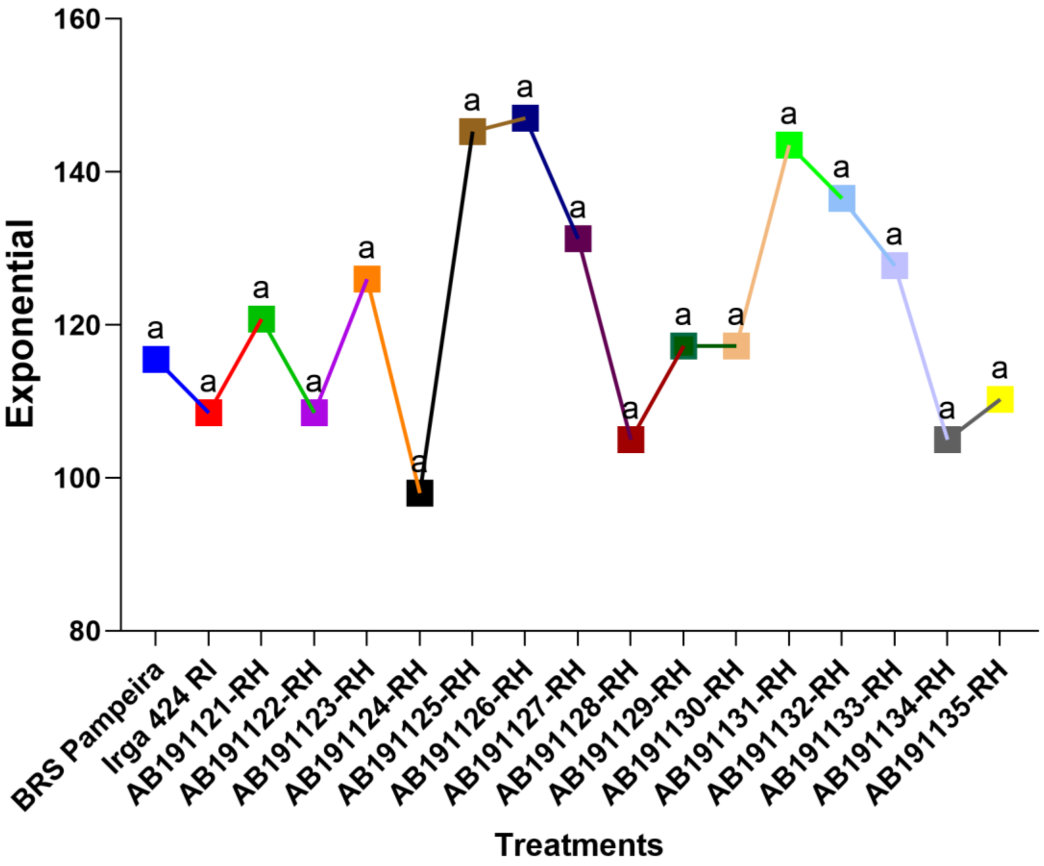

Figure 5. Exponential model–derived disease severity values for herbicide-resistant irrigated rice genotypes evaluated in the 2019/20 season under natural infection by *Rhizoctonia solani.* Each point represents the mean predicted severity for a genotype, and letters above points indicate statistical grouping according to Tukey's test ($p < 0.05$). Higher exponential values reflect faster initial disease increase. The comparison among genotypes illustrates the variability in early epidemic behavior, supporting the identification of resistant, moderately resistant, and susceptible materials.

that Clearfield® cultivars often display slower disease progression and reduced lesion expansion, but still require complementary management strategies to maintain productivity under high pathogen pressure (Rangel et al., 2022; Ke et al., 2017a). The consistent performance of AB191124-RH across both seasons in our study reinforces these earlier observations and suggests that some Clearfield lines may harbor minor-effect resistance loci capable of slowing epidemic development. This agrees with recent genomic analyses showing that resistance in Clearfield backgrounds is governed by multiple additive QTLs (Nizamani, 2025). Recent genomic findings suggest that this stability may be explained by the presence of a set of minor-effect loci that work synergistically to slow down progression (Nizamani, et al., 2025).

The environmental factors that existed at the time when the trials were conducted were favorable to the development of sheath blight, especially high relative humidity (>74%) and intermediate temperatures (24-28 °C). The close connection between climatic factors and disease occurrence supports the past findings according to which sheath blight severity is extremely reliant on the environmental factors (Mishra et al., 2020; Senapati et al., 2022). The Monomolecular model was the most useful in characterizing the epidemic process and shows the importance of initial inoculum in how the disease is structured. The model has found extensive application in epidemiological research, and is suitable for diseases where the pathogen does not replicate exponentially on the host (Khan, 2020) (Campbell & Madden, 1990). The fact that the early disease progress curve in this study looked like the Exponential model is not surprising when the severity values are relatively low over the time of observation. The comparison between trials in Lagoa da Confusão (with fungicides) and Formoso do Araguaia (without fungicides) demonstrated the productivity benefit of fungicide application. The use of fungicides led to a reduction in the disease severity, and plots treated with fungicides produced higher yields with an overall average yield of about 30 percent. No fungicides have yet been registered in Brazil against sheath blight in rice, but systemic fungicides used in the management of other diseases will incidentally control it (Li, et al., 2021; Mishra, 2020). There is also evidence pointing to the potential of biocontrol agents like Bacillus amyloliquefaciens that can modulate plant defence response and prevent *R. solani* infection (Molla, 2020; Van der Plank, 2013). These alternatives can supplement the use of fungicides and decrease the use of chemicals in the long term. Future research should focus on field validation of promising biocontrol agents like Bacillus amyloliquefaciens and their integration with partially resistant Clearfield® genotypes, potentially creating a more sustainable and durable sheath blight management strategy for floodplain systems. The consistent performance of AB191124-RH across both seasons in our study reinforces these earlier observations and suggests that some Clearfield lines may harbor minor-effect resistance loci capable of slowing epidemic development.

For instance, our finding that certain lines (e.g., AB191122-RH, AB191124-RH) maintained lower AUDPC values aligns with reports by Rangel et al. (2022) on the moderate field resistance of the Clearfield® cultivar BRS A706 CL. However, unlike studies that reported a trade-off between herbicide resistance and disease susceptibility, our results identify specific genotypes where both traits are favorably combined, addressing a key gap in the literature. This agrees with recent genomic analyses showing that resistance in Clearfield backgrounds is governed by multiple additive QTLs (Nizamani, 2025).

The inconsistency of the severity of the disease among years would be indicative of the fact that the quantity of initial inoculum is an important factor in the onset and progression of the disease (Martins, Lima, Cardoso, Viana, & Ootani, 2018). *R. solani* can generate sclerotia that remain in soil and crop residues allowing it to persist beyond several consecutive cropping seasons (Shu et al., 2019; Singh et al., 2016). Crop rotations of soybean, beans and watermelon in Tocantins preserve inoculum levels and increase sheath blight pressure. Here is the significance of integrated disease management, where crop rotation planning, application of fungicides, and resistant cultivars are all integrated. The observed negative relationships between the AUDPC and the yield of genotypes like AB191122-RH demonstrate that disease severity is directly linked to productivity losses. Conversely, positive correlations in certain genotypes may relate to tolerance mechanisms where plants endure the presence of the disease. These differences highlight the importance of distinguishing between resistance and tolerance in breeding programs. Advances in transcriptomic and QTL mapping are expected to facilitate the identification of candidate genes associated with resistance and tolerance mechanisms (Nizamani et al. 2025).

In general, this research indicates that the genotypes of Clearfield(r) rice respond differently to sheath blight, and some of these lines can achieve effective weed control while also exhibiting partial resistance to the disease. Combining epidemiological modelling with genotype assessment was useful in understanding disease patterns and host resistance. The results are part of the enhanced breeding strategies and management of the production of rice in the floodplain areas of Brazil.

CONCLUSION

This study demonstrates that sheath blight is a significant limitation to irrigated rice in the floodplain areas of Tocantins., and no genotype is resistant to this pathogen. Nevertheless, genotypes AB191132-RH, AB191122-RH, and AB191124-RH had lower AUDPC, less maximum severity, and higher yields, which is a partial resistance and possibly a source of resistance in breeding programs. The monomolecular model explained most effectively the course of a disease, and the initial inoculum strengthened the role of early inoculation in the dynamics of an epidemic. Fungicide application significantly reduced disease impact and boosted productivity, which highlights its importance in an integrated management where cultivar resistance is ineffective. However, the durability of *R. solani* in soil and crop residues in the long term demonstrates the necessity of integrating the resistant genotypes, crop-rotation strategies, and chemical or biological control strategies. In general, genotypes of the Clearfield(r) rice varieties that were tested in this experiment showed different tolerance to sheath blight, with certain varieties exhibiting good tolerance levels and still being productive. The results are valuable to breeding programs and integrated management strategies to maintain rice production within disease prone floodplain ecosystems. Also, the discovery of biocontrol agents is a sustainable alternative. Our preliminary in vitro screening has discovered bacteria isolates, including the Bacillus sp. presented herein (Figure 5) which have strong growth capabilities, making it worthwhile to conduct further research on the isolate to understand their effectiveness in integrated disease management protocols.

AUTHOR’S CONTRIBUTION

Performed the experiment: David Ingsson Liveria Andrade de Farias and Anila Kanwal analyzed the data: Muhammad Bilal and Muhammad Rizwan, contributed in material: Dalmarcia de Souza C. Mourão and Paulo R.S Fernandes, designed the experiment & wrote the paper: David Ingsson and Gil Rodrigues Santos, correspondence of the paper: Gil Rodrigues Santos. All authors approved the final draft.

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AVAILABILITY OF DATA AND MATERIAL

The collected and analyzed data is presented in the form of figures.

ETHICS APPROVAL AND CONSENT TO PARTICIPATE

The current study was checked and approved by the relevant team.

CONSENT FOR PUBLICATION

All authors have reviewed the manuscript and approved it for publication.

CONFLICT OF INTERESTS

The authors declare no conflict of interest.

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REFERENCES

Amorim, L., Rezende, J.A.M., Bergamin Filho, A., & Camargo, L.E.A. (Eds.). (2016). *Manual of phytopathology: diseases of cultivated plants* (Vol. 2). Ouro Fino, Brazil: Agronômica Ceres.

Andres, A., Machado, S. L. O., Mariot, C. H., & Gomes, A. S. (2017). Clearfield® rice: Weed control, agronomic performance, and sustainability. Planta Daninha, 35, e017163731.

Awlachew, H., & Mengistie, T. (2022). Advances in rice breeding and management practices to improve productivity. Agriculture, 12(4), 509.

Bhaskar Rao, T., Chopperla, R., Prathi, N. B., Balakrishnan, M., Prakasam, V., Laha, G. S., . . . Mangrauthia, S. K. (2020). A comprehensive gene expression profile of pectin degradation enzymes reveals the molecular events during cell wall degradation and pathogenesis of rice sheath blight pathogen Rhizoctonia solani AG1-IA. Journal of fungi, 6(2), 71.

Chen, J., Xuan, Y., Yi, J., Xiao, G., Yuan, D. P., & Li, D. (2023). Progress in rice sheath blight resistance research. Frontiers in Plant Science, 14, 1141697.

Conab. (2022). Rice production statistics. Retrieved from https://www.conab.gov.br

Fragoso, D. B. (2019). Irrigated rice cultivation in Tocantins: Challenges and opportunities. Revista Agro@mbiente On-line, 13(1), 10-20.

Germani, C., André, A., Laryssa Barbosa Xavier da, S., Thaís Stradioto, M., Alexssandra Dayane Soares de, C., & Camila Silveira, S. (2022). Carryover de [imazapic+imazapyr] sob diferentes sistemas de produção em terras baixas com arroz tolerante a ALS. Agrária - Revista Brasileira de Ciências Agrárias, 17(3), e2127. doi:10.5039/agraria.v17i3a2127

Gustavo Castilho Beruski, A. B. P., David Souza Jaccoud-Filho, Felipe Fadel Sartori, Paulo Cesar Sentelhas. (1990). Effects of Climate and Agricultural Practices on Temporal Progress of Sclerotinia sclerotiorum for Soybean in Brazil. Agricultural Sciences, Vol.7 (No.7). Retrieved from https://www.scirp.org/reference/referencespapers?referenceid=1799831

Jia, L., Yan, W., Zhu, C., Agrama, H. A., Jackson, A., Yeater, K., . . . McClung, A. (2012). Allelic analysis of sheath blight resistance with association mapping in rice. Plos one, 7(3), e32703.

Ke, Y., Deng, H., & Wang, S. (2017). Advances in understanding broad-spectrum resistance to pathogens in rice. The Plant Journal, 90(4), 738-748.

Ke, Y., Deng, H., & Wang, S. (2017). Advances in understanding rice resistance to sheath blight. Rice Science, 24(1), 15-24.

Khan, M. (2020). Epidemology of Plant Diseases. In (pp. 01-16).

Li, D., Li, S., Wei, S., & Sun, W. (2021). Strategies to manage rice sheath blight: Lessons from interactions between rice and Rhizoctonia solani. Rice, 14(1), 21.

Martins, M. V. V., Lima, J. S., Cardoso, J. E., Viana, F. M. P., & Ootani, M. A. (2018). Powdery mildew progress according to cashew phenology. Summa Phytopathologica, 44, 178-184.

Mishra, D., Rajput, R. S., Zaidi, N. W., & Singh, H. (2020). Sheath blight and drought stress management in rice (Oryza sativa) through Trichoderma spp. Indian Phytopathology, 73(1), 71-77.

Molla, K. A. (2020). Rice sheath blight: Insights into host pathogen interaction and resistance breeding. Rice, 13, 60.

Molla, K. A., Karmakar, S., Molla, J., Bajaj, P., Varshney, R. K., Datta, S. K., & Datta, K. (2020). Understanding sheath blight resistance in rice: the road behind and the road ahead. Plant biotechnology journal, 18(4), 895-915.

Nizamani, M. M. (2025). Decoding Rhizoctonia spp.: Genomic insights into taxonomy, pathogenicity, and diversity. Phytopathology Research, 7, 15.

Nizamani, M. M., Zhang, Q., Asif, M., Khaskheli, M. A., Wang, Y., & Li, C. (2025). Decoding Rhizoctonia spp. in-depth genomic analysis, pathogenic mechanisms, and host interactions. Phytopathology Research, 7(1), 12.

Rangel, P. H. N., Colombari-Filho, J. M., Ferreira, M. E., Magalhães Junior, A. M. d., Abreu, G. B., Pereira, J. A., . . . Fagundes, P. R. R. (2022). Imidazolinone resistance, yield potential and agronomic performance of the irrigated rice cultivar BRS A706 CL. Crop Breeding and Applied Biotechnology, 22, e42782237.

Senapati, M., Tiwari, A., Sharma, N., Chandra, P., Bashyal, B. M., Ellur, R. K., . . . Singh, A. K. (2022). Rhizoctonia solani Kühn pathophysiology: status and prospects of sheath blight disease management in rice. Frontiers in Plant Science, 13, 881116.

Shu, C., Zhao, M., Anderson, J. P., Garg, G., Singh, K. B., Zheng, W., . . . Zhou, E. (2019). Transcriptome analysis reveals molecular mechanisms of sclerotial development in the rice sheath blight pathogen Rhizoctonia solani AG1-IA. Functional & Integrative Genomics, 19(5), 743-758.

Singh, P. (2019). Genetic basis of sheath blight resistance in rice: Progress and prospects. Rice Science, 26(1), 1-14.

Singh, P. K., Nag, A., Arya, P., Kapoor, R., Singh, A., Jaswal, R., & Sharma, T. R. (2018). Prospects of Understanding the Molecular Biology of Disease Resistance in Rice. International Journal of Molecular Sciences, 19(4), 1141. Retrieved from https://www.mdpi.com/1422-0067/19/4/1141

Singh, R. (2016). Sheath blight of Rice: a review. International Journal of Agricultural Invention, 1(2), 161-169.

Srinivasachary, Willocquet, L., & Savary, S. (2011). Resistance to rice sheath blight (Rhizoctonia solani Kühn) [(teleomorph: *Thanatephorus cucumeris* (AB Frank) Donk.] disease: current status and perspectives. Euphytica, 178(1), 1-22.

Van der Plank, J. E. (2013). Plant diseases: epidemics and control: Elsevier.

Wang, A., Shu, X., Jing, X., Jiao, C., Chen, L., Zhang, J., . . . Li, S. (2021). Identification of rice (Oryza sativa L.) genes involved in sheath blight resistance via a genome-wide association study. Plant biotechnology journal, 19(8), 1553-1566.

Works, A. P. S. C. o. P. (1923). Report: Australian Government Publishing Service.

Xavier, M. C. G., Araújo, J. C., da Silva Menezes, B. R., & Júnior, P. C. D. (2022). CORRELAÇÕES CANÔNICAS ENTRE CARACTERÍSTICAS MORFOLÓGICAS E DE PRODUÇÃO EM TIPOS ESPECIAIS DE ARROZ. Revista Caatinga, 35(4), 764-771.

Zhang, S. (2019). The impact of fungal diseases on rice yield and quality. Plant Disease, 103(8), 1867-1876.