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A Review of *Calimoviridae* Family Viruses in Crop Plants: Impacts on Environment, Agriculture, and Human Health

Aryan Moradi

Department of Plant Protection, College of Agriculture, University of Guilan, Rasht, Iran.

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Abstract

The *Caulimoviridae* family consists of plant viruses characterized by circular double-stranded DNA genomes ranging in size from 7.1 to 9.8 kilobases, lacking a viral envelope. These viruses mainly infect monocot and dicot plants, though each species typically has a restricted host range. Some members of this group are responsible for economically impactful diseases in tropical and subtropical crops, with *Cauliflower mosaic* disease being among the most prominent examples. The viral genome is packaged by coat proteins into either isometric or cylindrical virions. Natural transmission predominantly occurs via aphids, while laboratory conditions enable artificial transmission through mechanical methods. These viruses are classified as pararetroviruses due to their reliance on reverse transcription during replication. Additionally, endogenous viral elements derived from this family are integrated into plant genomes and may become activated under stress, leading to infections. Common symptoms of infection include irregular chlorotic spotting and mosaic patterns on leaves. Infected cells exhibit non-membranous spherical or oval-shaped viral inclusions within their cytoplasm. Control strategies typically involve insecticide application, removal of infected plants, and measures aimed at curbing vector activity. Nevertheless, achieving complete control remains difficult owing to rapid transmission facilitated by insects.

Key words: *Calimoviridae* , Plant viruses , Double-stranded circular DNA genome , *Cauliflower mosaic* , Mechanical transmission

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*Corresponding Author: E-mail:

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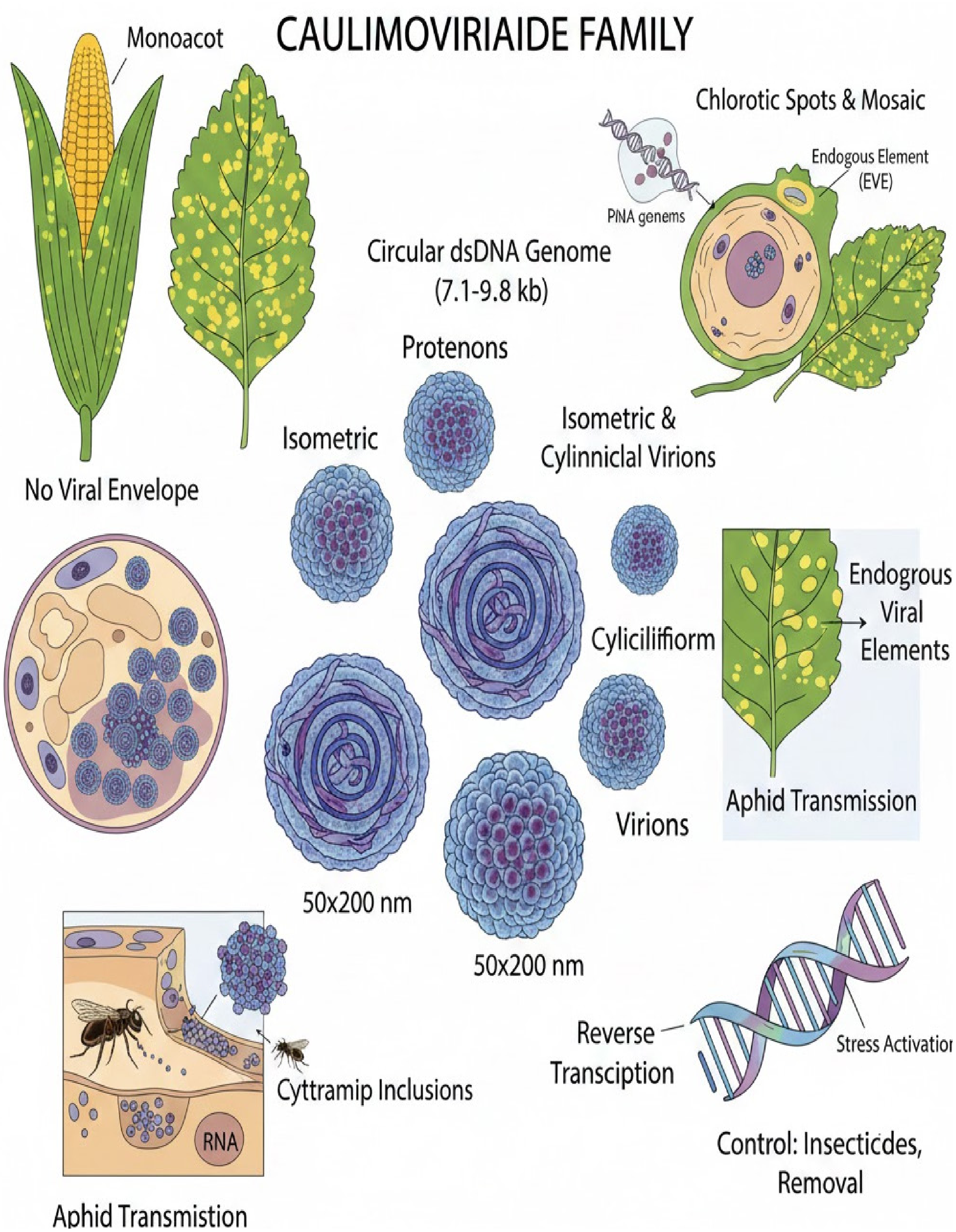
Graphical Abstract



Introduction

Plant viruses are one of the biggest biological threats to global agricultural productivity, especially in farming systems that heavily rely on vulnerable crop species. These pathogens can cause serious yield losses, lower crop quality, and disrupt local and international food markets (Jones & Naidu, 2019). Over the past few decades, the emergence and re-emergence of several viral families have raised significant concerns about plant health and sustainable crop production. Among these, the *Calimoviridae* family has gained increased attention from scientists due to its growing host range and the rising number of reported outbreaks in various agroecosystems (McDonald & Stukenbrock, 2016). Members of the *Calimoviridae* family show considerable structural and genetic diversity, which helps them adapt and infect many plant species successfully. Many viruses in this family infect staple crops that are essential for food security in different parts of the world (Serfraz, 2021). Their ability to spread quickly, survive in the environment, and evade host defenses highlights their role as emerging plant pathogens. A solid understanding of their biological features, such as genome organization, replication methods, transmission paths, and host interactions, is crucial for managing disease effectively. Additionally, the ecological behavior of these viruses, particularly how they interact with insect vectors and environmental factors, complicates control efforts (Hančinský et al., 2020). Climate change, global trade, and changes in farming practices may also promote their spread across geographical boundaries. Given these challenges, there is an increasing need for integrated approaches that connect virology, plant pathology, ecology, and agricultural science (Howden et al., 2007). This review summarizes the current knowledge about *Calimoviridae* viruses, focusing on their impact on agriculture, environmental health, and, indirectly, human well-being. By pointing out existing research gaps and new trends, this article aims to support the development of sustainable, science-based management strategies for these increasingly significant plant pathogens.

Taxonomy and Biological Characteristics

The *Calimoviridae* family includes a group of viruses that infect plants. They are classified based on unique genomic, structural, and evolutionary traits. Most members have single-stranded RNA genomes that code for various proteins (Bousalem et al., 2008). These proteins play roles in viral replication, moving between cells, suppressing host defenses, and assembling new virus particles. In terms of evolution, *Calimoviridae* viruses share a close lineage with other plant RNA viruses, but they show significant diversity (Serfraz, 2021a).This diversity leads to differences in which hosts they can infect and how pathogenic they are. Their capsids are structured to maintain stability in changing environmental conditions. This structure also allows for effective transmission through insects or mechanical means. Their replication cycle takes place entirely within host cells. It relies heavily on factors from the host to enable genome replication, translation, and spreading throughout the plant. These biological traits influence the infection process and affect the patterns of disease spread and severity. Understanding their taxonomy and molecular behavior is essential for improving virus detection, creating resistant crop varieties, and developing targeted management plans (Figure1)(Fereres & Raccah, 2015).

Host Range and Crop Plants Affected

Calimoviridae viruses infect many types of plants, including cereals, legumes, vegetables, and various horticultural crops (Kakareka et al., 2020). Susceptibility varies among species and cultivars due to genetic and physiological differences. Infection causes different disease symptoms, from mild yellowing to severe stunting and major yield loss. Crops like wheat, maize, tomato, and soybean are some of the most affected, marking this virus family as important for global food security (Jones, 2021).

Figure1: Schematic of Taxonomy and Biological Characteristics

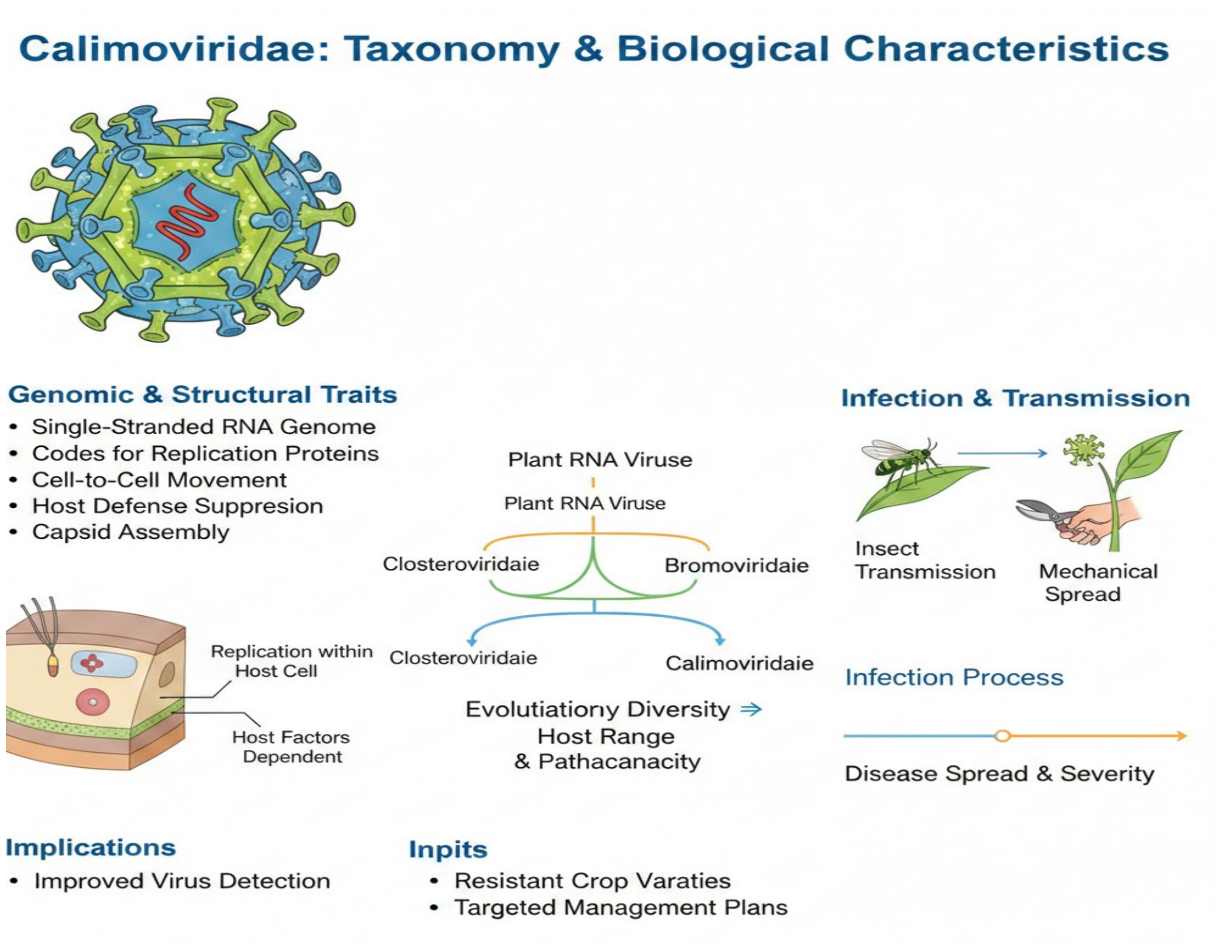


Table1: Host Range and Major Crop Plants Affected by *Calimoviridae* Viruses

Plant Group	Examples of Crops	Susceptibility / Notes	Common Symptoms	References
Cereals	Wheat, Maize	Susceptibility varies among cultivars due to genetic diversity	Yellowing, stunting, severe yield reduction	Kakareka et al., 2020
Legumes	Soybean, Pea	Variable sensitivity; affects growth and seed quality	Mosaic patterns, growth suppression	Jones, 2021
Vegetables	Tomato, Pepper	Some cultivars highly susceptible; major economic impact	Chlorosis, leaf curling, reduced fruit quality	Kakareka et al., 2020
Horticultural Crops	Various fruit and ornamental plants	Reported in diverse orchard and garden settings	Discoloration, necrotic spotting	Jones, 2021

Figure1: The environmental impacts of *Calimoviridae* viruses extend beyond plant health. Increased use of insecticides is causing water and soil pollution and reducing biodiversity, and climate change is exacerbating this threat.

Management and Control Strategies

Effective management of *Calimoviridae* viruses requires a multifaceted approach that integrates genetic resistance, cultural practices, and ecological pest management (Soni et al., 2024). Developing resistant cultivars remains one of the most reliable long-term strategies, achieved through conventional breeding, marker-assisted selection, and advanced biotechnological tools such as RNA interference and CRISPR-based genome modification (Singh et al., 2020). Resistance genes that disrupt viral replication or hinder movement proteins show particular promise in reducing infection severity. Complementing genetic resistance, cultural practices play a crucial role in limiting virus spread within agricultural systems. These measures include crop rotation, removal of infected plants, improved sanitation, and the optimization of planting schedules to minimize exposure to vectors. Managing volunteer plants and weed species is also essential, as these can act as reservoirs that maintain the virus between growing seasons (Angon et al., 2023). Additionally, integrated pest management (IPM) provides a sustainable framework for controlling vector populations through a combination of monitoring programs, biological control agents, and carefully targeted pesticide applications. Improving farmer education and strengthening extension services further enhance the effectiveness of IPM, ensuring practical and long-lasting disease management across diverse cropping environments (Deguine et al., 2021).

Environmental Impacts

The spread of *Calimoviridae* viruses indirectly influences environmental health. Increased insecticide use aimed at controlling vectors results in soil degradation, contamination of water resources, and reduced beneficial insect populations. Virus-induced shifts in plant communities may also alter ecosystem balance and biodiversity. Climate change, including rising temperatures and shifting precipitation patterns, is expected to enhance vector activity and expand the geographical range of these viruses.

Potential Human Health Impacts

Although *Calimoviridae* viruses do not infect humans directly, their influence on human health is indirect but significant. Increased pesticide exposure elevates risks of acute and chronic health conditions among agricultural workers and nearby communities. Additionally, reduced crop nutritional quality and food availability can contribute to dietary deficiencies. Economic pressures on farming communities may also have long-term societal and health implications.

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Transmission Mechanisms

There are several ways that *Calimoviridae* viruses can spread. Many species spread quickly within and between fields thanks to insect vectors like aphids, leafhoppers, and whiteflies. Plant-to-plant contact, contaminated tools, and farming activities all contribute to mechanical transmission. Certain viruses are persistent throughout growing seasons because they can spread through seeds or soil residues. Transmission efficiency is significantly influenced by environmental factors such as temperature, humidity, and vector population dynamics (Shah et al., 2015).

Impacts on Agriculture

Calimoviridae viruses exert substantial impacts on agricultural systems by reducing both crop yield and quality while creating persistent management challenges for farmers. Infected plants frequently experience significant yield losses, which in severe cases may exceed 50%, largely due to reduced biomass, malformed fruits, impaired seed development, and overall stunted growth. These losses translate into major economic consequences that extend beyond the field, influencing supply chains, commodity market stability, and food availability across affected regions. In addition to reducing yield, the viruses also compromise crop quality, leading to uneven ripening, poor texture, deformation of produce, and diminished nutritional value (Shahbazi et al., 2025). Such deterioration lowers marketability, reduces storage and processing efficiency, and limits export potential. Managing these viruses is further complicated by their wide host range, stable environmental persistence, and the activity of various insect vectors that facilitate rapid spread. Smallholder farmers, who often lack access to advanced diagnostic tools and resistant cultivars, face even greater difficulty in implementing effective control measures, making *Calimoviridae* infections a significant threat to sustainable agriculture (Tatineni & Hein, 2023)..

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Conclusion

Viruses of the *Calimoviridae* family, as emerging agents of plant diseases, pose a serious threat to global agricultural production. Their high genetic diversity, wide host range, and environmental adaptability increase their ability to infect major crops and severely reduce yield and quality. The important role of insect vectors and multiple transmission routes make these diseases difficult to control and cause rapid spread of infection. The consequences of these viruses are not limited to crop damage but also affect the economy, environment, and food security. Consequently, the development of rapid detection methods, better understanding of molecular mechanisms, production of resistant cultivars, and scientific management are essential to create sustainable solutions and maintain food security.

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