

REVIEW

Diagnosis and management of bacterial stripe in maize: Current limitations and perspectives for the control of *Acidovorax avenae* subsp. *avenae*

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Abstract: Maize (*Zea mays* L.) is one of the most important cereal crops worldwide, playing a fundamental role in food security, animal nutrition, and industrial production. Among the bacterial diseases affecting maize, bacterial stripe caused by *Acidovorax avenae* subsp. *avenae* has emerged as a significant phytosanitary concern due to its wide host range, seedborne nature, and capacity to survive in crop residues and alternative hosts. This review aimed to synthesize current knowledge regarding the biology, epidemiology, symptomatology, diagnosis, and management of *A. avenae* subsp. *avenae*, highlighting existing limitations and future perspectives for disease control. A narrative literature review was conducted using scientific publications indexed in national and international databases, with emphasis on studies published between 2020 and 2026. The pathogen causes characteristic water-soaked lesions that develop into elongated chlorotic and necrotic stripes, leading to reductions in photosynthetic capacity and crop performance. Recent advances in molecular diagnostics, including polymerase chain reaction (PCR), quantitative PCR (qPCR), sequencing technologies, and genomic approaches, have improved pathogen detection and epidemiological investigations. However, disease management remains challenging due to the limited availability of resistant cultivars and the inconsistent efficacy of chemical and biological control measures. Integrated disease management, combining cultural practices, pathogen-free seeds, biological control agents, host resistance, and disease monitoring, currently represents the most effective strategy. Emerging technologies such as remote sensing, artificial intelligence, precision agriculture, and gene-editing tools offer promising opportunities for improving disease detection, surveillance, and control. Future research should focus on pathogen diversity, host-pathogen interactions, resistance mechanisms, and climate change effects to support the development of sustainable management strategies for bacterial stripe in maize production systems.

Keywords: Bacterial stripe; Maize pathology; Molecular diagnosis; Integrated disease management; Plant-pathogenic bacteria.

1. Introduction

Maize (*Zea mays* L.) occupies a strategic position in global food security, serving as a staple for human consumption, animal feed, and as a raw material for numerous industrial sectors (Wani et al., 2022; Wang; Zhang, 2024). The increasing global demand for grain has driven the intensification of production systems, which has simultaneously favored the emergence and spread of diseases caused by phytopathogenic bacteria. Among these diseases, bacterial stripe, caused by *Acidovorax avenae* subsp. *avenae* (Aaa), has attracted growing attention due to its broad host range, high survival capacity, and potential to cause significant economic losses in cultivated grasses, including maize, rice, sorghum, and sugarcane (Zhao et al., 2023).

Acidovorax avenae subsp. *avenae* belongs to the family Comamonadaceae and is characterized as a Gram-negative, aerobic bacterium, motile by means of polar flagella and capable of colonizing both vascular and parenchymatic tissues of host plants (Osdaghi, 2023; Sawada et al., 2025). Recent studies have demonstrated that the genetic diversity observed among isolates of the species contributes to differences in virulence, environmental adaptation, and host specificity, complicating the development of universal management strategies. Furthermore, the occurrence of genetic and morphological variants highlights the high evolutionary plasticity of the pathogen, facilitating its persistence across diverse agroecosystems (Zhao et al., 2023).

Symptoms of bacterial stripe in maize typically include elongated, water-soaked, translucent lesions that develop into brown to dark-brown necrotic streaks, often accompanied by chlorosis and a reduction in photosynthetically active leaf area. Under favorable conditions of high temperature and elevated relative humidity, the disease may progress rapidly, impairing vegetative growth and reducing crop yield potential. Transmission through infected seeds and contaminated crop residues represents an important mechanism for bacterial dissemination among production regions, making the disease particularly difficult to eradicate once established (Somda et al., 2001).

Accurate diagnosis of *A. avenae* subsp. *avenae* remains one of the major challenges for researchers and plant pathologists (Verma et al., 2022). The similarity of symptoms to those caused by other bacterial and fungal pathogens may lead to misdiagnosis when only visual assessments are employed. In this context, molecular techniques have assumed a central role in pathogen identification, including conventional PCR, Bio-PCR, analysis of the 16S–23S ITS region, 16S rRNA gene sequencing, multilocus sequence typing

(MLST), and more recent genomic approaches. These tools substantially improve the sensitivity and specificity of detection, enabling early identification of the bacterium even in asymptomatic plant material (Zhang et al., 2025; Zhao et al., 2023).

In recent years, advances in molecular biology, comparative genomics, and proteomics have expanded our understanding of the pathogenicity mechanisms of *A. avenae* subsp. *avenae*. Recent investigations have revealed the involvement of bacterial secretion systems, virulence factors, and regulatory metabolites in the colonization of plant tissues and suppression of host defense responses. Knowledge of these mechanisms has contributed to the development of new monitoring and control strategies, although significant gaps remain regarding pathogen–host interactions and the environmental factors influencing disease severity (Masum et al., 2017).

Management of bacterial stripe continues to rely predominantly on preventive measures, as curative control options exhibit limited effectiveness. The principal strategies include the use of certified seed, crop rotation, removal of infected crop residues, adoption of cultivars with higher levels of resistance, and continuous phytosanitary monitoring (Zhang et al., 2023). However, the lack of highly resistant cultivars and the limited availability of bactericides specifically registered for disease control hinder the implementation of effective management programs. In addition, climate change and the intensification of agricultural systems may favor the geographical expansion of the pathogen, increasing the frequency of epidemic outbreaks (Zhao et al., 2023).

Simultaneously, new technologies associated with digital agriculture are being explored to improve the early detection of diseases in maize. Tools based on remote sensing, multispectral drone imagery, artificial intelligence, and deep learning have demonstrated potential for identifying physiological changes associated with infection before visible symptoms appear. These approaches represent promising opportunities for integrating real-time monitoring systems and data-driven decision-making, thereby contributing to the sustainability of phytosanitary management programs (Mall et al., 2023).

Given the growing economic and phytosanitary importance of bacterial stripe in maize, it is essential to compile and critically analyze recent advances related to the diagnosis, epidemiology, and management of *Acidovorax avenae* subsp. *avenae*. Therefore, this review aims to synthesize the current knowledge regarding the disease, discuss the existing limitations of control methods, and present future perspectives that

may contribute to the development of more effective and sustainable strategies for managing bacterial stripe in modern maize production systems.

2. Methodology

2.1. Narrative review design and literature search

This study was conducted as a narrative literature review with a qualitative and descriptive approach, aiming to synthesize and critically discuss the scientific knowledge currently available regarding the diagnosis, epidemiology, pathogenicity, and management of bacterial stripe in maize caused by *Acidovorax avenae* subsp. *avenae*. Narrative reviews are particularly suitable for providing a comprehensive understanding of a given topic, allowing the integration of theoretical, conceptual, and empirical evidence from multiple scientific sources without the methodological restrictions associated with systematic review protocols (Rother, 2007).

This approach is especially relevant for plant diseases that have received comparatively limited attention in the scientific literature and for which information remains dispersed across different disciplines, including plant pathology, microbiology, molecular diagnostics, crop protection, and disease epidemiology. The review was guided by the following research question: What are the current advances, limitations, and future perspectives regarding the diagnosis and management of bacterial stripe in maize caused by *Acidovorax avenae* subsp. *avenae*?

To address this question, a comprehensive bibliographic survey was conducted using national and international scientific databases, including SciELO, Portal de Periódicos CAPES, Web of Science, Scopus, PubMed/MEDLINE, Google Scholar, and the Biblioteca Digital Brasileira de Teses e Dissertações (BDTD). Searches were performed using isolated and combined descriptors in English, Portuguese, and Spanish. The main search terms included: "*Acidovorax avenae* subsp. *avenae*", "bacterial stripe of maize", "maize bacterial diseases", "corn bacterial stripe", "plant pathogenic bacteria", "maize disease diagnosis", "molecular detection of *Acidovorax*", "bacterial disease management", "fitobactérias do milho", "estria bacteriana do milho", and "diagnóstico molecular de fitobactérias". Boolean operators (AND, OR) were used to refine and expand the search strategy.

The temporal scope included studies published between 2020 and 2026, prioritizing recent scientific advances in pathogen detection, epidemiology, host-pathogen interactions, disease monitoring, and integrated disease management. However, seminal studies published before this period were also consulted when necessary to

provide historical context and support fundamental concepts related to the biology and taxonomy of *A. avenae* subsp. *avenae*. Eligible publications included original research articles, review papers, book chapters, theses, dissertations, conference proceedings, and technical-scientific documents available in English, Portuguese, or Spanish and directly related to bacterial stripe and other diseases associated with *Acidovorax* spp. Publications lacking scientific rigor, duplicate records, commercial dissemination materials, and studies not directly related to the proposed topic were excluded from the analysis.

Following the identification and selection of relevant studies, the retrieved information was subjected to qualitative content analysis. To facilitate data interpretation and synthesis, the literature was organized into five thematic categories: (i) taxonomy, biology, and pathogenicity of *Acidovorax avenae* subsp. *avenae*; (ii) epidemiology and symptomatology of bacterial stripe in maize; (iii) diagnostic methods and advances in pathogen detection; (iv) management and disease control strategies; and (v) current limitations, knowledge gaps, and future research perspectives. This thematic organization enabled the identification of convergences, divergences, and emerging trends within the scientific literature, contributing to a broader understanding of the disease and its implications for maize production systems.

The synthesis of evidence was performed through critical and interpretative analysis, emphasizing the relationships among pathogen biology, environmental conditions, host susceptibility, diagnostic technologies, and disease management practices. Particular attention was given to recent advances in molecular diagnostics, epidemiological monitoring, integrated disease management, biological control approaches, and emerging technologies such as remote sensing, genomics, and artificial intelligence-based disease detection systems. This integrative perspective sought to identify the principal challenges currently limiting the effective control of bacterial stripe in maize and to highlight future opportunities for improving disease management under modern agricultural production systems.

3. *Acidovorax avenae* Review

3.1. Symptoms and diagnosis of *Acidovorax avenae* subsp. *avenae*

The disease caused by *Acidovorax avenae* subsp. *avenae* (Aaa), commonly referred to as bacterial stripe, represents an important bacterial disease affecting maize and several other graminaceous hosts (Table 1). The pathogen colonizes leaf tissues and may spread systemically under favorable environmental conditions, particularly in regions characterized by high temperatures and prolonged periods of leaf wetness. Disease outbreaks

are often associated with tropical and subtropical production systems where elevated humidity promotes bacterial multiplication and dissemination (Zhao et al., 2023).

Table 1. Biological characteristics of *Acidovorax avenae* subsp. *avenae*.

Characteristics	Description
Gram	Negative
Shape	Rod-shaped
Motility	Polar flagellum
Hosts	Corn, rice, sorghum, sugarcane, etc.

Source: Authors, 2026.

The initial symptoms of bacterial stripe in maize typically appear as small, water-soaked lesions on the leaf blade. As infection progresses, these lesions elongate parallel to the veins, forming narrow translucent streaks that later become chlorotic and necrotic (Resmi; Kanhirala, 2024). In advanced stages, the lesions acquire a brown to reddish-brown coloration and may coalesce, resulting in extensive foliar blighting and reduction of the photosynthetically active area. Severe infections can compromise plant vigor, particularly when environmental conditions remain favorable for pathogen development throughout the growing season (Bertani et al., 2024; Zhao et al., 2023).

Symptom expression can vary according to maize genotype, environmental conditions, bacterial strain, and plant developmental stage. Similar symptoms have also been reported in other hosts infected by Aaa, including rice, sorghum, sugarcane, turfgrass, oats, and millet, indicating a broad host range and considerable phenotypic variability of the pathogen. This variability frequently complicates field diagnosis because bacterial stripe symptoms may resemble those caused by fungal leaf blights, nutrient deficiencies, abiotic stress factors, or infections caused by other phytopathogenic bacteria (Hernández-Juárez et al., 2021; Ogonkov et al., 2023; Zhao et al., 2023).

Accurate diagnosis based solely on visual assessment is therefore challenging and often insufficient for definitive pathogen identification. Conventional diagnosis generally begins with the observation of characteristic lesions followed by isolation of the bacterium from symptomatic tissues. On nutrient agar media, colonies of Aaa are usually circular, smooth, translucent, and cream-colored, although yellow-pigmented variants have also been reported. Microscopic

examination reveals Gram-negative rod-shaped cells possessing a single polar flagellum, a feature associated with bacterial motility and host colonization (Zhao et al., 2023).

Advances in molecular diagnostics have substantially improved the detection and identification of *A. avenae* subsp. *avenae*. Polymerase chain reaction (PCR)-based methods targeting the 16S–23S rDNA internal transcribed spacer (ITS) region are currently among the most widely employed techniques due to their high specificity and sensitivity. Species-specific primers have been successfully used to amplify characteristic DNA fragments from infected plant tissues, enabling reliable pathogen detection even when bacterial populations are low or symptoms are not fully developed (Jariwala, 2025; Netsu et al., 2022; Zhao et al., 2023).

In addition to conventional PCR, sequencing of the 16S rRNA gene, multilocus sequence typing (MLST), restriction fragment length polymorphism (RFLP), repetitive sequence-based PCR (rep-PCR), and whole-genome approaches have become increasingly important for epidemiological studies and strain characterization. These methodologies allow the differentiation of pathogen populations, identification of genetic diversity patterns, and monitoring of pathogen dissemination among production regions. Recent studies have demonstrated substantial genetic variability among Aaa isolates from different hosts and geographic locations, suggesting the existence of distinct evolutionary lineages with potential differences in aggressiveness and host adaptation (Jariwalaa, 2025; Zhao et al., 2023).

Emerging technologies are also contributing to disease diagnosis and surveillance. Remote sensing platforms, hyperspectral imaging, unmanned aerial vehicles (UAVs), and artificial intelligence-based image analysis systems are being investigated as tools for early disease detection. These approaches can identify physiological alterations in plants before visible symptom expression, offering opportunities for rapid disease monitoring over large agricultural areas. Although still under development for bacterial stripe specifically, such technologies may significantly enhance disease management and epidemiological surveillance in modern maize production systems (Mall et al., 2023).

Despite significant progress in diagnostic technologies, important limitations remain. The lack of standardized diagnostic protocols, restricted availability of molecular tools in many production regions, and the potential occurrence of asymptomatic infections continue to hinder accurate disease assessment. Therefore, integrated diagnostic approaches combining symptom observation, pathogen isolation, molecular confirmation, and advanced monitoring technologies are currently

considered the most reliable strategy for the identification and surveillance of bacterial stripe caused by *A. avenae* subsp. *avenae* in maize production systems (Zhao et al., 2023).

3.2. Epidemiology of *Acidovorax avenae* subsp. *avenae*

The epidemiology of bacterial stripe caused by *A. avenae* subsp. *avenae* is strongly influenced by the interaction among environmental conditions, pathogen survival mechanisms, host susceptibility, and agricultural management practices.

This bacterium is widely distributed in tropical, subtropical, and temperate regions and has been reported to infect numerous monocotyledonous hosts, including maize, rice, sorghum, millet, oats, sugarcane, rye, and turfgrasses. The broad host range of *Aaa* contributes significantly to its persistence in agricultural ecosystems and facilitates the maintenance of inoculum between cropping seasons. Recent phylogenetic studies have demonstrated substantial genetic diversity among populations collected from different hosts and geographic regions, suggesting the existence of host-adapted lineages that may influence disease dynamics and epidemic development (Zhao et al., 2023; Ogonkov et al., 2023).

The pathogen survives in infected crop residues, volunteer plants, alternative grass hosts, and contaminated seeds, which constitute the primary sources of inoculum for new disease outbreaks. Seedborne transmission is considered one of the most important mechanisms for long-distance dissemination, allowing the movement of bacterial populations across production regions and international borders. Several studies have demonstrated the occurrence of *Aaa* in naturally infected seed lots of gramineous crops, highlighting the epidemiological importance of seed health in disease management programs. The ability of the bacterium to remain viable in seeds and plant debris significantly enhances its survival during unfavorable periods and promotes the initiation of primary infections during subsequent growing seasons (Somda et al., 2001; Zhao et al., 2023).

Environmental conditions play a decisive role in disease development. High temperatures, generally ranging from 25 to 35 °C, combined with prolonged periods of leaf wetness, rainfall, overhead irrigation, and elevated relative humidity, create optimal conditions for bacterial multiplication and infection. Under these circumstances, bacterial populations rapidly colonize leaf surfaces and penetrate host tissues through natural openings such as stomata, hydathodes, and wounds caused by mechanical damage, hail, wind abrasion, or insect feeding. Epidemics are frequently associated with seasons characterized by intense rainfall and warm temperatures, conditions commonly observed in tropical

maize-producing regions (Li et al., 2014; Zhao et al., 2023).

Secondary dissemination within fields occurs primarily through rain splash, irrigation water, contaminated agricultural equipment, human activities, and direct contact between infected and healthy plants. Wind-driven rain can transport bacterial cells over considerable distances, increasing disease incidence and accelerating epidemic progression. Dense plant populations and reduced air circulation within crop canopies further contribute to disease establishment by prolonging leaf wetness duration and creating favorable microclimatic conditions for bacterial survival and infection. Consequently, agronomic practices that increase canopy humidity may indirectly favor disease outbreaks (Zhao et al., 2023).

Host susceptibility represents another critical epidemiological factor. Although bacterial stripe has been reported in numerous gramineous species, disease severity may vary substantially among cultivars and host species. Genetic variability among pathogen populations, coupled with differences in host resistance mechanisms, can result in distinct levels of symptom expression and pathogen aggressiveness. Recent investigations have demonstrated that different *Aaa* strains possess variable pathogenic capacities and may induce distinct disease severities even under similar environmental conditions, suggesting that pathogen genetic diversity is an important driver of epidemic behavior (Ogonkov et al., 2023).

Advances in molecular biology have expanded the understanding of epidemiological processes associated with *Aaa*. Genomic and transcriptomic studies have identified several virulence-associated genes, secretion systems, and effector proteins involved in host colonization and symptom development. These molecular determinants influence bacterial fitness, adaptation to environmental conditions, and interactions with host defense mechanisms. Comparative genomic analyses have revealed substantial variation among isolates obtained from different hosts and geographic regions, supporting the hypothesis that local adaptation may contribute to disease emergence and persistence in specific agroecosystems (Li et al., 2014; Nakamura et al., 2021).

Climate change is increasingly recognized as a factor capable of modifying the epidemiology of bacterial diseases, including those caused by *Acidovorax* species. Rising temperatures, altered rainfall patterns, increased frequency of extreme weather events, and prolonged periods of environmental stress may favor pathogen survival, dissemination, and infection processes. These environmental changes may expand the geographical distribution of bacterial stripe and increase disease

incidence in areas previously considered less favorable for pathogen establishment. Consequently, future epidemiological studies should integrate climatic variables into predictive models to improve disease forecasting and support the development of sustainable disease management strategies (Zytyńska et al., 2020; Zhao et al., 2023).

Despite recent advances, significant knowledge gaps remain regarding the epidemiology of bacterial stripe in maize. Information concerning pathogen survival under different soil and residue management systems, interactions with the crop microbiome, quantitative effects of environmental variables on epidemic progression, and the role of asymptomatic hosts remains limited. Addressing these gaps will be essential for improving epidemiological models, enhancing disease monitoring programs, and developing integrated management strategies capable of reducing the impact of *Acidovorax avenae* subsp. *avenae* in modern maize production systems (Nakamura et al., 2021; Zhao et al., 2023).

3.3. Management of bacterial stripe caused by *Acidovorax avenae* subsp. *avenae*

The management of bacterial stripe caused by *A. avenae* subsp. *avenae* remains challenging due to the absence of highly effective curative measures and the ability of the pathogen to survive in infected seeds, crop residues, alternative hosts, and environmental reservoirs. Consequently, disease management relies primarily on integrated approaches that combine preventive, cultural, genetic, biological, and chemical strategies. Recent studies have emphasized that no single control measure provides complete disease suppression, highlighting the importance of integrated disease management programs tailored to local production systems (Zhao et al., 2023; Torres, 2024).

3.3.1 Chemical control

Chemical control of bacterial diseases caused by *Acidovorax* species has traditionally been based on the application of copper-based compounds and, in some regions, antibiotics authorized for agricultural use. However, the effectiveness of these products is often inconsistent because bacterial infections frequently occur within plant tissues, limiting product penetration and reducing control efficiency. Furthermore, repeated applications may increase selection pressure for tolerant bacterial populations and raise environmental concerns associated with copper accumulation in agricultural soils (Torres, 2024).

Recent investigations have evaluated alternative

chemical compounds, resistance inducers, and combinations of bactericides as complementary tools for disease management. Salicylic acid and other defense-activating molecules have demonstrated potential to stimulate plant defense responses and reduce symptom severity in host-pathogen systems involving *A. avenae* subsp. *avenae*. Although promising, these approaches still require validation under field conditions and across different maize-growing environments before large-scale adoption can be recommended (Zhao et al., 2023).

The effectiveness of chemical control is strongly dependent on its integration with preventive practices, including the use of pathogen-free seed lots, crop residue management, sanitation of agricultural equipment, and reduction of conditions favorable to bacterial dissemination. Therefore, chemical treatments should be viewed as complementary components of integrated disease management rather than as standalone solutions (Monachesi et al., 2024; Torres, 2024).

3.3.2 Biological control

Biological control has emerged as a promising and environmentally sustainable alternative for managing bacterial diseases in agricultural systems. Beneficial microorganisms, including species of *Bacillus*, *Pseudomonas*, *Streptomyces*, and other plant growth-promoting rhizobacteria (PGPR), can suppress phytopathogenic bacteria through mechanisms such as antibiosis, nutrient competition, niche exclusion, biofilm formation, and induction of systemic resistance in plants (Lee et al., 2023).

Although studies specifically targeting *A. avenae* subsp. *avenae* in maize remains limited, evidence from related bacterial pathosystems indicates that microbial antagonists may significantly reduce pathogen populations and disease severity. The increasing understanding of plant microbiomes has also opened new opportunities for the development of microbial consortia capable of enhancing plant resilience and suppressing bacterial pathogens under field conditions. These approaches are particularly attractive within sustainable and low-input agricultural systems (Lee et al., 2023; Zytyńska et al., 2020).

Recent advances in microbial ecology and biotechnology have facilitated the identification of beneficial microorganisms with multiple modes of action. However, challenges related to environmental stability, formulation, shelf life, and field performance continue to limit the widespread adoption of biological products for bacterial stripe management. Further research is required to optimize application methods and evaluate interactions among microbial agents, host plants, and environmental conditions (Lee et al., 2023).

3.3.3 Genetic control

Genetic resistance is widely regarded as the most effective, economical, and environmentally sustainable strategy for the long-term management of bacterial diseases. The deployment of resistant or tolerant cultivars reduces pathogen multiplication, limits disease dissemination, and decreases reliance on chemical inputs. Consequently, breeding programs have increasingly focused on identifying resistance sources and incorporating favorable alleles into commercially competitive cultivars (Zhao et al., 2023).

Studies conducted in sugarcane, where *A. avenae* subsp. *avenae* has caused significant economic losses, have demonstrated that cultivar resistance remains the cornerstone of disease management. Similar strategies are expected to play a crucial role in maize production systems. However, the considerable genetic diversity observed among Aaa populations may complicate resistance breeding efforts because pathogen variability can lead to differential host responses and potential resistance breakdown over time (Zhao et al., 2023).

Advances in genomics, molecular breeding, and gene-editing technologies offer new opportunities for the development of resistant maize cultivars. Marker-assisted selection, genomic selection, and CRISPR-based approaches may accelerate the identification and incorporation of resistance traits into elite germplasm. Nevertheless, additional research is necessary to elucidate the genetic basis of host resistance and the molecular mechanisms underlying interactions between maize and *A. avenae* subsp. *avenae* (Nakamura et al., 2021; Bertani et al., 2024).

3.3.4 Integrated disease management

Given the complexity of bacterial stripe epidemiology and the limitations associated with individual control measures, integrated disease management (IDM) represents the most effective approach currently available. IDM programs should combine certified pathogen-free seeds, crop rotation, destruction of infected crop residues, sanitation of tools and machinery, balanced fertilization, disease monitoring, biological control agents, and resistant cultivars whenever available. Such integration reduces inoculum sources, limits pathogen dissemination, and enhances the sustainability of maize production systems (Torres, 2024; Monachesi et al., 2024).

Future disease management strategies are expected to incorporate precision agriculture, remote sensing technologies, artificial intelligence-based disease detection systems, and predictive epidemiological

models. These innovations may improve early diagnosis, optimize intervention timing, and enhance the overall effectiveness of bacterial stripe management under changing environmental conditions and increasingly intensive agricultural systems (Zhao et al., 2023).

3.4. Current limitations and future perspectives for the control of *Acidovorax avenae* subsp. *avenae*

Despite recent advances in plant pathology, molecular biology, and disease management, the control of bacterial stripe caused by *A. avenae* subsp. *avenae* remains a significant challenge for maize production systems worldwide. The complexity of the host–pathogen interaction, the broad host range of the bacterium, its capacity to survive in crop residues and seeds, and the limited availability of effective control measures contribute to the persistence of the disease in agricultural environments. Furthermore, the increasing intensification of agricultural systems and the expansion of maize cultivation into new production areas may create favorable conditions for disease establishment and dissemination (Zhao et al., 2023).

One of the principal limitations associated with disease management is the lack of highly resistant commercial maize cultivars. Although variability in host susceptibility has been reported, resistance sources remain poorly characterized, and few breeding programs have specifically targeted bacterial stripe resistance. The substantial genetic diversity observed among Aaa populations further complicates resistance breeding because pathogen variability may result in differential virulence and potential resistance breakdown over time. Consequently, the identification of stable and durable resistance genes remains a priority for future research (Bertani et al., 2024; Zhao et al., 2023).

Another important constraint involves disease diagnosis and monitoring. Symptom similarity with other foliar diseases often results in misdiagnosis, particularly under field conditions where laboratory confirmation is unavailable. Although molecular diagnostic techniques such as PCR, quantitative PCR (qPCR), and genomic sequencing have improved pathogen detection, these technologies are not always accessible in developing agricultural regions due to infrastructure and cost limitations. Therefore, the development of rapid, affordable, and field-deployable diagnostic tools remains essential for improving disease surveillance and early detection programs (Nakamura et al., 2021; Zhao et al., 2023).

Chemical control also presents significant limitations. Copper-based bactericides and other antimicrobial compounds generally provide only partial suppression of bacterial populations and are highly dependent on

application timing and environmental conditions. Moreover, repeated use of these products may contribute to the emergence of tolerant bacterial strains and increase concerns regarding environmental contamination and soil accumulation of chemical residues. As a result, chemical control alone is insufficient to ensure long-term disease management and should be integrated with other strategies (Torres, 2024).

Biological control represents a promising alternative; however, its practical implementation remains limited. Although several beneficial microorganisms have demonstrated antagonistic activity against phytopathogenic bacteria, relatively few studies have specifically evaluated their effectiveness against *A. avenae* subsp. *avenae* under field conditions. Variability in environmental conditions, microbial survival, formulation stability, and interactions with native microbiota continue to restrict the large-scale adoption of biological products. Additional research is needed to identify effective microbial agents and optimize their application in maize production systems (Lee et al., 2023).

Climate change introduces an additional layer of complexity to disease management. Rising temperatures, altered precipitation regimes, and the increasing frequency of extreme weather events may favor bacterial survival, dissemination, and infection processes. These environmental changes could expand the geographic distribution of bacterial stripe and increase disease incidence in regions where the pathogen was previously considered of minor importance. Consequently, future disease forecasting systems should incorporate climatic variables to improve epidemiological predictions and support decision-making processes (Zhao et al., 2023; Zytynska et al., 2020).

Despite these challenges, several emerging technologies offer promising opportunities for improving bacterial stripe management. Advances in genomics, transcriptomics, proteomics, and comparative genome analyses are expanding knowledge regarding pathogen virulence mechanisms and host resistance pathways. These approaches may facilitate the identification of resistance-associated genes, molecular markers, and novel targets for disease control. In addition, next-generation sequencing technologies are enabling more detailed studies of pathogen population structure and evolutionary dynamics, providing valuable information for epidemiological monitoring and resistance breeding programs (Bertani et al., 2024; Nakamura et al., 2021).

The integration of precision agriculture technologies also represents a major future perspective. Remote sensing, hyperspectral imaging, unmanned aerial vehicles (UAVs), machine learning algorithms, and artificial

intelligence-based disease detection systems have demonstrated considerable potential for identifying disease symptoms before they become visually apparent. These technologies may allow real-time disease monitoring, improve management timing, and reduce unnecessary pesticide applications, contributing to more sustainable crop protection systems (Mall et al., 2023).

Gene-editing technologies such as CRISPR/Cas systems may further accelerate the development of resistant maize cultivars. By enabling precise modifications of susceptibility genes or the introduction of resistance-associated traits, these tools offer unprecedented opportunities for enhancing host resistance. Although their application to bacterial stripe remains at an early stage, gene-editing approaches are expected to play an increasingly important role in future disease management programs (Bertani et al., 2024).

Overall, the future control of *Acidovorax avenae* subsp. *avenae* will likely depend on integrated disease management strategies that combine resistant cultivars, rapid diagnostic technologies, biological control agents, precision agriculture tools, and improved epidemiological forecasting models. Continued investment in multidisciplinary research will be essential to overcome current limitations and develop sustainable solutions capable of minimizing the impact of bacterial stripe on global maize production systems (Zhao et al., 2023).

4. Conclusion

Acidovorax avenae subsp. *avenae* is an emerging bacterial pathogen of increasing importance in maize production systems worldwide. Its ability to survive in seeds, crop residues, and alternative hosts, combined with favorable environmental conditions, contributes to disease persistence and dissemination. Advances in molecular diagnostics have substantially improved pathogen detection and epidemiological studies; however, significant challenges remain regarding disease monitoring, early detection, and effective control under field conditions.

Current management strategies rely primarily on preventive and integrated approaches, including the use of healthy seeds, cultural practices, biological control agents, and host resistance whenever available. Nevertheless, the limited availability of resistant maize cultivars and the inconsistent effectiveness of chemical and biological control measures highlight the need for further research. Emerging technologies such as genomics, precision agriculture, artificial intelligence, remote sensing, and gene-editing tools offer promising opportunities for improving disease diagnosis and management.

Future efforts should focus on understanding pathogen diversity, host–pathogen interactions, resistance mechanisms, and the effects of climate change on disease epidemiology. The integration of advanced technologies with sustainable crop management practices will be essential for reducing the impact of bacterial stripe and ensuring the long-term productivity and resilience of maize production systems.

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