

Sorghum mosaic disease: Epidemiology, transmission, and management challenges of sorghum mosaic caused by sorghum mosaic virus in tropical agricultural systems

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Abstract

Sorghum (*Sorghum bicolor* L. Moench) is a crop of major relevance for food security, animal production, and bioenergy, particularly due to its high tolerance to water deficit and adaptability to adverse environmental conditions. However, its productivity is significantly constrained by viral diseases, among which sorghum mosaic, caused by Sorghum mosaic virus, stands out as one of the most economically important. In this context, this study aimed to critically review the epidemiology, transmission mechanisms, and management challenges associated with SrMV in tropical agricultural systems. This work was conducted as a qualitative literature review, based on a systematic search of scientific articles, books, dissertations, theses, and technical reports published between 2020 and 2025, retrieved from national and international scientific databases. The findings indicate that SrMV, a member of the genus Potyvirus, exhibits high genetic variability, which enhances its adaptive potential and contributes to its widespread distribution. The virus is primarily transmitted by aphids in a non-persistent manner, with epidemiological dynamics strongly influenced by tropical environmental conditions, the abundance of alternative host plants, and the continuous presence of susceptible grass species in cropping systems. Disease management is largely dependent on preventive and integrated strategies, including the deployment of resistant cultivars, effective vector control, eradication of inoculum sources, and the implementation of integrated pest management (IPM) practices. Overall, the study highlights that a comprehensive understanding of the epidemiological behavior and transmission biology of SrMV is essential for the development of sustainable and effective management strategies, thereby supporting the stability and productivity of sorghum-based cropping systems in tropical regions.

Keywords: sorghum mosaic virus, sorghum, viral epidemiology, aphids, integrated management.

Doença do mosaico do sorgo: Epidemiologia, transmissão e desafios no manejo do sorghum mosaic virus em sistemas agrícolas tropicais

Resumo

O sorgo (*Sorghum bicolor* L. Moench) é uma cultura de grande relevância para a segurança alimentar, produção animal e geração de bioenergia, destacando-se pela elevada tolerância ao déficit hídrico e pela adaptabilidade a condições ambientais adversas. Entretanto, sua produtividade é significativamente limitada por doenças virais, entre as quais se destaca o mosaico do sorgo, causado pelo Sorghum mosaic virus, considerado uma das viroses de maior importância econômica. Nesse contexto, este estudo teve como objetivo realizar uma revisão crítica sobre a epidemiologia, os mecanismos de transmissão e os desafios no manejo do SrMV em sistemas agrícolas tropicais. O trabalho foi conduzido como uma revisão bibliográfica de abordagem qualitativa, baseada em busca sistemática de artigos científicos, livros, dissertações, teses e relatórios técnicos publicados entre 2020 e 2025, obtidos em bases de dados científicas nacionais e internacionais. Os resultados indicam que o SrMV, pertencente ao gênero

Potyvirus, apresenta elevada variabilidade genética, o que favorece seu potencial adaptativo e contribui para sua ampla disseminação. A transmissão ocorre principalmente por afídeos, de forma não persistente, sendo fortemente influenciada por condições ambientais típicas de regiões tropicais, pela abundância de plantas hospedeiras alternativas e pela presença contínua de gramíneas suscetíveis nos sistemas de cultivo. O manejo da doença depende, em grande parte, de estratégias preventivas e integradas, incluindo a utilização de cultivares resistentes, o controle eficiente de vetores, a eliminação de fontes de inóculo e a adoção de práticas de manejo integrado de pragas (MIP). De modo geral, o estudo evidencia que a compreensão abrangente do comportamento epidemiológico e da biologia de transmissão do SrMV é essencial para o desenvolvimento de estratégias de controle sustentáveis e eficazes, contribuindo para a estabilidade e a produtividade dos sistemas de cultivo de sorgo em regiões tropicais.

Palavras-chave: sorghum mosaic virus, sorgo, epidemiologia viral, afídeos, manejo integrado.

1. Introduction

Sorghum bicolor belongs to the Poaceae family, which includes some of the world's most economically important cereal crops, such as wheat, rice, and maize (Karimi; Saeidi, 2022; Kazungu et al., 2023; Nemera et al., 2022). This crop exhibits high adaptability to adverse environmental conditions, particularly in tropical and subtropical regions, due to its tolerance to water deficit and its ability to produce under low to moderate soil fertility conditions (Spindel et al., 2018).

In recent decades, sorghum cultivation has expanded significantly, especially in developing countries, driven by its hardiness and versatile uses (Hossain et al., 2022). The crop stands out for its broad climatic adaptation and multiple applications in grain production, forage, silage, and bioenergy, reinforcing its importance in agricultural systems, including in Brazil (Silva et al., 2024).

Sorghum represents a strategic alternative in agricultural systems exposed to climatic stress, particularly in arid and semi-arid regions, due to its well-documented drought tolerance and high water-use efficiency (Hadebe et al., 2017). In addition, it is a relatively short-cycle crop, ranging from 90 to 120 days to harvest, depending on the cultivar and environmental conditions (Silveira, 2023). Its physiological efficiency supports its use in crop rotation systems, enhancing agricultural sustainability (Santos et al., 2020).

From a socioeconomic perspective, sorghum serves as a staple food for more than half a billion people worldwide, contributing significantly to global food security, and also holds strong industrial potential, particularly for bioethanol production (Mathure et al., 2017). In the context of climate change, its importance becomes even more evident due to its resilience and ability to maintain productivity under adverse conditions, making it a strategic crop for vulnerable agricultural systems (Khalifa; Eltahir, 2023; Hossain et al., 2022).

Despite its resilience, sorghum productivity can be severely affected by diseases, particularly viral infections. Among them, sorghum mosaic, caused by Sorghum mosaic virus, stands out as one of the most important diseases affecting the crop. The virus belongs to the genus *Potyvirus* and the family Potyviridae, and is widely distributed in sorghum- and sugarcane-producing regions across Africa, Asia, and the Americas (Lu et al., 2021). The epidemiology of SrMV is complex and influenced by multiple factors, including viral genetic variability, host diversity, and favorable environmental conditions (Xu et al., 2023). The presence of alternative hosts, such as maize and sugarcane, as well as susceptible wild grasses, plays a key role in maintaining and spreading viral inoculum (Lu et al., 2021).

Under field conditions, SrMV incidence can reach high levels, resulting in significant yield losses. In tropical and subtropical regions, high temperatures, continuous host cultivation, and the presence of volunteer plants favor virus survival and year-round dissemination (Xu et al., 2021). Transmission occurs primarily through insect vectors, especially aphids, which spread the virus in a non-persistent manner during feeding on infected plants, a mechanism typical of potyviruses and highly efficient in rapid field dissemination (Mauck et al., 2018). Recent studies indicate that the use of resistant cultivars remains the most effective management strategy, contributing to reduced viral incidence and mitigation of yield losses (Hussain et al., 2022; Lu et al., 2021).

In this context, an integrated understanding of SrMV epidemiology, transmission mechanisms, and management challenges is essential for the development of sustainable and effective control strategies in tropical agricultural systems. Given the importance of sorghum and the impacts caused by Sorghum mosaic virus in production systems, this study is characterized as an integrative literature review. This methodological approach allows for the synthesis and critical analysis of the available scientific knowledge, bringing together evidence from different research designs. Thus, it aims to integrate and systematize information on the epidemiology, transmission mechanisms,

and management challenges of SrMV in tropical agricultural systems, contributing to a broader and more up-to-date understanding of the topic and providing support for more efficient and sustainable control strategies.

2. Materials and Methods

This study was designed as an integrative literature review with a qualitative approach, aiming to systematically collect, critically appraise, and synthesize current scientific evidence on the epidemiology, transmission dynamics, and management strategies of Sorghum mosaic virus in tropical agricultural systems.

The integrative review framework was selected due to its capacity to incorporate diverse methodological designs, including experimental, observational, and theoretical studies, thereby enabling a comprehensive and multidimensional understanding of complex plant-virus interactions. This approach supports evidence integration across disciplinary boundaries, facilitating the identification of epidemiological patterns, research gaps, and methodological convergences within the scientific literature. A qualitative interpretative perspective was adopted to allow in-depth examination of conceptual, ecological, and epidemiological dimensions, prioritizing contextualized understanding over statistical aggregation (Minayo, 2012).

2.1 Information sources and search strategy

A systematic and structured bibliographic search was conducted across multiple international and multidisciplinary scientific databases, including Google Scholar, ScienceDirect, PubMed, SciELO, SpringerLink, and MDPI. These platforms were selected due to their broad coverage of plant pathology, virology, agronomy, and agricultural epidemiology literature.

The search strategy was constructed using controlled and free-text descriptors in both Portuguese and English, combined through Boolean operators (AND, OR) to maximize sensitivity and specificity. Keywords included: “Sorghum mosaic virus”, “mosaico do sorgo”, “*Potyvirus*”, “plant viral epidemiology”, “aphid-borne transmission”, “integrated pest management”, “viral diseases in grasses”, and “sorghum”.

Advanced search combinations were implemented to refine retrieval, including: “Sorghum mosaic virus AND epidemiology”, “*Potyvirus* AND aphid transmission”, “plant virus ecology AND sorghum”, and “sorghum mosaic OR Sorghum mosaic virus”. Searches were iteratively adjusted to ensure coverage of epidemiological, molecular, and agronomic dimensions of the topic.

2.2 Eligibility criteria

Studies were considered eligible if they met the following criteria: (i) peer-reviewed scientific articles, review papers, books, dissertations, theses, and technical reports; (ii) full-text availability; (iii) publication between 2012 and 2026; and (iv) explicit focus on epidemiology, molecular characterization, transmission biology, vector ecology, or integrated management of SrMV and related *Potyvirus* species infecting grasses.

Exclusion criteria comprised duplicate records, conference abstracts without full methodological description, non-peer-reviewed materials, studies not directly related to plant viral diseases in grasses, and publications outside the defined temporal scope. Classical and foundational references were retained when deemed essential for theoretical and conceptual framing.

2.3 Study selection and synthesis approach

Retrieved records were initially screened based on title and abstract relevance, followed by full-text evaluation according to eligibility criteria. Although not structured as a meta-analysis, data extraction followed a qualitative synthesis approach, focusing on recurring epidemiological mechanisms, transmission pathways, and management strategies reported across studies.

Extracted information was organized into thematic categories, including: (i) viral diversity and genetic variability, (ii) host range and reservoir dynamics, (iii) aphid-mediated transmission mechanisms, and (iv) integrated disease management strategies. This thematic synthesis enabled cross-study comparison and the identification of consistent epidemiological trends under tropical agricultural conditions.

3. Viral diseases in cultivated grasses

Viral diseases represent one of the major biotic constraints limiting productivity in cultivated grasses, particularly in tropical agricultural systems, where environmental conditions favor vector activity and the persistence of alternative host plants, thereby intensifying disease epidemiology. In this context, viruses belonging to the genus *Potyvirus* are especially relevant, as they are widely associated with economically important crops such as sorghum, maize, and sugarcane, and are frequently linked to significant yield losses across major production regions (Lu et al., 2021; Xu et al., 2023).

The spread of these viruses in grasses is closely associated with insect vectors, particularly aphids (Aphididae), which transmit the virus in a non-persistent manner during feeding on infected plant tissues. This transmission mode promotes rapid field dissemination, especially in systems characterized by high host density, extensive monocultures, and continuous cultivation of susceptible species (Mauck et al., 2018). In addition, transmission efficiency may be influenced by abiotic and biotic factors, including temperature, host plant phenological stage, and plant community composition, contributing to the high epidemiological complexity of these diseases (Fingu-Mabola; Francis, 2021).

Another critical aspect of the epidemiology of these viruses is the high genetic variability observed within the genus *Potyvirus*, characterized by elevated mutation and recombination rates. These evolutionary processes favor the emergence of viral variants with enhanced adaptive plasticity, capable of overcoming host resistance barriers in cultivated plants. Consequently, this variability poses a major challenge to plant breeding programs and integrated management strategies, as it may reduce the durability of resistance in commercial cultivars (Xu et al., 2023).

4. Characterization of sorghum mosaic virus (SrMV)

Sorghum mosaic virus (SrMV) Figure 1 and Table 1 is a plant virus belonging to the genus *Potyvirus* and the family *Potyviridae*, a group that comprises the largest collection of plant viruses with a positive-sense single-stranded RNA (+ssRNA) genome. This family includes more than 200 species distributed across different viral genera, with *Potyvirus* representing the largest and most economically important genus, encompassing over 180 recognized species associated with major diseases in globally important crops (Inoue-Nagata et al., 2022; Klein; Smith, 2020).

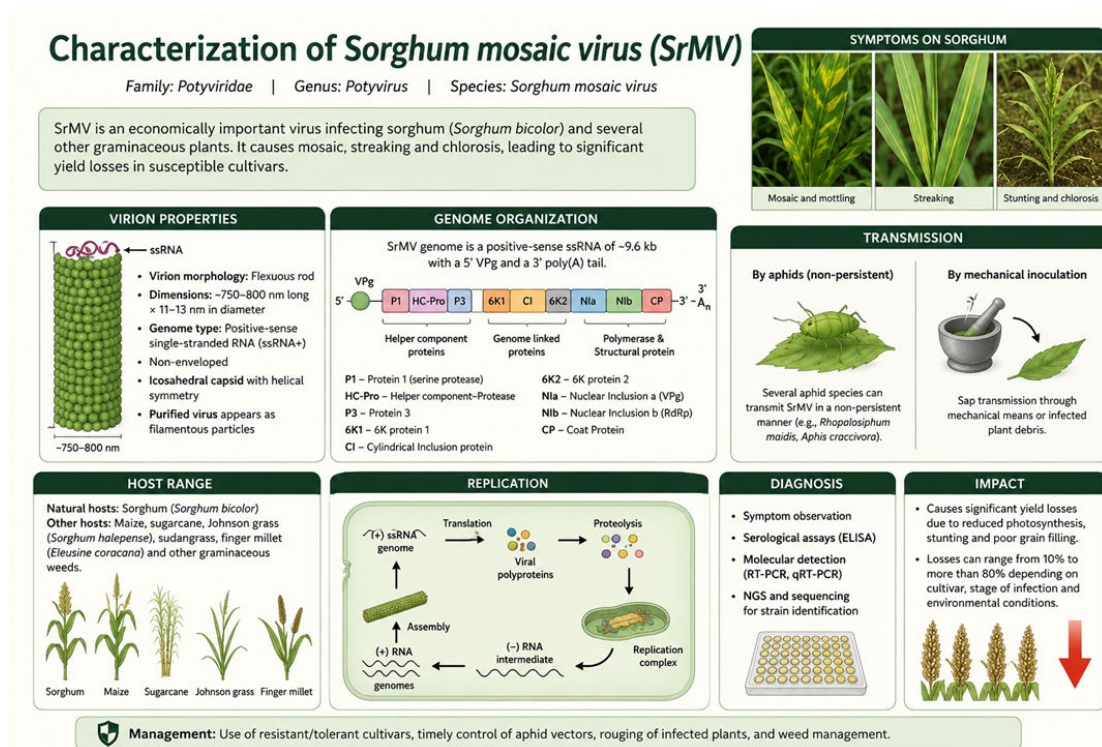


Figure 1. Characterization of Sorghum mosaic virus (SrMV). Source: Authors, 2026.

Table 1. Key characteristics of Sorghum mosaic virus (SrMV), including taxonomy, genome, host range, transmission, diagnostic methods, and management strategies.

Aspect	Information
Family	Potyviridae
Genus	Potyvirus
Genome	Positive-sense single-stranded RNA (ssRNA+)
Vectors	Aphididae species, especially <i>Rhopalosiphum maidis</i> and <i>Toxoptera graminum</i>
Main hosts	<i>Sorghum bicolor</i> , <i>Saccharum officinarum</i> , <i>Zea mays</i> and other Poaceae species
Diagnostic methods	ELISA, RT-PCR, IC-RT-PCR, qRT-PCR and RT-LAMP
Management	Resistant cultivars, integrated pest management (IPM), vector control, elimination of inoculum sources and phytosanitary monitoring

Source: Authors, 2026.

Structurally, SrMV particles are non-enveloped and exhibit flexible filamentous morphology, a hallmark of potyviruses. Its genome consists of a positive-sense single-stranded RNA molecule containing a single open reading frame (ORF), which encodes a large polyprotein subsequently cleaved by viral proteases into functional proteins essential for the infection cycle. This genomic organization is highly conserved within the genus *Potyvirus*, reflecting its evolutionary efficiency and adaptability (Mäkinen et al., 2023).

From an evolutionary perspective, SrMV displays high genetic variability among isolates, driven by mutation, recombination, natural selection, genetic drift, and geographic isolation. These processes contribute to the emergence of viral variants with differing levels of virulence, adaptability, and ability to overcome host genetic resistance in cultivated species (Lu et al., 2021; Xu et al., 2023).

The host range of SrMV includes mainly sorghum, sugarcane, and maize, as well as ornamental and forage species such as *Miscanthus sinensis*. Infection is associated with typical symptoms of viral diseases in grasses, including leaf mosaic, chlorosis, green and yellow mottling, leaf deformation, and reduced plant growth. In severe cases, infection significantly impairs photosynthesis, reduces biomass accumulation, and decreases sugar content in sugarcane, leading to substantial economic losses in production systems (Agyemang et al., 2025; Viswanathan et al., 2023).

SrMV detection can be performed using different diagnostic approaches, including serological and molecular methods such as ELISA, RT-PCR, IC-RT-PCR, qRT-PCR, and RT-LAMP. Among these, molecular amplification-based techniques, particularly IC-RT-PCR, exhibit higher sensitivity and diagnostic accuracy compared to conventional serological assays such as ELISA and Dot-ELISA, and are widely recommended for early detection in plant tissue samples (Lu et al., 2021).

4.1 Genome and proteins encoded by Sorghum mosaic virus (SrMV)

Sorghum mosaic virus (SrMV) belongs to the genus *Potyvirus* and the family Potyviridae. Its genome consists of a positive-sense single-stranded RNA (+ssRNA) molecule approximately 9.6 – 10.0 kb in length, carrying a covalently linked protein at the 5' end known as VPg (viral protein genome-linked) and a poly(A) tail at the 3' end. The genome contains a single open reading frame (ORF) that is translated into a large polyprotein, which is subsequently cleaved into mature functional proteins (Xu et al., 2023; Zhang et al., 2016). These proteins include P1, HC-Pro, P3, 6K1, CI, 6K2, VPg, NIa-Pro, NIb, and CP, as well as the PIPO protein generated through a transcriptional frameshift mechanism within the P3 coding region. The genomic organization of SrMV follows the conserved pattern observed in potyviruses, with proteins expressed in the following order: P1–HC-Pro–P3–6K1–CI–6K2–VPg–NIa-Pro–NIb–CP. Maturation of these proteins occurs through proteolytic cleavage mediated by the viral proteases P1, HC-Pro, and NIa-Pro (Mei et al., 2019; Parizipour et al., 2025; Xu et al., 2023).

4.2 Biological Functions of the Proteins Encoded by SrMV

4.2.1 P1 (Proteinase 1)

P1 is a serine protease responsible for the autocatalytic cleavage of the N-terminal region of the viral polyprotein. Beyond its proteolytic role, P1 contributes to host adaptation, expansion of host range, and enhancement of viral translation and replication efficiency. Studies on potyviruses have also demonstrated that P1 potentiates HC-Pro-mediated suppression of RNA silencing (Cui; Wang, 2016).

4.2.2 HC-Pro (Helper Component-Proteinase)

HC-Pro is a multifunctional protein essential for successful viral infection. It acts as a protease, facilitates aphid-mediated transmission, promotes systemic movement of the virus, and functions as a potent suppressor of RNA silencing, allowing the virus to evade host antiviral defense mechanisms (Widyasari et al., 2020).

4.2.3 P3 (Protein 3)

The P3 protein is involved in viral replication and interactions with host cellular factors. Research indicates that P3 recruits plant proteins required for the assembly of viral replication complexes and contributes to intracellular viral movement. In addition, the P3 coding region gives rise to the PIPO protein, which is associated with cell-to-cell movement (Widyasari et al., 2020).

4.2.4 6K1

The 6K1 protein is a small peptide of approximately 6 kDa associated with viral replication complexes. Although its complete function remains unclear, available evidence suggests that it participates in the early formation of replication complexes and is required for efficient viral genome replication (Cui; Wang, 2016).

4.2.5 CI (Cylindrical Inclusion Protein)

CI possesses helicase activity and plays a fundamental role in viral RNA replication. It also directly participates in cell-to-cell movement through the formation of cylindrical inclusions ("pinwheel" structures), characteristic of potyviruses, which facilitate viral transport through plasmodesmata (Widyasari et al., 2020).

4.2.6 6K2

The 6K2 protein is a transmembrane protein that induces the reorganization of host cell membranes to form viral replication vesicles. These vesicles serve as specialized platforms for viral RNA synthesis. Furthermore, 6K2 is involved in systemic movement and establishment of infection within host plants (Zhang et al., 2019).

4.2.7 VPg (Viral Protein Genome-Linked)

VPg is covalently attached to the 5' end of the viral RNA. This protein plays essential roles in viral translation, replication, and movement. It interacts with plant translation initiation factors, particularly eIF4E and eIF(iso)4E, thereby promoting viral protein synthesis. VPg also contributes to the assembly of replication complexes (Widyasari et al., 2020).

4.2.8 NIa-Pro (Nuclear Inclusion a Protease)

NIa-Pro is the principal protease encoded by the viral genome and is responsible for cleaving most of the polyprotein into mature functional proteins. This activity is indispensable for the potyvirus infection cycle because it ensures the proper release of structural and non-structural viral proteins (Goh; Hahn, 2021).

4.2.9 NIb (Nuclear Inclusion b)

NIb functions as the RNA-dependent RNA polymerase (RdRp), the key enzyme responsible for viral genome replication. It synthesizes new copies of viral RNA and recruits host proteins to replication complexes. NIb is regarded as one of the most highly conserved proteins within the family Potyviridae (Majer et al., 2014).

4.2.10 CP (Coat Protein)

The coat protein (CP) is responsible for encapsidating and protecting the viral RNA. In addition to its structural role, CP participates in aphid-mediated transmission, cell-to-cell and systemic movement, virion assembly, and interactions with host proteins. In SrMV, the CP region is widely used in phylogenetic and genetic diversity studies (Xu et al., 2023).

5. Epidemiology and transmission

The epidemiology of Sorghum mosaic virus is driven by complex interactions among susceptible hosts, insect vectors, and environmental conditions. In tropical regions, factors such as high temperatures, irregular rainfall patterns, and the continuous availability of host plants contribute to the year-round persistence of viral inoculum, favoring recurrent epidemics in sorghum and sugarcane production systems (Mollov et al., 2025; Xu et al., 2023; Yin et al., 2026). SrMV transmission occurs predominantly through aphids (Aphididae), particularly *Rhopalosiphum maidis* and *Toxoptera graminum*, via a non-persistent mechanism. In this transmission mode, virus acquisition and inoculation occur during short feeding periods, without viral replication within the vector, resulting in high transmission efficiency and rapid spatial spread of the disease (Lu et al., 2021).

In addition to vector transmission, SrMV can also be mechanically disseminated through contaminated agricultural tools, plant-to-plant contact, and infected propagation materials. Following initial infection, the virus spreads systemically through the phloem, reaching different plant tissues such as leaves, stems, and meristems, which facilitates widespread colonization and rapid symptom expression under field conditions (Lu et al., 2021). Vector population dynamics, combined with climatic factors and host density, directly influence virus dissemination rates and may significantly accelerate epidemic development over short time periods (Bueno et al., 2024).

6. Management of sorghum mosaic disease

The management of viral diseases in agricultural systems is inherently complex, as no curative measures are available for infected plants. Therefore, control strategies are essentially preventive and rely on integrated approaches aimed at reducing disease incidence and viral spread in the field (Souza et al., 2020). Among the main management strategies, the use of genetically resistant cultivars is highlighted. However, the effectiveness of this approach may decline over time due to the high genetic variability of the virus and the emergence of new variants capable of overcoming host resistance mechanisms (Okosun et al., 2021). In this context, integrated pest management (IPM) plays a central role, including vector population reduction, use of certified virus-free seeds, and elimination of inoculum sources in the cropping environment (Chavula, 2022).

Additionally, cultural practices such as the management of alternative hosts, adjustment of planting schedules, and removal of volunteer plants contribute to reducing infection pressure. At the same time, emerging technologies, including precision agriculture and phytosanitary monitoring systems, have been incorporated into management strategies, enabling improved decision-making and enhanced control efficiency in production systems (Bueno et al., 2024).

7. Economic impact of Sorghum mosaic virus (SrMV)

The economic impact of Sorghum mosaic virus (SrMV) is associated with reductions in crop productivity, forage quality, and industrial processing efficiency, particularly in sorghum and sugarcane production systems. As a member of the genus *Potyvirus*, SrMV interferes directly with plant physiological processes, including chlorophyll synthesis, photosynthesis, carbohydrate translocation, and biomass accumulation. Consequently, infected plants exhibit reduced vigor, stunted growth, and lower productive potential, resulting in significant economic losses under favorable epidemic conditions (Che et al., 2025; Lu et al., 2021; Yin et al., 2026).

One of the most important consequences of SrMV infection is reduced crop yield. Viral infection compromises photosynthetic efficiency by causing mosaic symptoms and chlorotic lesions, reducing the production and allocation of assimilates required for plant growth and grain filling. Field studies conducted in sugarcane-producing regions have demonstrated that mosaic diseases associated with SrMV can significantly reduce cane yield, with losses varying according to cultivar susceptibility, environmental conditions, and disease incidence. In susceptible genotypes, reductions in cane production and sucrose yield have been reported, highlighting the direct impact of the virus on agricultural profitability (Rice; Hoy, 2020; Lu et al., 2021). Furthermore, recent reviews indicate that viral diseases in sugarcane continue to represent an important constraint to productivity and economic sustainability in tropical agroecosystems (Yin et al., 2026).

The reduction in biomass production is another relevant economic consequence of SrMV infection. Viral interference with photosynthesis and plant metabolism leads to shorter plants, reduced leaf area, lower stem development, and diminished accumulation of dry matter. These effects are particularly important in forage sorghum systems, where biomass production is directly related to silage yield and animal feed availability. Reduced vegetative growth limits the amount of forage harvested per unit area, negatively affecting livestock production systems that rely on sorghum as a source of conserved feed (Lu et al., 2021; Yin et al., 2026).

In sugarcane, the economic impact extends beyond reductions in stalk yield. Mosaic diseases involving SrMV have been associated with decreases in juice quality and sucrose concentration due to impaired carbohydrate metabolism and reduced photosynthetic performance. Lower sugar accumulation directly affects industrial efficiency and profitability, reducing sugar and bioethanol production. Studies have demonstrated that mosaic-infected sugarcane plants frequently exhibit lower sucrose content and juice quality, which may substantially compromise industrial returns, especially when disease incidence is high within commercial plantations (Rice; Hoy, 2020; Lu et al., 2021).

The implications of SrMV infection are also relevant for silage production systems. Besides reducing forage biomass, viral infection may alter the nutritional value of harvested material by decreasing carbohydrate accumulation and overall plant quality. Lower forage yield and quality can reduce silage fermentation efficiency and nutritive value, potentially affecting animal performance and increasing feed supplementation requirements. Although studies specifically evaluating SrMV effects on sorghum silage remain limited, the physiological damage caused by potyvirus infections suggests a negative influence on forage productivity and conservation potential (Lu et al., 2021).

In addition to production losses, SrMV generates indirect economic costs associated with disease management. Producers must invest in certified planting material, resistant cultivars, phytosanitary monitoring programs, vector surveillance, and integrated pest management practices. Although aphid control alone is generally insufficient due to the non-persistent transmission mechanism of potyviruses, continuous monitoring and preventive measures remain essential to reduce epidemic risk. Consequently, disease management increases production costs while requiring long-term investments in breeding programs and phytosanitary research aimed at developing durable resistance and sustainable control strategies (Lu et al., 2021; Yin et al., 2026).

Overall, the economic impact of SrMV encompasses direct yield losses, reductions in biomass accumulation, decreases in sucrose content, impairment of forage and silage production, and additional management expenditures. These combined effects reinforce the importance of integrated disease management and the development of resistant cultivars to ensure the sustainability and profitability of sorghum- and sugarcane-based production systems in tropical regions.

8. Conclusions

Sorghum mosaic virus is one of the main viral agents associated with significant yield losses in sorghum and other economically important grasses, particularly in tropical and subtropical regions. Its wide geographical distribution, combined with high genetic variability and efficient aphid transmission, favors recurrent epidemic outbreaks and poses substantial limitations to the development of durable control strategies.

This review highlights that the epidemiology of SrMV results from the dynamic interaction among susceptible hosts, insect vectors, and environmental conditions that favor viral inoculum persistence and spread. The presence of alternative host plants, continuous grass cultivation, and typical tropical climatic conditions play a central role in sustaining and intensifying the virus epidemiological cycle. Given the absence of curative measures for infected plants, disease management must rely on preventive and integrated approaches. In this context, the use of resistant cultivars, vector monitoring and control, elimination of inoculum sources, and proper management of alternative hosts represent essential pillars for reducing the impact of sorghum mosaic disease.

In addition, advances in molecular diagnostic tools and phytosanitary monitoring systems have contributed to early virus detection and improved management strategies. However, the high genetic plasticity of potyviruses reinforces the need for continued research focused on molecular characterization of viral isolates, development of new sources of genetic resistance, and a better understanding of environmental factors that drive disease epidemiology. It is therefore concluded that integrating epidemiological, virological, and agronomic knowledge is essential for developing more efficient and sustainable management strategies, contributing to sorghum yield stability and global food security in tropical agricultural systems.

9. Authors' Contributions

Osvaldo Mascarenhas Neto: conceptualization; methodology; data curation; investigation. *Alinne Crisóstomo de Moraes*: conceptualization; methodology; writing – original draft; writing – review & editing. *Claudio Roberto da Silva Junior*: investigation; data curation; writing – review & editing. *Hellen Dias Neres*: investigation; data curation. *Jéssica Tatielle Martins Freitas*: validation; writing – review & editing. *José Saraiva Lucena Júnior*: supervision; project administration; validation. *Rian Freitas Veríssimo*: investigation; visualization; data curation. *Sophy Louise Lassance Dantas*: investigation; writing – original draft; visualization.

10. Conflicts of Interest

No conflicts of interest.

11. Ethics Approval

Not applicable.

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