

Plant Viruses: Diversity, Evolution, and Their Impact on Global Agriculture- A Comprehensive Review

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Abstract:

Plant viruses represent a major constraint to global agriculture, significantly affecting crop productivity, quality, and food security. These viruses display a high degree of variability in their morphology, genetic content, and transmission patterns, making them capable of infecting a wide variety of host plants in diverse agro-ecological environments. Studies in plant virology have shown a complex association between viruses and their hosts, including a high level of sophistication in their replication, spread, and subversion of host defense mechanisms. The emergence of plant viruses is a continuous process facilitated by their high mutation rates, genetic recombination, and adaptation to a wide variety of hosts and vectors. These factors have contributed to the development of new and more aggressive strains of plant viruses. Their spread is affected by several factors, including vector and agriculture-associated changes, and environmental conditions such as changes in climate. Consequently, plant viral diseases have become a serious challenge in their control. Effective management of plant viruses requires a holistic approach that includes cultural practices, vector management, crop resistance, and the use of modern biotechnological tools such as RNA interference and genome editing. In recent years, the use of advanced diagnostic tools such as modern molecular tools and next-generation sequencing has greatly contributed to the discovery and identification of plant viruses. This review provides a comprehensive overview of plant viruses, including their diversity, evolutionary patterns, and their impact on global agriculture. In addition, it discusses the management of plant viruses, and the challenges and prospects in managing plant viruses in a rapidly changing world.

Keywords — **Plant viruses; Diversity; Evolution; Disease management; Global agriculture**

I. INTRODUCTION

Viruses that infect plants are a heterogeneous group of obligate intracellular pathogens that need the host plant cells to replicate, transcribe, and move. Unlike bacteria and fungi, which are cellular organisms, plant viruses are acellular organisms consisting of a nucleic acid, which can either be DNA or RNA, encapsidated in a protein shell named the capsid, which is sometimes further encapsulated in a lipid membrane (Hull, 2014). From the composition of their genome, the majority of plant viruses possess a

genome consisting of a single-stranded nucleic acid, although a small percentage possess a double-stranded nucleic acid or a DNA genome (Adams & Antoniw, 2006). In terms of structure, plant viruses are highly diverse, with most being helical, icosahedral (isometric), or bacilliform. The variation in structure among plant viruses has a close relationship with the transmission, stability, and interaction with the host plants. After infecting the host cell, plant viruses replicate through the host cell ribosomes. The movement of plant viruses from one

cell to another occurs through the movement proteins, whereas the transport of plant viruses over a long distance occurs through the phloem tissue (Lucas, 2006). These symptoms of plant virus infection may take various forms, including mosaics, leaf curling, chlorosis, necrosis, vein clearing, and stunted growth. All of these result from alterations in the normal physiological processes of the plants, including photosynthesis, hormonal balance, and gene expression. An important new trend in plant virology is the understanding that plant viruses are not only causal agents of plant diseases, but are also part of plant ecosystems as a whole. It has been observed that many plant viruses are latent in plant populations and do not express any symptoms of infection, and this has been referred to as the “plant virome.” These latent viruses may affect plant tolerance to abiotic factors such as drought, heat, and salinity, and this may indicate a complex role for viruses in plant biology (Roossinck, 2015). This may emphasize the importance of plant viruses as a whole, not as plant pathogens. Some of the virus infections may occur without any symptoms, making them difficult to detect and thus posing a threat of their spread without being noticed (Scholthof et al., 2011). Another important dimension is the interaction between plant viruses, their hosts, and vectors within agroecosystems. Virus transmission is often mediated by insect vectors such as aphids, whiteflies, and leafhoppers, forming intricate tripartite interactions. These relationships are highly dynamic, with viruses capable of altering host plant physiology to enhance vector attraction and feeding efficiency, thereby promoting their own spread (Jones, 2021). Understanding these interactions is essential for developing effective disease management strategies. Besides their role as pathogens, plant viruses have also been recognized as useful in various applications in molecular biology and biotechnology. Advances in omics technologies, including genomics, transcriptomics, proteomics, and metabolomics, have greatly improved our understanding of plant viruses. Omics technologies have helped us to identify the host genes that control resistance and susceptibility to viruses, as well as the virus genes that control pathogenicity. For example, next-generation sequencing technologies have helped us to discover a number of unknown viruses, thereby improving our

understanding of virus diversity and evolution (Roossinck et al., 2015). They have been used as vectors for gene expression, functional genomics, and vaccine development, thus exhibiting their dual role as pathogens and useful tools in scientific applications (Hefferon, 2017).

A. Overview of Plant Viruses

Viruses that infect plants are a heterogeneous group of obligate intracellular pathogens that need the host plant cells to replicate, transcribe, and move. Unlike bacteria and fungi, which are cellular organisms, plant viruses are acellular organisms consisting of a nucleic acid, which can either be DNA or RNA, encapsidated in a protein shell named the capsid, which is sometimes further encapsulated in a lipid membrane (Hull, 2014). From the composition of their genome, the majority of plant viruses possess a genome consisting of a single-stranded nucleic acid, although a small percentage possess a double-stranded nucleic acid or a DNA genome (Adams & Antoniw, 2006). In terms of structure, plant viruses are highly diverse, with most being helical, icosahedral (isometric), or bacilliform. The variation in structure among plant viruses has a close relationship with the transmission, stability, and interaction with the host plants. After infecting the host cell, plant viruses replicate through the host cell ribosomes. The movement of plant viruses from one cell to another occurs through the movement proteins, whereas the transport of plant viruses over a long distance occurs through the phloem tissue (Lucas, 2006). These symptoms of plant virus infection may take various forms, including mosaics, leaf curling, chlorosis, necrosis, vein clearing, and stunted growth. All of these result from alterations in the normal physiological processes of the plants, including photosynthesis, hormonal balance, and gene expression. An important new trend in plant virology is the understanding that plant viruses are not only causal agents of plant diseases, but are also part of plant ecosystems as a whole. It has been observed that many plant viruses are latent in plant populations and do not express any symptoms of infection, and this has been referred to as the “plant virome.” These latent viruses may affect plant tolerance to abiotic factors such as drought, heat, and salinity, and this

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B. Historical Background

Plant virology, as a branch of science, was initiated in the late 19th century and has contributed significantly to the establishment of the science of virology as a whole. In 1886, tobacco mosaic disease was first described by Adolf Mayer, and it was proven that it could be transferred mechanically by means of inoculation of plant sap. Initially, Mayer thought that the causative agent of tobacco mosaic disease was bacterial in nature (Bos, 1999). However,

in 1892, Dmitri Ivanovsky made a breakthrough by showing that the infectious agent of tobacco mosaic disease was capable of passing through Chamberland porcelain filters, which were designed to retain bacteria, thus indicating the submicroscopic nature of the causative agent of tobacco mosaic disease. This was further developed by Martinus Beijerinck in 1898, when he introduced the term “contagium vivum fluidum,” which recognized viruses as a new class of infectious agents (Bos, 1999). Tobacco mosaic virus (TMV) crystals were first crystallized by Wendell Stanley in 1935, which showed that viruses are chemical substances (Stanley, 1935). This marked the beginning of the field of molecular virology. The invention of electron microscopy in the middle of the 20th century enabled the direct observation of viral particles, and the advances made in the field of molecular biology in the latter half of the century enabled the study of the viral genome and the replication process.

C. Scope and Objectives of the Review

In recent years, the introduction of high-throughput sequencing technologies, such as next-generation sequencing, has changed the field of plant virology. This has enabled the identification of new viruses, the study of the viral population, and the understanding of the evolutionary process of the viruses. The threat of plant viruses to food security is a major problem, and they have a great impact on crop yield, quality, and marketability. It is estimated that plant pathogens, including plant viruses, cause a great loss to crop yield every year, and the economic loss is in billions of dollars (Oerke, 2006). Rice, wheat, maize, cassava, and potato are the staple food crops of many developing countries, and they form the backbone of food security. Rice tungro disease, cassava mosaic disease, banana bunchy top disease, and tomato yellow leaf curl disease have caused devastating epidemics of plant viruses, and they have had a great impact on food security and economic stability of the affected countries. The severity of plant virus diseases is often increased by monoculture farming, lack of resistant varieties, and improper disease management. The globalization of trade and movement of plant materials has facilitated the rapid spread of plant viruses across geographical

boundaries. Additionally, climate change has emerged as a critical factor influencing plant virus epidemiology. Changes in temperature, rainfall patterns, and atmospheric conditions affect the distribution, population dynamics, and behaviour of insect vectors such as aphids, whiteflies, and leafhoppers, thereby altering virus transmission patterns (Jones, 2021). Beyond direct crop losses, plant viruses also impact agricultural sustainability by increasing reliance on chemical inputs for vector control and reducing the efficiency of crop production systems. Finally, the integration of advanced biotechnological tools, such as RNA interference (RNAi), CRISPR/Cas-mediated genome editing, and transgenic resistance, represents a promising frontier in plant virus management. These technologies offer precise and sustainable solutions for developing virus-resistant crops, although their adoption is often influenced by regulatory, ethical, and socio-economic considerations. This underscores the need for environmentally sustainable and integrated approaches to virus management.

This review is intended to provide a comprehensive and integrated understanding of plant viruses by addressing their diversity, their molecular biology, their evolution, and their overall impact on global agriculture. The review is a synthesis of knowledge on the classification, structure, and genome

II. DIVERSITY OF PLANT VIRUSES

Plant viruses are considered one of the most diverse plant pathogens, and their genomes differ in many ways, including their composition, structure, and evolutionary strategies. This diversity allows plant viruses to infect a wide range of plant species and adapt to different environmental and ecological niches. The diversity of plant viruses is important in classifying, diagnosing, and managing plant viruses effectively (Hull, 2014; Roossinck et al., 2015).

A. Classification and Taxonomy

The classification and taxonomic structure of plant viruses are mainly regulated by the International Committee on Taxonomy of Viruses (ICTV). It is a universal standard system used to classify and name plant viruses according to their genetic, structural, and biological properties (Adams & Antoniw, 2006).

In the early attempts at classifying plant viruses, the basis was largely biological or pathological, including symptom expression, host ranges, and vector specificity. Although these approaches provided a good basis for identification, they were not very accurate because of the variable expression of plant virus symptoms under different environmental conditions (Agrios, 2005). The International Committee on Taxonomy of Viruses (ICTV) now uses genome sequence-based phylogenetics as the primary classification criterion. Viruses are grouped into realms, orders, families, genera, and species based on evolutionary relationships (Adams et al., 2017). Based on their evolutionary origin and replication strategies, currently, six major viral realms are recognized, but plant viruses are present only in a subset of these three realms (Riboviria, Monodnaviria, Pararnavirae). The remaining realms (Duplodnaviria, Varidnaviria, Adnaviria) do not include plant-infecting viruses, highlighting that plant viruses occupy a distinct evolutionary subset of the global virosphere (Koonin et al., 2020).

TABLE I
DISTRIBUTION OF PLANT VIRUSES ACROSS VIRAL
REALMS BASED ON EVOLUTIONARY ORIGIN AND
REPLICATION STRATEGY

VIRAL REALM	GENOME TYPE / REPLICATION STRATEGY	PLANT VIRUS PRESENCE	EXAMPLES OF PLANT VIRUS GROUPS	KEY FEATURES	REFERENCE
Riboviria	RNA viruses (ssRNA, dsRNA) and reverse-transcribing RNA viruses; encode RNA-dependent RNA polymerase (RdRp) or reverse transcriptase	Present (major realm)	<i>Tobamovirus</i> , <i>Potyvirus</i> , <i>Tospovirus</i>	Largest realm of plant viruses; high mutation rates and rapid evolution; includes most economically important plant pathogens	Koonin et al., 2020
Monodnaviria	Single-stranded DNA (ssDNA) viruses; rolling-circle replication	Present	<i>Geminiviridae</i> (e.g., <i>Begomovirus</i>), <i>Nanoviridae</i>	Important group of plant DNA viruses; often circular ssDNA; commonly transmitted by insect vectors such as whiteflies	Koonin et al., 2020
Pararnavirae	Double-stranded DNA viruses replicating via RNA intermediate (reverse transcription)	Present	<i>Caulimoviridae</i> (e.g., Cauliflower mosaic virus)	Plant-infecting pararetroviruses; complex replication involving reverse transcription; nucleus–cytoplasm cycle	Koonin et al., 2020
Duplodnaviria	Double-stranded DNA viruses with HK97-fold capsid proteins	Absent in plants	None known in plants	Mainly bacteriophages and animal viruses; structurally and evolutionarily distinct from plant viruses	Koonin et al., 2020
Varidnaviria	Double-stranded DNA viruses with vertical jelly-roll capsid proteins	Absent in plants	None known in plants	Infects marine eukaryotes, animals, and large DNA viruses; not associated with plants	Koonin et al., 2020
Adnaviria	Archaeal viruses with A-form DNA and unique virion structures	Absent in plants	None known in plants	Restricted to archaeal hosts in extreme environments; highly specialized lineage	Koonin et al., 2020

This modern system has replaced older symptom based classification and has led to the discovery of hundreds of new plant viruses through metaviromics (Koonin et al., 2020). There are different classification criteria used to classify plant viruses, which include genome composition, such as DNA or RNA, strandedness, which is divided into single or double strands, sense, which is divided into positive or negative sense, segmentation, capsid symmetry, and transmission types. For example, the Potyviridae family of plant viruses is classified according to their composition of a positive-sense, single-stranded genome, which is transmitted by aphid vectors, while the Geminiviridae family is classified according to their circular, single-stranded genome composition, which is transmitted by whitefly vectors (Hull, 2014). Recent advances in molecular biology and sequencing technologies have significantly improved virus classification by enabling phylogenetic analysis based on genome sequences. This has led to the discovery of numerous novel viruses and the reclassification of existing taxa, highlighting the dynamic nature of virus taxonomy (Roossinck et al., 2015).

B. Genome Types (DNA vs RNA Viruses)

The genomic composition of plant viruses is a fundamental aspect in the definition of their biological properties, including their mode of replication, rate of mutation, interaction with the host, and evolutionary potential. Based on the composition of their genetic material, plant viruses can be classified as RNA and DNA viruses. The majority of plant-infecting viruses belong to the RNA virus class, as opposed to the DNA virus class (Hull, 2014).

RNA Viruses- RNA viruses dominate the plant virosphere and are responsible for a large proportion of economically important plant diseases. Their genomes are typically composed of single-stranded RNA (ssRNA), although double-stranded RNA (dsRNA) viruses are also reported in certain families (Hull, 2014).

RNA viruses can be categorized based on genome polarity into:

- Positive-sense RNA (+ssRNA) viruses, whose genomes can function directly as messenger

RNA (mRNA) and are immediately translated upon entry into the host cell.

- Negative-sense RNA (-ssRNA) viruses, which require transcription into complementary RNA before protein synthesis can occur.
- Double-stranded RNA (dsRNA) viruses, which contain segmented genomes in some cases (Roossinck et al., 2015).

Additionally, RNA genomes may be monopartite (single segment) or multipartite (divided into multiple segments, often packaged into separate virions). Multipartite genomes can enhance genetic reassortment and contribute to viral evolution and adaptability. The replication of an RNA virus mainly takes place in the cytoplasm of an infected plant cell. An important characteristic of an RNA virus is that it requires an enzyme known as an RNA-dependent RNA polymerase, which plays a role in the synthesis of an RNA strand from an RNA template. This enzyme is encoded by the virus. This process of replication of an RNA virus is known as RNA-dependent RNA synthesis. The most important characteristic of an RNA-dependent RNA polymerase is that it does not have a proofreading function, resulting in a high mutation rate. This phenomenon results in the formation of quasispecies. This genetic variability provides RNA viruses with a remarkable capacity to: Adapt rapidly to new hosts, overcome plant defense mechanisms, and develop resistance to antiviral measures. The high rate of mutation and short generation time in RNA viruses result in their high evolutionary dynamics. This allows RNA viruses to rapidly adapt to environmental pressures such as host resistance genes and vector availability. This is why RNA viruses are often associated with emerging and re-emerging plant diseases, a wide host range in some species, and High transmissibility by vectors such as aphids, whiteflies, and thrips (Agrios, 2005). These characteristics make RNA viruses particularly challenging to manage in agricultural systems.

DNA Viruses-

In contrast to RNA viruses, DNA viruses are less diverse and less abundant in plants but remain

significant plant pathogens. Their genomes consist of either single-stranded DNA (ssDNA) or double-stranded DNA (dsDNA). Plant DNA viruses can be broadly divided into:

- **ssDNA viruses**, such as those belonging to the family *Geminiviridae*, which typically possess circular genomes and replicate via rolling-circle replication.
- **dsDNA viruses**, such as members of the family *Caulimoviridae*, which are unique in that they replicate through an RNA intermediate despite having DNA genomes. These are often referred to as pararetroviruses (Hull, 2014).

DNA virus replication typically occurs inside the nucleus of the infected cell, with a strong dependence on cellular machinery, especially DNA polymerases. In the case of pararetroviruses, their replication process includes a step called reverse transcription, during which an RNA intermediate is converted back into a DNA copy with the help of an enzyme called reverse transcriptase. Thus, the two-stage replication of these viruses, which includes both nuclear and cytoplasmic components, makes their life cycle more complex compared with other DNA viruses. When it comes to their genetic stability and evolution, as compared to RNA viruses, DNA viruses exhibit lower mutation rates due to the proofreading activity of DNA polymerases, greater genetic stability, and slower rates of evolution. As a result, DNA viruses tend to maintain more stable interactions with their host plants over time (Domingo & Holland, 1997). However, they can still cause severe diseases, particularly in tropical and subtropical crops, often mediated by insect vectors such as whiteflies. Understanding the differences in the genome is essential for advancing plant virology research and improving strategies for managing viral diseases in crops, as they influence disease epidemiology, host-virus interactions, development of resistant crop varieties, and strategies for virus detection and control.

C. Structural Diversity of Plant Viruses

Plant viruses exhibit remarkable structural diversity, which plays a critical role in determining their stability, transmission, and interaction with host plants. In terms of structure, most plant viruses are simple entities that contain a genome of nucleic acid encapsulated in a protein layer called the capsid, which is composed of repeating units. Plant viruses are usually non-enveloped entities, a characteristic that is quite distinct from most other plant virus types. This is a characteristic that provides plant viruses with environmental stability, enabling their persistence in the environment even outside their host plants. They can be transmitted through mechanical injury of plants, contaminated equipment, or vectors. This is in contrast to most other viruses that are enveloped. The structure of plant virus entities is usually ordered and follows a particular pattern of symmetry. The most common of these is the helical structure, icosahedral structure, and complex structure. The structure of most plant virus entities is critical for their classification; however, it is also critical for their infectivity, movement within the host, and evolution.

Helical (Rod-shaped and Filamentous) Viruses:

Helical viruses are characterized by a capsid protein arranged in a spiral around the viral nucleic acid, forming rigid rod-like or flexible filamentous particles. A classic example is Tobacco mosaic virus (TMV), which has a rigid, rod-shaped structure and a positive-sense RNA genome. In contrast, members of the *Potyviridae* family, such as Potato virus Y (PVY), form flexuous (flexible) filamentous particles. These helical structures are advantageous because they allow efficient packaging of long RNA genomes while maintaining structural stability. They also facilitate movement within plant tissues, particularly through plasmodesmata (Revers & García, 2015). Helical viruses may also be rigid or flexible in nature. Filamentous forms are particularly common in plant viruses. These forms help in efficient motility in plant tissue, especially through plasmodesmata. This increases the efficiency of infection in plants (Hull, 2014; Lucas, 2006). The assembly of helical capsids is a highly efficient process. This is because of the interactions between the viral capsid proteins and the nucleic acid. This reduces the complexity of assembly processes (Caspar & Klug, 1962). This efficiency is one of the reasons for the evolutionary success of helical plant viruses.

Icosahedral (Spherical) Viruses: Icosahedral viruses have a highly symmetrical 20-sided shape with 20 triangular surfaces. This is a geometrically optimal solution to encapsulate the viral genetic material with a limited number of proteins. This maximizes the viral stability and minimizes the viral cost (Caspar & Klug, 1962; Flint et al., 2015). Icosahedral viruses are also highly stable and compact. They are highly resistant to environmental stress. This maximizes their efficiency in persistence and transmission. This is especially true in the case of insect-borne viruses such as aphids and beetles (Ng & Falk, 2006). The structural inflexibility of icosahedral viruses also contributes to their ability to cope with changes in temperature, pH, and enzymatic degradation, thus allowing them to survive in a variety of environmental conditions (Agrios, 2005).

Geminate (Twin Particle) Viruses: A unique structural form is found in the family Geminiviridae, which produces geminate (twin icosahedral) particles. These virions consist of two joined incomplete icosahedral units, forming a distinctive “double particle” shape. Viruses such as Tomato yellow leaf curl virus (TYLCV) and Cassava mosaic virus (CMV) exhibit this structure. The geminate form is believed to enhance genome packaging of circular single-stranded DNA and may facilitate transmission by whiteflies (*Bemisia tabaci*) (Hanley-Bowdoin et al., 2013).

Bacilliform and Bullet-shaped Viruses: Some plant viruses display bacilliform (rod-like but shorter) or bullet-shaped structures, particularly within the Rhabdoviridae family. These viruses possess negative-sense RNA genomes and are often transmitted by insect vectors such as leafhoppers and planthoppers. For example, Rice yellow stunt virus shows a bacilliform morphology. The bullet-shaped structure is associated with efficient encapsidation of segmented genomes and is similar to animal rhabdoviruses, indicating evolutionary conservation across kingdoms (Jackson et al., 2005).

Complex and Flexible Structural Forms: Complex viruses, which do not display strict helical or icosahedral symmetry, are rare among plant viruses. Complex plant viruses have unusual or additional structural components. The low incidence of complex plant viruses might result from evolutionary pressure related to plant cell walls as well as transmission

modes. In contrast with plant viruses, which do not need complex structures for infection, bacteriophages, as well as certain animal viruses, need complex structures for infection, which might not be required for plant viruses, as they are transmitted mechanically or by vectors, as suggested by Koonin et al. (2020). Certain plant viruses exhibit highly flexible or complex virion structures, including extremely long filamentous particles. Members of the *Closteroviridae*, such as Citrus tristeza virus (CTV), are among the largest and most structurally complex plant RNA viruses. These viruses have long, thread-like particles that can exceed 2,000 nm in length. Their structure is associated with phloem-limited infection and specialized transmission by aphids or whiteflies (Bar-Joseph et al., 1989).

Overall, the structural diversity in plant virus morphology is a result of a balance between simplicity and functional efficiency. The lack of an envelope makes plant viruses more durable, while changes in symmetry affect genome packaging, transmissibility, and interactions with hosts. Advances in structural biology, like cryo-electron microscopy and X-ray crystallography, have helped to gain insights into the morphology of plant viruses, which is important in understanding virus evolution and managing plant viral diseases effectively (Baker et al., 1999; Rossmann & Johnson, 1989; Hull, 2014; Flint et al., 2015). Moreover, virion morphology influences transmission mode, environmental stability, and host range, making structural classification an essential component of plant virology (Hull, 2014; Elena et al., 2014).

D. Major Plant Virus Families

Plant viruses are distributed across numerous taxonomic groups, but a relatively small number of families account for the majority of agriculturally important diseases. These families differ in genome organization, replication mechanisms, vector associations, and host interactions, reflecting their evolutionary diversification. In RNA viruses, the most important and prevalent group of plant viruses is the family of **Potyviridae**. The most important characteristic of these viruses is that they contain a single strand of RNA that carries a large protein that is later divided into smaller units (Revers & García,

2015). The most important of these is Potato virus Y (PVY) and Turnip mosaic virus (TuMV), causing yield loss in solanaceous and cruciferous crops. The virus is transmitted through aphids in a non-persistent mode, enabling rapid spread of the virus in the field. The second most important virus is the **Geminiviridae** family of single-stranded circular DNA (ssDNA) viruses. They are differentiated from other single-stranded DNA viruses due to their geminate morphology. They replicate via a rolling circle mechanism in the nucleus of infected plant cells (Hanley-Bowdoin et al., 2013). The most important of these is the Tomato yellow leaf curl virus (TYLCV) and the Cassava mosaic virus (CMV), transmitted through whiteflies (*Bemisia tabaci*). They are most devastating in tropical and subtropical regions of the world. They have the capability to manipulate the cell cycle of the host plant, contributing to pathogenicity and persistence.

The family **Tombusviridae** comprises small, icosahedral, positive-sense RNA viruses without envelopes, which are transmitted mechanically or through soil. These viruses, despite their simple genome structure, have evolved complex virus replication and RNA recombination processes (White & Nagy, 2004). These viruses include Tomato bushy stunt virus, which has been a model system in the study of RNA virus replication. The **Tospoviridae**, now classified under the order Bunyavirales, comprise a critical class of negative-sense RNA viruses infecting plants. Tomato spotted wilt virus, a prominent member of the class, is transmitted by thrips in a propagative manner (Adkins, 2000). These viruses have segmented genomes, which result in reassortment, thus providing a source of genetic diversity and new strains. The family **Closteroviridae** comprises some of the largest and most complex plant RNA viruses, with long filamentous virions and large genomes. Citrus tristeza virus (CTV), a member of this family, has caused widespread destruction of citrus industries globally (Bar-Joseph et al., 1989). These viruses are typically transmitted by aphids or whiteflies and are restricted to phloem tissues, influencing their pathogenic effects.

Another notable group is **Caulimoviridae**, which includes plant pararetroviruses with double-stranded DNA genomes that replicate via reverse transcription. Unlike retroviruses, they do not integrate obligatorily

into the host genome but replicate episomally (Hull, 2014). Cauliflower mosaic virus (CaMV) is a well-studied member and has contributed significantly to understanding gene expression in plants, including the widely used CaMV 35S promoter in plant biotechnology.

Other important groups include Luteoviridae, **Rhabdoviridae**, and **Secoviridae**, which add to the diversity of plant viruses. Each has unique modes of transmission, which include vector specificity, aphids, beetles, nematodes, and fungi, which influence their ecological niches (Ng & Falk, 2006).

E. Host range and Specificity

The host range of plant viruses is a critical determinant of their ecological success, epidemiology, and agricultural impact. Plant viruses exhibit a continuum of host specificity, ranging from highly specialized viruses that infect a single plant species or genotype to generalist viruses capable of infecting a broad spectrum of hosts across multiple plant families (Elena et al., 2014). Host specificity is governed by a series of molecular interactions between viral components and host cellular machinery. Successful infection requires the virus to overcome multiple barriers, including entry into the host cell, replication compatibility, movement within the plant, and evasion or suppression of host defense mechanisms. Viral proteins such as movement proteins, replicases, and suppressors of RNA silencing play essential roles in determining host compatibility (Pallas & García, 2011). Generalist viruses, such as Cucumber mosaic virus (CMV), have exceptionally broad host ranges, infecting over 1,000 plant species. This adaptability is often associated with flexible genome organization and the ability to interact with conserved host factors. In contrast, specialist viruses may evolve highly optimized interactions with specific hosts, resulting in efficient replication but limited host range. Such specialization can arise from co-evolutionary processes between virus and host, leading to finely tuned molecular compatibility (Woolhouse et al., 2001). Host range is also influenced by the presence of resistance (R) genes in plants, which can recognize specific viral proteins and trigger defense responses such as the hypersensitive response (HR). However, viruses can overcome host resistance through

mutations, recombination, or reassortment, leading to the emergence of resistance-breaking strains (Brown et al., 2015). This evolutionary “arms race” between plant hosts and viruses drives diversification on both sides.

For example, aphid-transmitted viruses often infect a wide range of herbaceous plants, whereas viruses transmitted by specialized vectors such as certain nematodes or fungi may have more restricted host distributions (Ng & Falk, 2006). Latent infections further complicate the understanding of host range. Some viruses can infect plants without causing visible symptoms, allowing them to persist undetected and serve as reservoirs for future outbreaks. These asymptomatic hosts play a significant role in virus epidemiology and the emergence of new diseases. Environmental factors, including temperature, humidity, and agricultural practices, also influence host range expression. Climate change, in particular, is expected to alter virus–host interactions by expanding the geographical range of both viruses and their vectors, potentially exposing new plant species to infection (Jones, 2016).

III. TRANSMISSION AND EPIDEMIOLOGY

A. Modes of Transmission

Plant viruses are disseminated through multiple transmission pathways, including vector-mediated, mechanical, and vertical (seed and pollen) transmission. These mechanisms operate at different ecological and temporal scales and collectively determine virus spread, persistence, and epidemic development. Recent advances in plant virology highlight that transmission efficiency is strongly

influenced not only by virus biology but also by vector ecology, host physiology, and environmental change (Jones & Naidu, 2019; Moreno & López-Moya, 2020).

2021). Recent studies emphasize that vector behavior and viral proteins jointly determine transmission efficiency, making virus–vector interactions highly co-evolved systems (Moreno & López-Moya, 2020).

Mechanical Transmission

Mechanical transmission occurs through physical damage to plant tissues, allowing virus entry via wounds. This mode is common in agricultural systems where human activities such as pruning, grafting, and handling contaminated tools facilitate virus spread.

Vector relationships further complicate host range dynamics. Many plant viruses rely on specific vectors for transmission, and the feeding behavior and host preferences of these vectors indirectly define the effective host range of the virus. For

Vector-Mediated Transmission (Insects, Nematodes, and Fungi)

Vector-mediated transmission is the most important and widespread mode of plant virus dissemination. A wide range of biological vectors—including aphids, whiteflies, leafhoppers, planthoppers, and thrips facilitate virus movement between host plants. Depending on the virus–vector interaction, transmission is classified as non-persistent, semi-persistent, or persistent. Non-persistent transmission involves rapid acquisition and inoculation during brief feeding probes, as seen in Potyviridae members such as Potato virus Y (PVY). Persistent transmission requires longer acquisition periods and may involve circulation or replication within the vector, as observed in Tomato spotted wilt virus (TSWV) transmitted by thrips and many Geminiviridae transmitted by whiteflies (Ng & Falk, 2006; Adkins, 2000). In addition to insects, nematodes transmit viruses belonging mainly to Secoviridae and Tobravirusidae, while soil-inhabiting fungi such as *Polymyxa* and *Olpidium* act as vectors for root-infecting viruses. These vectors contribute to long-term soil persistence and localized spread of viral diseases. These soil-associated vectors contribute to long-term environmental persistence and are increasingly recognized as important reservoirs in agroecosystems (Thresh & Cooter,

2021). Viruses such as Tobacco mosaic virus (TMV) are highly stable and can remain infectious on surfaces for extended periods. Mechanical transmission can also occur naturally through wind abrasion, insect feeding damage, and herbivory. Although non-specific, this mode can lead to rapid local spread in intensively cultivated crops (Hull, 2014).

Seed and Pollen Transmission

Vertical transmission through seeds and pollen is crucial for long-distance dispersal and

intergenerational persistence of plant viruses. Seed transmission enables viruses to survive between growing seasons and spread through global seed trade networks. Viruses such as Barley stripe mosaic virus (BSMV) and several luteoviruses are well-documented seed-transmitted pathogens. Pollen transmission can also introduce viruses into developing seeds or infect maternal tissues during fertilization. Recent studies emphasize that asymptomatic seed infection is a major hidden driver of global virus spread, particularly in grain and vegetable crops (Zhou & Tzanetakis, 2020).

B. Epidemiological Factors Influencing Virus Spread

The epidemiology of plant virus infections is a multifaceted phenomenon, depending on the interplay between the host plant, vector, environment, and human activities in agricultural settings. The density of the host plant and its genetic homogeneity are also crucial in the build-up of a plant virus epidemic, as monoculture provides a constant source of susceptible hosts. The vector population is also a crucial factor in the epidemiology of plant virus infections, as their population varies in seasons, migration, and feeding behavior, which can affect the rate of virus transmission. Studies have also indicated that recent changes in land use and increased agricultural activities have increased vector populations in many regions, which can enhance virus transmission (Jones & Naidu, 2019). International trade in plants also plays a role in the long-distance transmission of new viral pathogens (Bhat et al., 2021).

C. Role of Environment and Climate Change

Environmental factors have been shown to greatly influence plant virus epidemiology, with factors like temperature greatly affecting plant virus epidemiology by determining the replication rate of the virus and the development of the vector. Climate change has been identified as a major driver in the emergence and spread of plant viruses. Changes in temperature and rainfall patterns have been shown to increase the spread of plant viruses like those transmitted by the whitefly and aphid, which have been shown to spread diseases caused by the Geminiviridae virus and others

like the economically important virus groups. Climate change has been shown to stress plants, making them more susceptible to disease (Moreno & López-Moya, 2020; Jones, 2016). Global analysis has shown that changes in the vector population would greatly influence plant virus epidemiology in the coming decades (Thresh & Cooter, 2021).

D. Disease cycles in Agrosystems

Virus disease cycles are dynamic systems, which are constantly involved in a process of continuous interaction with their environment. In many instances, plant viruses have the ability to survive between crop seasons in alternative hosts, including weeds and wild plants. The idea of a “green bridge” has been a fundamental concept of plant virus diseases, with volunteer crops as well as weeds serving as a source of plant virus populations during periods outside of the growing seasons. When a new crop is established, vectors will pick up plant viruses from the volunteer crops or weeds, thus initiating a new cycle of infection. In recent times, studies have indicated that the complexity of plant virus diseases has been increased by mixed cropping systems, climatic changes, and globalisation, which have made it more unpredictable (Zhou & Tzanetakis, 2020; Thresh & Cooter, 2021). Systemic infection of plant cells has also played a critical role in the spread of plant virus diseases, thus ensuring their transmission. These interconnected processes create highly dynamic and often region-specific disease cycles that are becoming increasingly difficult to manage under modern agricultural conditions.

IV. SYMPTOMS AND DIAGNOSIS OF PLANT VIRAL DISEASES

A. Common Symptoms in Infected Plants

Plant virus infections produce a wide range of visible and physiological symptoms that reflect disruptions in host metabolism, gene expression, and cellular function. The most common symptoms include mosaic patterns, chlorosis, leaf curling, vein clearing, stunting, enations, necrosis, and abnormal fruit development.

These symptoms often arise due to interference with chloroplast development, hormonal imbalance, and impaired phloem transport (Hull, 2014). Recent studies emphasize that symptom expression is strongly influenced by virus strain, host genotype, environmental conditions, and mixed infections, making visual diagnosis alone unreliable in many cases. For example, infections caused by Geminiviridae often result in severe leaf curling and stunting in tomato and cotton, while Potyviridae members typically induce mosaic and mottling symptoms in a wide range of crops (Jones & Naidu, 2019).

B. Symptom Variability and Latent Infections

Symptom expression in plant virus infections is highly variable and may range from severe disease to complete absence of visible symptoms. This variability is influenced by host resistance genes, environmental stress, virus concentration, and co-infection with other pathogens. Latent infections, where viruses are present without visible symptoms, are increasingly recognized as a major epidemiological challenge. Modern research using high-throughput sequencing has revealed that many economically important crops harbour cryptic or asymptomatic viral infections that can later become symptomatic under stress conditions such as drought, heat, or nutrient deficiency (Bhat et al., 2021; Zhou & Tzanetakis, 2020). Furthermore, mixed infections can lead to synergistic interactions, where one virus enhances the replication or pathogenicity of another, significantly increasing disease severity and complicating field diagnosis (Moreno & López-Moya, 2020).

C. Conventional Diagnostic Methods

Traditional plant virus diagnosis relies on biological, serological, and microscopic techniques. Biological indexing involves mechanical inoculation of indicator plants to observe symptom development, while electron microscopy allows direct visualization of virion morphology. Serological methods such as Enzyme-Linked Immunosorbent Assay (ELISA)

remain widely used due to their simplicity, affordability, and ability to process large sample numbers. ELISA-based detection is particularly effective for routine screening of viruses such as Potyvirus and Begomovirus species (Hull, 2014). However, conventional methods have limitations, including low sensitivity, inability to detect mixed infections, and failure to identify novel or divergent viruses, which restricts their use in modern diagnostics.

D. Molecular Diagnostic Techniques (PCR, ELISA, NGS)

Modern plant virology increasingly relies on molecular diagnostic techniques, which offer higher sensitivity, specificity, and speed compared to conventional approaches.

PCR and qPCR-based detection

Polymerase Chain Reaction (PCR) and quantitative PCR (qPCR) are widely used for detecting viral DNA and RNA with high precision. These methods allow early detection of infections even before symptom development and are now standard tools in plant quarantine and certification programs (Jones & Naidu, 2019).

Loop-mediated isothermal amplification (LAMP)

LAMP has emerged as a rapid, field-deployable diagnostic method that does not require sophisticated laboratory infrastructure. Recent studies highlight its usefulness for on-site detection of viruses in resource-limited agricultural systems, enabling faster disease management decisions (Bhat et al., 2021).

Next-Generation Sequencing (NGS) and Metagenomics

NGS has revolutionized plant virus diagnostics by enabling unbiased detection of known, unknown, and novel viruses directly from plant tissues. Metagenomic sequencing allows comprehensive profiling of plant viromes, revealing complex viral communities and uncovering asymptomatic infections that traditional methods fail to detect (Zhou & Tzanetakis, 2020). Recent advances also demonstrate that NGS is critical for understanding emerging plant viruses, recombination events, and mixed infections, which are increasingly important under climate change and

global trade scenarios (Bhat et al., 2021; Nicaise, 2022).

5. EVOLUTION OF PLANT VIRUSES

A. Genetic Variation and Mutation Rates

Plant viruses exhibit extremely high levels of genetic variation, primarily driven by rapid mutation rates, especially in RNA viruses. The lack of proofreading activity in RNA-dependent RNA polymerases leads to frequent replication errors, generating diverse viral populations known as quasispecies. This high variability enables rapid adaptation to changing environmental and host conditions (Elena et al., 2014). Recent studies confirm that RNA plant viruses such as members of Potyviridae and Tombusviridae evolve much faster than DNA plant viruses, allowing them to overcome host resistance and environmental pressures quickly (Jones & Naidu, 2019).

B. Recombination and Reassortment

Genetic recombination is a major evolutionary mechanism in plant viruses, particularly in single-stranded DNA viruses such as Geminiviridae and RNA viruses like Potyviridae. Recombination occurs when two related viral genomes infect the same host cell and exchange genetic material, producing novel genotypes with altered fitness. In segmented RNA viruses, reassortment provides an additional mechanism of evolution, where entire genome segments are exchanged between viral strains. These processes are strongly associated with the emergence of new viral variants and increased virulence in agricultural systems (Moreno & López-Moya, 2020).

C. Virus Adaptation to Hosts and Vectors

Plant viruses continuously adapt to both their host plants and insect vectors, thereby increasing transmission efficiency and host-range expansion. Viral proteins involved in movement and replication often undergo selection pressure to enhance compatibility with host cellular machinery. Similarly, adaptation to vectors such as aphids, whiteflies, and thrips has been widely documented. For example, begomoviruses (Geminiviridae) show strong adaptation to whitefly vectors, which has contributed

to their global spread in tropical and subtropical regions (Jones & Naidu, 2019).

D. Co-evolution with Host Plants

Plant viruses and their hosts engage in a continuous co-evolutionary arms race, where host plants develop resistance genes while viruses evolve counter-defense strategies. This dynamic interaction shapes both viral diversity and host immune responses. Host RNA silencing mechanisms constitute a major defence strategy, whereas viruses counteract this by encoding silencing suppressor proteins. Recent research highlights that this molecular arms race is a key driver of viral diversification and long-term evolutionary stability in plant-virus systems (Nicaise, 2022).

E. Emergence of New Viral Strains

The emergence of new plant viral strains is primarily driven by mutation, recombination, host switching, and vector expansion. Agricultural intensification, global trade, and climate change have significantly accelerated the appearance of novel viral diseases. Modern metagenomic studies have revealed that many newly emerging plant viruses originate from previously unrecognized reservoirs in wild plants and weeds. Climate-driven expansion of vector populations further facilitates the spread of these novel strains into new geographic regions, increasing global agricultural risk (Zhou & Tzanetakis, 2020; Bhat et al., 2021).

5. IMPACT ON GLOBAL AGRICULTURE

Plant viruses are among the most damaging plant pathogens globally, causing substantial yield losses across staple, horticultural, and cash crops. Their impact is not only limited to direct reduction in yield but also includes quality degradation, post-harvest losses, trade restrictions, and increased production costs. Recent global analyses show that plant viral diseases contribute to significant economic burdens, particularly in regions dependent on agriculture for livelihood and food security (Jones & Naidu, 2019). Plant viruses cause severe economic losses in major crops such as rice, wheat, maize, potato, tomato, cassava, and legumes. For example, Potato virus Y

(PVY) and Potato leafroll virus (PLRV) can reduce potato yields by up to 80% under severe infections, while cassava mosaic disease and cassava brown streak disease collectively threaten food security in Africa. Similarly, Begomoviruses affecting tomato and cotton lead to major production losses in tropical and subtropical regions (Thresh & Cooter, 2021). These losses are further amplified by increased costs of vector control and seed replacement.

Several plant viral diseases illustrate the global impact of plant viruses. Cassava mosaic disease in Africa, caused by Geminiviridae, has historically led to devastating yield reductions and food shortages. Rice tungro disease in Asia, caused by a virus complex transmitted by leafhoppers, remains a major constraint on rice production. Another important case is Tomato yellow leaf curl disease (TYLCD), which has spread globally due to whitefly expansion and climate change, severely affecting tomato productivity in multiple continents (Moreno & López-Moya, 2020). These case studies highlight how virus–vector–environment interactions drive large-scale epidemics. Plant viruses directly threaten global food security by reducing staple crop productivity and destabilizing agricultural systems. Unlike many fungal or bacterial diseases, viral infections are often systemic and irreversible, making infected plants difficult to recover. In smallholder farming systems, particularly in developing countries, viral outbreaks can lead to complete crop failure. Recent studies emphasize that climate change, limited access to certified seed, and weak diagnostic infrastructure further intensify food insecurity risks associated with plant viruses (Bhat et al., 2021). The impact of plant viruses varies significantly across regions. Tropical and subtropical regions experience higher virus pressure due to favorable conditions for vector populations, especially whiteflies and aphids. Africa faces severe challenges from cassava and banana viruses, while Asia is heavily affected by rice and vegetable viruses. In contrast, temperate regions experience periodic outbreaks linked to seasonal vector activity. On a global scale, increased trade, climate change, and agricultural intensification have facilitated the rapid emergence and spread of plant viruses across continents, making

them a transboundary agricultural threat (Jones & Naidu, 2019; Moreno & López-Moya, 2020).

6. MANAGEMENT AND CONTROL STRATEGIES

Management of plant viral diseases is challenging because viruses cannot be directly controlled by chemical treatments once infection occurs. Therefore, effective control relies on an integrated approach combining cultural, biological, genetic, and biotechnological strategies. Cultural practices such as crop rotation, removal of infected plants, use of certified virus-free seed material, and weed management are fundamental in reducing initial inoculum sources. Vector control remains critical, involving insecticide use, biological control agents, reflective mulches, and habitat management to reduce vector populations. However, sole reliance on insecticides is often ineffective due to rapid virus transmission and insect resistance issues (Jones & Naidu, 2019). Host plant resistance remains the most sustainable strategy, achieved through conventional breeding and marker-assisted selection for virus-resistant cultivars. Cross protection, where mild viral strains are used to protect against severe strains, has also been successfully applied in certain crops such as citrus and papaya. Recent advances in biotechnology have introduced powerful tools such as RNA interference (RNAi) and CRISPR/Cas-based genome editing, which enable targeted disruption of viral genomes or host susceptibility genes, offering promising long-term solutions (Nicaise, 2022; Bhat et al., 2021). Modern plant virus management increasingly relies on Integrated Disease Management (IDM), which combines multiple strategies including host resistance, vector monitoring, ecological approaches, and molecular diagnostics for early detection. IDM is considered the most effective and sustainable approach under current agricultural conditions, especially in the context of climate change and evolving viral populations.

7. CHALLENGES AND FUTURE PERSPECTIVES

Plant virology is facing new challenges because of the rapid evolution of viruses, changes in agricultural practices, and global environmental changes. The first challenge facing plant virology is the constant emergence of new strains of viruses. The emergence of new strains is attributed to the high mutation rate, recombination, and reassortment of viruses. These processes allow viruses to rapidly escape resistance in their hosts and colonize new ecological niches. This has made it difficult to control plant viruses in the long term (Jones & Naidu, 2019). The second challenge facing plant virology today is the effects of climate change. Climate change has affected the geographical distribution, abundance, and periodic occurrence of insect vectors, including aphids, whiteflies, and thrips. The increase in temperature and changes in rainfall patterns have led to the geographical extension of several economically important viruses, especially those in the Geminiviridae family. This has resulted in increased occurrence and severity of viral diseases in regions previously regarded as low-risk (Moreno & López-Moya, 2020; Thresh & Cooter, 2021). Globalization and trade in plant materials further complicate virus management by facilitating the rapid introduction of emerging and invasive viruses into new regions.

Many outbreaks are linked to the movement of infected planting material, often before symptoms become visible, highlighting the limitations of current quarantine and certification systems. A persistent limitation in many developing agricultural systems is the lack of affordable and rapid diagnostic infrastructure, which delays early detection and allows viruses to spread unchecked. In addition, over-reliance on chemical vector control has become less effective due to widespread insecticide resistance and environmental concerns, emphasizing the need for more sustainable approaches. Looking forward, the future of plant virology will depend on the development of integrated, climate-resilient disease management systems that combine host resistance, improved surveillance, and ecological vector management. Strengthening global monitoring networks, improving seed health systems, and promoting the use of resistant or genetically improved

crops will be essential to reduce the impact of plant viral diseases. In conclusion, it will be essential to address all these problems through a multi-disciplinary approach that incorporates virology, ecology, climatology, and biotechnology to ensure that the management of plant viruses keeps pace with the ever-changing environment.

8. CONCLUSIONS

Plant viruses are one of the most significant constraints to global agricultural productivity due to their variability, rapid evolution, and efficiency of spread via various biological and environmental mechanisms. The adaptability of plant viruses to overcome any barrier to resistance via rapid evolution through mutation, recombination, and selection pressure by the host plant results in the continuous emergence of novel strains of plant viruses that are more virulent. The effects of plant viruses are not limited to yield loss, but they are also responsible for lowering the quality of crops, increasing the cost of crop production, and affecting global food security. These problems are further complicated by the effects of climate change, which are affecting the distribution, period of spread, and geographic range of some of the economically important groups of plant viruses. Furthermore, the global movement of plant products is facilitating the spread of newly emerging viral diseases. Despite advances in the understanding of plant virus biology, the control of plant viruses is proving to be challenging due to the fact that there are no curative measures available once the plant becomes infected. Therefore, the control of plant viruses relies on integrated approaches to plant virus management. The way forward in the study of plant virology in the future involves strengthening global surveillance, enhancing seed certification, and establishing lasting resistance through sophisticated breeding and technology. A multidisciplinary and proactive approach in the study of plant virology, ecology, climatology, and agricultural management will be vital in addressing the rising global burden of plant viral diseases.

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