



Unravelling the Current Status of Alfalfa Mosaic Virus: Its Geographical Spread, Biology, Epidemiology, and Management

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Abstract

Alfalfa Mosaic Virus (AMV), a member of the *Bromoviridae* family, is a significant global pathogen affecting a wide range of economically important crops, particularly alfalfa (*Medicago sativa*). First identified in 1931, AMV has since expanded its host range to over 700 plant species, including potato, tomato, and various legumes. The virus is characterized by its tripartite RNA genome, comprising three segments (RNA1, RNA2, and RNA3), with RNA3 also producing a sub-genomic RNA (RNA4) that facilitates replication and movement within host plants. AMV is primarily transmitted by aphids in a non-persistent manner, complicating control efforts. Symptoms of infection include yellow mosaic patterns, stunted growth, and necrosis, leading to substantial economic losses that can reach up to 100% in severe cases. Management strategies focus on preventing the proximity of susceptible crops to alfalfa fields and utilizing resistant plant varieties. Recent advances in detection methods, including Next Generation Sequencing (NGS), have enhanced the ability to identify AMV quickly and accurately. Understanding the biology and transmission dynamics of AMV is crucial for developing effective management strategies to mitigate its impact on agriculture industry.

Introduction

Alfalfa Mosaic Virus (AMV), family *Bromoviridae*, is globally the most prevalent virus in alfalfa (*Medicago sativa*), (Lloveras, 2020; Wang et al., 2023). AMV is also known as *Lucerne mosaic virus* or *Potato calico virus*, is a significant phytopathogen that affects a wide range of plant species, including many economically important crops. AMV is a tripartite virus possessing three segments of its genome, namely RNA1, RNA2, and RNA3, with RNA1 and RNA2 encoding essential replication protein, while RNA3 encodes the movement protein and coat protein. Notably, RNA3 also produces a sub-genomic RNA (RNA4) that aids in the virus's replication and movement within host plants (Alvarado

Marchena, 2022). AMV is transmitted by a number of species of aphid, in a non-persistent manner.

First identified in 1931 by Weimer J.L. in alfalfa, AMV is the sole member of the *Alfamovirus* genus within the family *Bromoviridae* (Weimer, 1931). Since 1931, its host range is increasing with the passage of time covering a significant number of economical important crops and plants from agricultural as well as horticultural plants used for landscaping. AMV was first isolated in the United States and has since been reported in multiple nations, including Australia, New Zealand, Saudi Arabia, North and South America, France, England, Italy, Greece, Egypt, China, and Iran, resulting in varying degrees of economic losses (Al-Shahwan, 2002; Che et al., 2020; Fletcher, 2001; Maina et

al., 2019; MASOUMI et al., 2012; Sawalha & Mansour, 1996). In July 2018, soybean (*Glycine max*) plants exhibiting yellow mottling patterns or vein yellowing were observed at the university trial field in Harbin, Heilongjiang, China (Che et al., 2020). The virus is commonly found in alfalfa, which serves as the primary reservoir, but it can also infect over 700 different plant species, including potato, tomato, pepper, and various legumes such as chickpea and lentil. Symptoms of AMV infection include striking yellow mosaic patterns on leaves, stunted growth, and in severe cases, deformed or unmarketable fruit. Infected plants may exhibit mottling, leaf curling, and necrosis, leading to substantial economic losses in affected crops. The AMV presents considerable economic difficulties for alfalfa cultivation and other crops, especially legumes. Infection by AMV can result in significant yield reductions, with research suggesting losses may vary from 30% to 100%, influenced by factors including the viral strain and climatic circumstances (Mulenga, 2022). Late infection in faba beans have caused a 45% decrease in seed output, while lentils infected by AMV have exhibited declines of 81% to 87% in seed yield and 74% to 76% in shoot dry weight (Jones & Congdon, 2024). The economic consequences are significant, as AMV not only reduces the volume of harvestable yield but also diminishes quality, resulting in additional financial detriment for farmers dependent on these products for livelihood and sustenance. The factors influencing genetic and viral population structure are linked to evolutionary dynamics including mutation, genetic diversity, selection, and genetic drift.

In summary, AMV poses a significant threat to various crops through its wide host range and efficient transmission methods via aphids. Understanding its biology, symptoms, and management strategies is crucial for mitigating its impact on agriculture.

Symptomatology and Host range

Infected alfalfa plants are usually asymptomatic, but they may occasionally exhibit symptoms such as mosaic patterns, yellowing and curling or distortion of the leaves (Xu et al., 2019). AMV is not limited to this crop and may infect more than 700 other species representing more than 70 plant families (Demirel; Guo et al., 2022). The AMV impacts numerous host plants, resulting in diverse symptoms that might differ dramatically depending on the plant type, viral strain, and environmental factors. Typical symptoms include yellow mosaic patterns and mottling on leaves, frequently accompanied by leaf bending, stunting, and necrosis (Fig. 1). Infected potatoes tend to have corky regions in their tubers, whereas peppers may present bright yellow mottling alongside potential leaf distortion. In legumes such as chickpea, AMV can cause severe shoot tip necrosis, while faba bean may display chlorosis and stunted growth (Dell'Olmo et al., 2023). Other hosts, such as tomato and potato, may have necrotic lesions and generalized plant

stunting. The symptoms can sometimes mimic those of nutrient deficiencies or herbicide damage, complicating diagnosis. Typically, early infections lead to more severe symptoms, although specific plant species may recover from first infections while still retaining the virus's genome.

AMV, or *Lucerne mosaic virus*, commonly referred to as *Potato calico virus*, is a notable plant viral pathogen that impacts a diverse array of host plants, including alfalfa, potato, pepper, tomato, and various ornamental species. In nature, AMV infects weeds such as *Datura stramonium*, *Solanum nigrum*, *Chenopodium quinoa*, *Melilotus species*, and cultivated plants including *Solanum tuberosum*, *Medicago sativa*, and *Capsicum annum*.

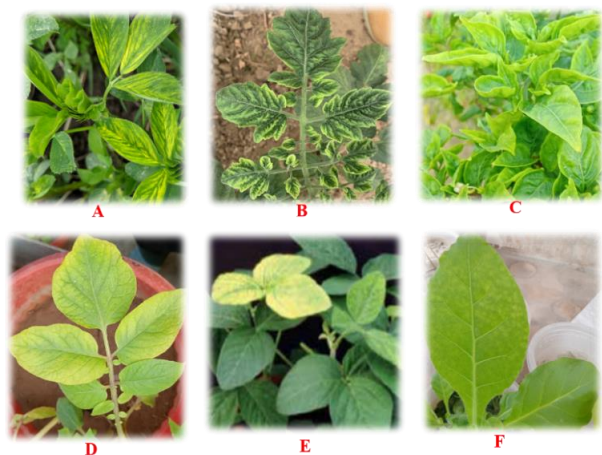


Figure 1. Picture showing different symptoms on different host of AMV, A (Alfalfa), B (Tomato), C (Chilli), D (Potato), E (Soybean), F (Tobacco)

Transmission

AMV is transmitted by at least 20 species of aphid in a non-persistent manner (Che et al., 2020; Janecek, 2023), and *Alate morphs* are thought to play a major role in its dispersion due to their high mobility and tendency to probe multiple plants before eventually locating a suitable host for feeding. The three prevalent species, namely *Acyrtosiphon pisum*, *Aphis craccivora*, and *Therioaphis trifolii*, have been reported as AMV vectors (Li et al., 2022; Meseguer et al., 2024), so they may significantly contribute to its spread within the field over time (Gao et al., 2022) and to other alfalfa fields in the surrounding landscape. Additionally, this is also transmitted through seed and also mechanical transmission (Amin et al., 2023). The initial preliminary evidence for seed transmission of AMV in faba bean was documented, indicating a transmission rate of 0.04 % (Dawit et al., 2024). In the Western Australia, seed transmission of AMV was detected in *Lathyrus cicera*, *Lathyrus sativus*, *Vicia benghalensis*, *Vicia narbonensis*, *Vicia sativa*, and

lucerne seeds 2, 4, 0.9, 0.1, 0.7, 0.7, and 1.9 per cent respectively (Abdalla et al., 2020; Latham & Jones, 2001). AMV is seed-borne in alfalfa (Meseguer et al., 2024), and low incidences have been recorded on commercial seed lots, which are probably the main source of primary inoculum (Abdalla et al., 2020). Meanwhile, non-grown and unwanted plants (weeds) serve as secondary host as well as alternate host for AMV (Abdalla et al., 2020).

Detection and Identification

Most commonly practiced techniques are biological, serological, and molecular based, with the recent advances in the detection techniques a significant number of newly developed techniques have been identified but the most authentic and reliable basic techniques are mentioned above. In the most conventional and old method of identifying the viral pathogen onto relating the response of indicator plant, while in serological protein-based identification is practiced, and in molecular characterization gene specific primers are used to amplify a selected region of any viral pathogen (Abdalla et al., 2020). From the latest rapid detection techniques Next Generation Sequencing (NGS) and High Throughput Sequencing (HTS), both can be practiced to know the disease causing agent in a very short period of time with authentic genomic map, particularly if the viral agent is unknown (Amin et al., 2023).

Genomic Organization

The viral structure of AMV consists of icosahedral particles measuring 30–57 nm in length and 18 nm in diameter. The RNA-based AMV genome comprises three single-stranded positive-sense RNA components: RNA1, RNA2, and RNA3. The replicase subunits P1 and P2 are encoded by RNA1 and RNA2 molecules, respectively. The mobility protein and coat protein are encoded by the RNA3 molecule. The CP is translated by the supplementary sub-genomic component RNA4 and is essential for RNA translation and binding, viral transport throughout the nucleus and cytoplasm, virion assembly, and systemic viral dissemination (Herranz et al., 2012).

Management Strategies

Plant viruses represent significant diseases threatening world agriculture and food security. Utilizing eco-friendly antiviral drugs may serve as an alternative method to stimulate the development of innate resistance in plants against viruses. Management strategies focus on preventing the proximity of susceptible crops to alfalfa fields and utilizing resistant plant varieties where possible. Chitosan is a natural biopolymer with significant biological advantages attributed to its distinctive properties, including a positive charge and the presence of reactive hydroxyl and amino groups. Chitosan is a safe and economical biocontrol agent owing to its bio-adhesive, biodegradable, and biocompatible characteristics (Hassan & Chang, 2017). Insecticides targeting aphids are ineffective in managing AMV.

Recommendations include planting healthy seed (some seed firms offer seed tested for AMV), managing weeds, refraining from cultivating crops near affected pastures, and using other cultural measures to mitigate AMV (Jenkins, 2011). Research has been conducted on the development of transgenic plants resistant to AMV. DNA obtained from AMV, which encodes the capsid protein, has been incorporated into alfalfa plants. This diminished the plants' vulnerability to AMV infection, hence reducing their capacity as a reservoir for viral transmission to other plants (Kalla et al., 2001).

Other Approaches

Accurate forecasting is crucial for preventing the AMV pandemic, with social media playing a key role in bridging communication between the public and plant pathology (Oakley, 2023). Scientists can leverage social media to engage with both the public and their peers. Current agricultural practices and rice cultivars are contributing to increased vector populations, which facilitate AMV infections, particularly when ratoon seedlings are thriving (Ito et al., 2018). Additionally, there is growing interest in using atmospheric pressure non-thermal plasma for treating plant diseases due to its strong antibacterial properties, which have been effective against pathogens like the *Tobacco Mosaic Virus* (Hanbal et al., 2018).

Effective plant disease management requires immediate actions to reduce disease outbreaks and long-term strategies to prevent the emergence of new pathotypes (Zhan et al., 2014). Thus, interdisciplinary collaboration among evolutionary plant pathologists and geneticists is essential for developing management strategies that enhance host defenses while minimizing pathogen evolution (Fig 2). By implementing these strategies, farmers can better manage AMV and its impact on alfalfa production, ultimately

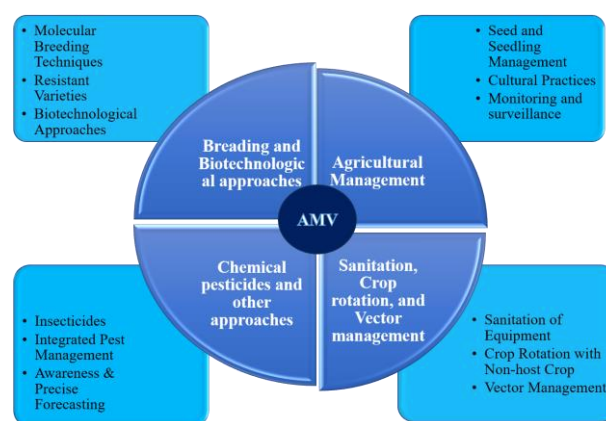


Figure 2. A visual framework has been developed to support early disease detection and the swift execution of control measures.

improving crop yields and promoting sustainable agriculture through adaptive and environmentally friendly practices.

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Conflict of Interest

The author declares no conflict of interest.

Authors' Contribution

The author is solely responsible for the conception, literature search, analysis, and interpretation of the reviewed material, as well as the preparation and writing of the manuscript. The author has read and agreed to the published version of the manuscript.

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