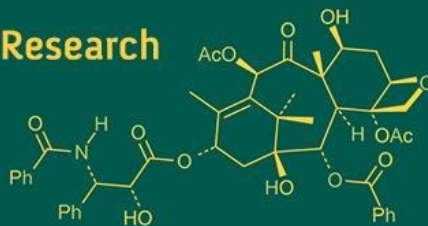
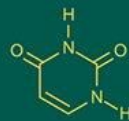
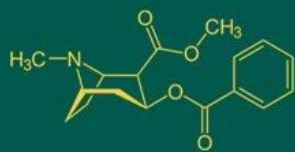


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Emerging cucurbit viruses

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Abstract

Cucurbits are essential components of global vegetable production; however, their cultivation faces increasing threats from a rapidly expanding complex of viral pathogens. Despite their importance in global nutrition, cucurbit survival is jeopardised by evolving viruses. This review examines the biology and transmission patterns of five significant pathogens cucumber green mottle mosaic virus (CGMMV; species *Tobamovirus viridimaculae*), cucurbit aphid-borne yellows virus (CABYV; *Polytomovirus CABYV*), cucumber mosaic virus (CMV; *Cucumovirus CMV*), papaya ringspot virus (PRSV; *Potyvirus papayanuli*), and tomato leaf curl New Delhi virus (ToLCNDV; *Begomovirus virussolanumdelhiense*) - that are currently transforming cucurbit farming. In many cases, isolated outbreaks have been replaced by complex virus incidences, involving multiple viruses that interact to produce more severe symptoms and substantial yield losses.

This changing landscape is driven by globalized seed trade, the instability of large-scale monocultures, and climate change altering the distribution of insect vectors. Since traditional treatments for plant viruses are unavailable, efforts must focus on developing sophisticated, multi-layered defense strategies. These strategies should extend beyond basic field hygiene to incorporate advanced agricultural technologies, including RNA interference (RNAi) and precise CRISPR/Cas9 gene editing. Ensuring the future of cucurbit production requires integrating these innovative tools with sustainable management practices.

Keywords: Cucurbitaceae, viral synergism, CGMMV, CABYV, ToLCNDV, Integrated disease management, climate change

1. Introduction

Cucurbits, a vital group of vegetable crops, are cultivated extensively worldwide, contributing significantly to global food production. The cucurbitaceae family includes over 130 genera and 800 species, with 30 species particularly crucial to global agriculture. They are low in calories, rich in vitamins, minerals, and antioxidants, making them valuable for hydration, heart health, and immune support. They are versatile in culinary use, contribute to digestive health, and are important crops with high yield and economic value. Major producers of cucurbits include Turkey, China, India, and the United States (Rolnik and Olas, 2020) ^[72]. Key crops such as watermelons, cucumbers, gherkins, and melons are increasingly cultivated, with global production rising from 209.8 million tons in 2017 to 223.2 million tons in 2022 (FAO, 2024) ^[26].

The expansion of cucurbit production has been accompanied by a rapid increase in the number of virus species infecting these crops. Viruses from genera such as *Begomovirus*, *Potyvirus*, *Cucumovirus*, and *Tobamovirus* pose significant threats to cucurbit cultivation worldwide. The known cucurbit-infecting virus species increased from approximately 20 in 1980 (Lovisolo, 1980) ^[56] to over 90 by 2019 (Desbiez, 2020) ^[19, 20]. Recently emerging viruses, including cucumber green mottle mosaic virus (CGMMV), cucurbit aphid-borne yellows virus (CABYV), cucumber mosaic virus (CMV), papaya ringspot virus (PRSV), and tomato leaf curl New Delhi virus (ToLCNDV), have become widespread and present new challenges for cucurbit production (Desbiez, 2020) ^[19, 20].

2. *Tobamovirus viridimaculae* (CGMMV)

Tobamovirus viridimaculae (cucumber green mottle mosaic virus) was first found in England in 1935, and it slowly spread across Europe, the Middle East, and Asia over the following decades. However, from 2007 to 2016, the virus spread rapidly to new regions, including

West Africa, North America, and Australia, marking a significant increase in its global distribution (Webster and Jones, 2022) ^[90].

The genome of CGMMV consists of a 6.4-kb single-stranded, positive-sense RNA, which is housed within a rigid, rod-shaped virion measuring approximately 300 nm in length and 18 nm in diameter, composed of roughly 2,000 capsid protein subunits (Hollings *et al.*, 1975) ^[71]. This genomic RNA is protected from enzymatic degradation by a methylated nucleotide cap at its 5' terminus and a tRNA-like structure at its 3' terminus. Within the genome, four open reading frames (ORFs) encode essential proteins, including two replication-related polypeptides: a 129-kDa protein containing methyltransferase and helicase motifs, and a 186-kDa protein generated through the suppression of a UAG termination codon which features an RNA-dependent RNA polymerase at its carboxyl end. Furthermore, two additional proteins, including the coat protein necessary for virion assembly, are translated from subgenomic mRNAs derived from ORFs located in the 3' region of the genome (Ishibashi and Ishikawa, 2016) ^[37].

Tobamoviruses have an evolutionary history marked by frequent cross-species transmission and a slower rate of evolution. Analysis by Gibbs *et al.* (2015) ^[29] of 29 Tobamoviruses revealed the existence of eight specific lineages that mirror the evolutionary history of their respective host plants. The study suggests that the majority of these viruses co-diverged alongside their primary plant hosts over a period exceeding 110 million years, resulting in three major clusters that target the asterid, rosid, and caryophyllid subdivisions of angiosperms. Within the rosid-infecting cluster, five viruses specialized for cucurbits were identified as distinct phylogroups; notably, both CGMMV and Cucumber mottle virus were found to form their own separate monophyletic groups, a finding that validates the classification of CGMMV as a uniquely divergent species (Gibbs *et al.*, 2015) ^[29].

The symptoms of CGMMV vary significantly across different cucurbit species and cultivars. In cucumbers, the virus causes green mottling on young leaves and fruits, potentially leading to plant collapse. Watermelons develop mottled and mosaic leaves, with brown necrotic lesions on stems, and fruits become unmarketable due to malformation and internal discoloration. Melons show initial mottle and mosaic on young leaves, which often fade as the plant matures, but fruits still develop mottling and surface netting. Pumpkins typically remain asymptomatic, while squash and zucchini may have discoloured and necrotic internal fruit tissue (Dombrovsky *et al.*, 2017) ^[23, 24]. CGMMV can also cause significant yield losses, up to 15 percent in cucumbers and over 50 percent in watermelons, even if the infected plants show no visible symptoms. The severity of symptoms depends on factors such as environmental conditions, the plant's growth stage at infection, and the viral strain, with early infections and specific strains causing more severe symptoms. CGMMV is more aggressive in warmer climates, spreading faster at higher temperatures, while drought conditions can limit its systemic movement within the plant. CGMMV spreads readily through contact because its virions are highly stable and can stay infectious on contaminated surfaces for long durations. The virus transmits via tiny wounds on healthy plants when they touch infected plants, plant debris, or contaminated objects such as machinery, tools, and clothing. It can also infect seedlings planted in

contaminated soil through small wounds on their roots (Mandal *et al.*, 2008) ^[57]. Seed transmission plays a crucial role in the virus's worldwide spread since CGMMV can contaminate seed coats and remain infectious for extended periods, although not all contaminated seeds will transmit the virus. According to a study by Constable *et al.* (2018) ^[11], CGMMV was detected in 22 out of 631 samples tested, representing 3.5 percent of the total. The virus was found in the seeds of different cucurbit crops, with detection rates of 7.8percent in cucumber seeds (8 out of 102 samples), 3.3percent in melon seeds (13 out of 393 samples), and 1.8percent in watermelon seeds (1 out of 57 samples).

CGMMV is also capable of infecting a wide range of alternate collateral hosts, including at least 15 weed species across nine plant families within the asterid, rosid, and caryophyllid subdivisions. The virus's stability and infectious nature raise concerns about its potential spread by beneficial insects, including biological pest control agents and pollinators like bumblebees and honey bees. Recent greenhouse studies demonstrated that honey bees could spread CGMMV from infected to healthy plants up to 30 meters away, indicating that pollinators might play a significant role in the virus's transmission, especially in areas where they are essential for cucurbit crop pollination (Darzi *et al.*, 2017) ^[13].

Initial detections of CGMMV in Australia occurred in 2014, when the virus was identified within four watermelon crops located in Katherine, Northern Territory. Following this emergence, a broader spread was documented between September 2014 and January 2016, during which the pathogen was confirmed in both weeds and cucurbit plantings across 26 different sites; this expansion affected 10 commercial farms spanning the Ti Tree, Katherine, and Darwin regions. In 2015, an agricultural research station also reported CGMMV infection in cucurbits. Most infected crops, primarily watermelon, were sourced from a Queensland nursery and exhibited symptoms like leaf mottling and mosaic, though some plants were asymptomatic. Strict quarantine measures were imposed, requiring the destruction of infected crops and a two-year ban on CGMMV host plantings. After 17 months of eradication efforts, the virus was detected in common weeds, leading to the lifting of quarantine restrictions in NT, though movement of plant material, soil, and equipment remained restricted (NTGOV, 2016) ^[67].

3. *Polerovirus CABYV*(CABYV)

The cucurbit aphid-borne yellows virus (CABYV) is classified under the genus *Polerovirus* within the *Solemoviridae* family. Although it was officially identified and described for the first time in France in 1992, researchers believe the virus had been circulating for at least ten years prior to its formal discovery (Lecoq *et al.*, 1992) ^[53]. CABYV primarily affects cucurbit crops and is now present worldwide, with the exception of some islands. The virus also infects a variety of wild species, including both cucurbit and non-cucurbit hosts, found in different agro-climatic environments.

CABYV was first identified in France and is now distributed globally, except for some isolated regions. It is divided into two main molecular groups: one consisting of Asian isolates and the other containing isolates from America, Africa, and Europe (Kassem *et al.*, 2013) ^[45]. The virus has also been responsible for a severe disorder in bitter melon known as

'Namamarako' in the Philippines, which is characterized by interveinal chlorosis, green vein banding, wrinkling, and thickening of younger leaves (Relevante *et al.*, 2012) [70]. In India, CABYV was initially identified as one of the first cucurbit-infecting poleroviruses to affect teasel gourd and bitter gourd crops within the state of Karnataka (Suveditha *et al.*, 2017) [83]. And very recently natural occurrence of CABYV in Snake gourd and Round gourd worldwide and Bottle gourd, Sponge gourd, and Ash gourd, in India was reported. (Verma *et al.*, 2023) [88].

The cucurbit aphid-borne yellows virus (CABYV) is characterized by icosahedral-shaped particles that measure roughly 25 nm across. These particles house a single-stranded, positive-sense RNA genome with a length of approximately 5.7 kb (D'Arcy and Domier, 2005) [12]. This genetic material is organized into seven open reading frames (ORFs) flanked by non-coding segments at the 5' and 3' ends. Translation of the first three ORFs (0, 1, and 2) occurs directly from the genomic RNA. Specifically, a leaky scanning process is used for ORF1, while the RNA-dependent RNA polymerase (RdRP) in ORF2 is produced as a fusion protein through a ribosomal frameshift (Smirnova *et al.*, 2015) [82]. The remaining genetic components are expressed through subgenomic RNAs. Subgenomic RNA1 is responsible for translating ORFs 3a, 3, 4, and 5; subgenomic RNA2 handles ORFs 6 and 7; and ORF7 can also be translated via subgenomic RNA3. Within this group, the ORF5 protein is expressed as a fusion product when translation continues past the ORF3 stop codon. Lastly, the P4 protein acts as the movement protein, which is the primary tool the virus uses to travel between cells and achieve systemic infection throughout the plant (Delfosse *et al.*, 2021) [16].

In cucurbit crops such as melon, cucumber, squash, and watermelon, CABYV typically induces yellow mottling and interveinal chlorotic patches on the leaves, which eventually coalesce, causing the leaves to become yellow, thickened, and brittle (Kassem *et al.*, 2007) [46]. The virus affects the yield of infected plants, often leading to blossom drop and reduced fruit numbers, although fruit quality is generally unaffected (Lecoq *et al.*, 1992) [53]. In some regions, like the Philippines and India, CABYV has caused significant yield reductions in bitter gourd and cucumber (Suveditha *et al.*, 2017; Menzel *et al.*, 2020) [61, 83].

Controlling the spread of cucurbit aphid-borne yellows virus (CABYV) relies heavily on understanding its unique relationship with its insect vectors and the development of resistant crop varieties. Unlike many other plant viruses, CABYV is not seedborne and cannot be spread through mechanical contact; instead, it remains strictly restricted to the plant's phloem (Lecoq and Desbiez, 2017).

The virus is spread in a circulative, non-propagative manner by specific aphid species, most notably *Aphis gossypii*, *Myzus persicae*, and *Macrosiphum euphorbiae* (Lecoq *et al.*, 1992; Kassem *et al.*, 2013) [45, 53]. During feeding, aphids pick up the virus from the phloem. The viral particles then move through the insect's digestive tract into the hemocoel, eventually reaching the accessory salivary glands before being injected into a new host plant. This process requires an acquisition period of several hours to a full day, after which the aphid remains capable of spreading the virus for the rest of its life, even though the virus does not multiply inside the insect or pass to its offspring (Sangeetha *et al.*, 2019) [75].

Interestingly, infection alters how aphids behave, favouring the virus. For instance, in cucumber plants, *Aphis gossypii* has been observed to feed for longer periods on infected hosts, thereby boosting virus uptake, before moving on to settle on healthy plants (Carmo-Sousa *et al.*, 2016) [8]. This behavioral shift significantly optimizes the spread of the pathogen throughout a field.

To combat this, breeding for resistance is the primary management strategy. While CABYV can undergo recombination with other viruses, such as melon necrotic spot virus (MNSV), to bypass current crop defense, resistance has been identified in squash, cucumber, bitter gourd, and melon (Miras *et al.*, 2014; Lecoq *et al.*, 1998; Relevante *et al.*, 2012) [54, 62, 70]. In melons specifically, researchers have identified three distinct genetic mechanisms for resistance (Boissot *et al.*, 2016) [6]. Notably, the *Vat* gene, which provides resistance against *Aphis gossypii*, has proven highly effective at lowering the occurrence of CABYV in field settings (Schoeny *et al.*, 2017) [76].

4. *Cucumovirus CMV* (CMV)

Cucumovirus CMV (cucumber mosaic virus) is a significant pathogen in the family *Bromoviridae* and genus *Cucumovirus*, recognized as one of the top 10 plant viruses worldwide. It poses a severe threat to cucurbit production due to its global distribution and diverse modes of transmission. CMV is a positive-sense single-stranded RNA (ssRNA) virus with a tripartite genome encapsidated in isometric particles about 30 nm in diameter with three genomic RNAs, designated as RNA 1, RNA 2, and RNA 3. RNA 1 and RNA 2 are encapsulated separately, while RNA 3 and its subgenomic RNA-4 are encapsidated within the same particle. These RNA segments encode several essential viral proteins, including the 1a protein (replicase), 2a protein, 2b protein, 3a protein (movement protein), and 3b protein (capsid protein). CMV is also known to support a satellite RNA (satRNA), designated as RNA 5 facilitating its spread along with the virus and its aphid vectors (ICTV, 2024).

This virus has an exceptionally wide host range, infecting over 800 species across 70 botanical families. In cucurbit crops, CMV's persistence is largely attributed to its ability to be transmitted by more than 70 aphid species in a non-persistent manner, through seed transmission, contact spread, and even by parasitic plants (Jacquemond, 2012) [38]. CMV is known for its variable and often severe symptoms across different host species. In vegetables like tomatoes, early-stage infection can cause chlorotic lesions, necrosis, and eventually plant death, while later infections may result in reduced growth, bushy appearance, and malformed fruits. In cucurbits, particularly melons, zucchini, and squash CMV induces strong mosaic symptoms, leaf distortion, and misshapen, unmarketable fruits. Mixed infections with other viruses often exacerbate these symptoms (Desbiez, 2020) [19, 20].

In tobacco species, the 1a protein of cucumber mosaic virus (CMV) functions as a critical factor in host-virus interactions by triggering programmed cell death. For instance, the Ns strain of CMV induces systemic necrotic spots and local necrotic lesions (NLLs) in several species, including *Nicotiana tabacum* cv. Xanthi, *N. glutinosa*, and *N. clevelandii* (Salánki *et al.*, 2007) [74]. Divéki *et al.* (2004) [22] identified the molecular determinant of this response, demonstrating that the amino acid at position 461 in the 1a protein governs the reaction: cysteine (C) at this site triggers

cell death, whereas arginine (R) does not. Beyond eliciting cell death, the genetic composition of CMV significantly affects symptom expression in other hosts such as zucchini squash. Differences in symptom severity and viral movement speed between the Sny and Fny strains have been attributed to RNA segments 1 and 2. Notably, in the Fny (IA) strain, a single mutation at position 267, substituting isoleucine (I) with threonine (T), shifts the pathology from chlorotic spots to mosaic symptoms in squash (Choi *et al.*, 2005).

5. *Potyvirus papayanuli* (PRSV)

Papaya ringspot virus (PRSV), part of the Potyvirus group in the Potyviridae family and once called Watermelon mosaic virus 1 (WMV1), is an important disease-causing virus. The virus is made of flexible, thread-like particles about 12 nm wide and 760 to 800 nm long (Herold and Weibel, 1962) [30]. Its genetic material is a single strand of RNA with about 10,000 building blocks. This RNA is used to make a large protein that is then cut into smaller functional parts, including a 36-kDa coat protein (CP) (Rodriguez *et al.*, 2008). Although the N-terminal region of the coat protein exhibits variability, its core remains highly conserved among isolates. Two primary strains exist: PRSV-P and PRSV-W. PRSV-P infects both cucurbits and papaya, mainly causing serious disease in papaya, while PRSV-W infects only cucurbits and does not infect papaya. Studies show that P-type strains probably came from W-type strains. This change in which plants the virus can infect can happen with a single mutation in the NIa-Pro protease, which is enough to switch the virus between P and W types (Chen *et al.*, 2008) [10].

Symptoms in cucurbits include intense mosaic patterns, leaf narrowing, and in severe cases, a shoestring effect similar to that seen in papaya. Infected fruits, such as yellow crookneck squash, display green blotches and deformities. In papaya, early symptoms include oily streaks and vein clearing on younger leaves, which later develop into intense mosaic symptoms and chlorosis. Transmission occurs primarily through aphids in a non-persistent manner, with over 20 aphid species, including *Myzus persicae* and *Aphis gossypii*, being capable of transmitting PRSV (Martins *et al.*, 2016) [58, 59]. Although PRSV was not traditionally considered seed-transmissible, a study in the Philippines reported a low incidence (0.15 percent) of seed transmission in 'Cavite papaya' strain (Bayot *et al.*, 1990) [4]. Weeds in cucurbit field may serve as reservoirs for aphid vectors, aiding in the spread of the virus.

PRSV is part of a cluster of cucurbit-infecting viruses, including Moroccan watermelon mosaic virus and zucchini tigre mosaic virus, which are geographically restricted mainly to Africa and the Middle East but are emerging in other regions, such as the Mediterranean Basin (Desbiez *et al.*, 2017) [17].

6. *Begomovirus solanumdelhiense* (ToLCNDV)

In recent decades, tomato leaf curl New Delhi virus (ToLCNDV) has surfaced as a primary threat to vegetable production, particularly within tropical and subtropical climates (Navas-Castillo *et al.*, 2011) [66]. As a member of the *Begomovirus* genus the most populous group in the *Geminiviridae* family ToLCNDV is distinguished by its "geminate" or twin-shaped particles. These structures consist of two conjoined, partial icosahedral heads made of 110 capsid protein molecules (Brown 2012).

The genetic blueprint of ToLCNDV is a bipartite, circular, single-stranded DNA genome divided into two segments: DNA-A and DNA-B, each roughly 2.5-2.6 kb. DNA-A possesses the machinery for independent replication and the creation of new virions, yet the virus requires DNA-B to establish a systemic infection throughout the host (Srivastava *et al.*, 1995) [94]. Furthermore, these viruses often associate with 1.3 kb satellite molecules known as beta satellites. These satellites carry a specific gene, β C1, which functions as a suppressor of the plant's gene-silencing defenses, thereby intensifying the viral impact (Singh *et al.*, 2012) [78].

Initially discovered in 1995 on tomato crops in North India (Srivastava *et al.*, 1995) [94], ToLCNDV has since expanded its host range across several plant families, including *Cucurbitaceae*, *Solanaceae*, and *Fabaceae*. It causes substantial damage to a variety of cucurbits, ranging from zucchini and cucumber to melon, watermelon, and various pumpkins (Venkataravanappa *et al.*, 2020; Siskos *et al.*, 2022) [80, 87]. Infected plants display distinct physical symptoms such as vein swelling, leaf curling, severe yellowing, and shortened internodes. The fruit itself often suffers in quality, exhibiting reduced size, skin roughness, and longitudinal cracks (Kiran *et al.*, 2021; Siskos *et al.*, 2022) [80].

The primary mode of dissemination for ToLCNDV is the whitefly (*Bemisia tabaci*), which transmits the virus in a persistent, circulative manner; while mechanical contact transmission has also been documented, the whitefly remains the most significant vector. The global spread of the virus is largely attributed to the highly adaptable "B type" whitefly biotype, which originated in the Mediterranean-Asian region (Navas-Castillo *et al.*, 2011) [66]. Once a whitefly acquires the virus through feeding a process taking several hours it can remain a carrier for days or even the rest of its life.

Regarding seed transmission, the evidence remains a subject of ongoing debate. While a 2023 study by Sáez *et al.* identified DNA-A and DNA-B components within the embryo and endosperm of melon seeds, they observed that seedlings germinating from these seeds did not develop intact viral genomic components in their leaves. Instead of seed transmission, the rapid emergence of ToLCNDV is more likely driven by its vast host range and the continuous presence of inoculum in year-round tomato crops and surrounding weeds (Nagendran 2021).

7. Virus Complex

A study by Kumari *et al.* (2021) [49] in Uttar Pradesh, India, analyzed 563 samples from 14 cucurbit crops. *Begomovirus* was the most prevalent (93percent), followed by *Potyvirus* (46percent), CGMMV (39percent), *Polerovirus* (9percent), CMV (2percent), and *Orthotospovirus* (2percent). Additionally, CMV, CGMMV, and *Polerovirus* showed host range expansion on cucurbit crops. Virus-infected cucurbit samples showed a higher incidence of mixed infections (65percent) compared to single infections (35percent). Among single infections, *Begomovirus* was the most common (90percent). In mixed infections, 61percent were double infections, primarily involving combinations with *Begomovirus*. Triple infections accounted for 31percent, and 8percent of samples had four-virus combinations. *Potyvirus* and/or CGMMV were frequently found with *Begomovirus* in mixed infections.

Field surveys in Tamil Nadu (2012-2014) revealed a high incidence of *Begomovirus* (98.6percent) in cucurbits,

followed by PRSV (32.1percent) and CGMMV (22.2percent). *Zucchini yellow mosaic virus* (ZYMV) and CMV were less frequent. Over 50percent of samples had mixed infections with two or three viruses. Sequencing identified ToLCNDV and *Squash leaf curl China virus* (SLCCNV). Mixed infections are common globally, with various combinations reported in different regions. In this study, co-infection of two potyviruses (PRSV + ZYMV) with begomovirus was rare, likely due to differences in potyvirus replication rates. (Nagendran *et al.*, 2017) ^[64, 65].

8. Factors Leading To Emergence

The recent increase in plant virus epidemics is closely linked to the shift toward large-scale monoculture. Agricultural practices aimed at maximizing yields and extending growing seasons have unintentionally created unstable ecosystems that facilitate more frequent disease outbreaks (Thresh, 1980) ^[85]. This instability is exacerbated by several contemporary factors. Foremost among these is the globalization of trade; rapid movement of plants and seeds by multinational companies often introduces pathogens into previously unexposed regions (Jones and Naidu, 2019) ^[42]. Additionally, crops relocated far from their centers of domestication frequently encounter novel local viruses in surrounding natural vegetation, against which they lack evolved defenses (Jones, 2020) ^[41].

Environmental shifts, particularly global warming, add another layer of complexity to this crisis. The "disease triangle"- the interaction between the host, the pathogen, and the environment- is being reshaped by rising temperatures (Hunjan and Lore, 2020) ^[34]. Warmer winters, for instance, allow weeds and insects to survive in larger numbers, creating a massive reservoir of viruses ready to infect crops the following season (Chappell *et al.*, 2013) ^[9]. While higher temperatures can sometimes speed up viral replication, they can also affect insect vectors. For example, a mere 2 degree rise in temperature can lead to five additional generations of aphids per year, significantly increasing their mobility and ability to spread diseases over long distances (Hullé *et al.*, 2010) ^[33]. Similarly, whitefly populations are expanding into previously cold regions, carrying viruses such as ToLCNDV (Navas-Castillo *et al.*, 2011) ^[66].

Human activity and the physical nature of the viruses themselves further complicate management. Poor farm hygiene such as using contaminated tools or failing to clear infected debris remains a major pathway for transmission (Wokorach *et al.*, 2018) ^[91]. This is especially dangerous with highly stable viruses like CGMMV, which can persist on surfaces, clothing, or in the soil for over a year without a host (Antignus, 2012) ^[3]. The rapid global dispersal of CGMMV over the last few decades serves as a prime example of how international seed trade, combined with a lack of strict quarantine and the pressures of climate change, can turn a localized issue into a worldwide agricultural threat (Dombrovsky and Smith, 2017) ^[23, 24].

9. Integrated Disease Management

Given the obligate intracellular nature of plant viruses, curative methods are often ineffective. Therefore, disease management strategies must prioritize risk reduction and prevention, taking into account the dynamic and evolvable nature of plant viruses. The design of management strategies for plant viruses should consider the nature of host plants, such as annuals or perennials and their types of propagation,

vector biology and ecology, transmission characteristics, and infection cycle of plant viruses.

Exclusion and avoidance

Managing the import and movement of plant material is crucial to prevent virus introduction. Exclusion through quarantine and certification at ports can stop infected plant materials from entering. Seed and plant material testing, including Next-Generation Sequencing (NGS), is vital for detecting all viruses in a sample, though large-scale use of NGS remains costly (Tatineni and Hein, 2023) ^[84]. India's plant quarantine measures are governed by the Destructive Insects & Pests Act of 1914, aimed at preventing the introduction of pests harmful to crops. Import of agricultural products is regulated through the Plant Quarantine Order of 2003, aligned with the New Policy on Seed Development and the WTO's Sanitary and Phytosanitary (SPS) Agreement. The scheme's objectives include preventing exotic pest entry, ensuring safe agricultural trade, and providing phytosanitary certification. With 73 quarantine stations across international entry points, India conducts inspections of imports and exports, undertakes pest risk analysis, and enforces post-entry quarantine protocols. Modern equipment at key stations aids in efficient quarantine operations, supporting both domestic and international trade compliance (DPPQS, 2023) ^[23].

Seed-transmitted viruses, often spread through seed coat infection, can be effectively managed with disinfection treatments using hydrochloric acid, trisodium phosphate, or sodium hypochlorite (Davino *et al.*, 2020) ^[15]. Soil fumigation and treatments like steam heat, ozone, and ultraviolet irradiation are essential for eliminating stable virions like CGMMV (Reingold *et al.*, 2016) ^[69]. Controlling weeds and volunteer cucurbits is crucial to prevent virus-carrying hosts. Planting non-host crops such as millet, maize, or barley in appropriate regions further reduces virus spread and prevents soil erosion (Antignus, 2012) ^[3].

Promoting natural enemies through the establishment of flower strips can help reduce vector populations, which is particularly important for controlling viruses like CMV, PRSV, CABYV, and ToLCNDV, whose primary spread is vector-mediated (Schoeny *et al.*, 2019) ^[77]. The use of insect nets or plastic mulch can also be effective in repelling aphids, though this is typically only effective for a few weeks before canopy cover renders the plastic ineffective.

Chemical treatments are common for controlling vector transmission but can be less effective against efficient vectors or viruses transmitted by nonpersistent methods due to rapid inoculation (Zaffaroni *et al.*, 2021) ^[93]. Concerns about their impact on soil fertility, drug-resistant pathogens, and pesticide residues have led to increased interest in biopesticides. These are more environmentally friendly, specific, and less likely to cause resistance. *Beauveria bassiana*, an entomopathogenic fungus, effectively controls aphids and whiteflies, offering a viable alternative for vector management (Singh *et al.*, 2020) ^[79].

Antiviral principles

Plant extracts, fungi, and bacteria offer sustainable control of plant viruses by targeting vectors, inhibiting virus replication, or altering biosynthetic pathways through gene expression regulation. Their antiviral activity involves techniques like cross-protection, induced systemic resistance, and the synthesis of biochemicals such as lipopeptides, phenolic compounds, and enzymes that activate defense mechanism.

Culture filtrate of Streptomycetal isolates has inhibited cucumber mosaic virus (CMV) in *Chenopodium amaranticolor*. *Beauveria bassiana* has shown potential against Zucchini yellow mosaic virus (ZYMV) in *Cucurbita pepo* L. (Jaber & Salem, 2014), while *Penicillium simplicissimum* (GP17-2) has been used to manage CMV infections in *Arabidopsis thaliana* and *Nicotiana tabacum* (Marina *et al.*, 2011).

Extracts from various plant parts, like leaves and roots, show antiviral effects. *Azadirachta indica* leaf extract is effective against whitefly (*Bemisia tabaci*) and inhibits Zucchini yellow mosaic virus (ZYMV) in *Citrullus lanatus* (Abbas *et al.*, 2020) [1]. Additionally, extracts from *Nigella sativa*, *Thuja orientalis*, and *Bougainvillea spectabilis* also target ZYMV (Elbeshehy, 2017) [25], and *Mirabilis jalapa* leaf extract controls cucumber mosaic virus in Brinjal (Bharathi, 2007) [5]. *Brahmi* (*Centella asiatica*) is also known for its antiviral properties.

Host resistance

Plants develop defense mechanisms to combat viral infections, with natural genetic resistance being the most effective and eco-friendly approach. Resistance genes, classified as dominant or recessive, in which dominant gene mostly effective against fungi and bacteria, with only a few targeting viruses (Huang, 2021) [32].

R genes encode NBS-LRR proteins that interact with avirulence (Avr) gene products in a direct gene-for-gene relationship, triggering a hypersensitive response (HR) which contains the pathogen through programmed cell death. Recessive resistance results from host factor loss or mutations, providing broader resistance compared to dominant R genes (Wang and Krishnaswamy, 2012) [89]. For example, recessive resistance genes like *cgmmv-1* and *cgmmv-2* in melon reduce CGMMV symptoms, though such resistance can be unstable due to temperature sensitivity or emerging virus strains (Lecoq and Katis, 2014) [51].

RNA Silencing: RNA silencing, or RNA interference (RNAi), involves Dicer-like ribonucleases producing siRNAs from dsRNAs, which then guide the RNA-induced silencing complex (RISC) to degrade complementary mRNA (Liu *et al.*, 2006) [55]. This mechanism provides antiviral defense by generating virus-specific siRNAs. RNAi technology can manage multiple viruses, as demonstrated in transgenic squash resistant to CMV, watermelon mosaic virus, and ZYMV (Fuchs *et al.*, 1998) [28]. Spray-induced gene silencing (SIGS) offers an alternative to GMO-based approaches by applying RNAi inducers directly to plants (Das and Sherif, 2020) [14].

Cross protection, where prior infection by one virus prevents subsequent infection by related viruses, was first explored by McKinney (1926) [60]. This approach has been used to protect crops, such as CGMMV-resistant cucumber and muskmelon, and is being developed commercially in Russia (Slavokhotova *et al.*, 2016) [81].

CRISPR/Cas Technology: CRISPR/Cas technology enables precise gene editing, which can disrupt viral susceptibility genes and create virus-resistant plants. This method can produce non-transgenic, consumer-acceptable resistant plants (Khan *et al.*, 2022) [47]. Alternatively, CRISPR/Cas can target viral genomes directly, as demonstrated in cucumbers against PRSV and ZYMV (Kalinina *et al.*, 2020) [44].

The IIVR (Indian Institute of Vegetable Research) Varanasi, recommends an integrated approach to managing

mosaic disease on cucurbits, emphasizing seed treatment with *Pseudomonas fluorescens* (10 g/kg of seed), soil application of FYM (10 kg/pit) and *P. fluorescens* (2.5 kg/ha) in planting pits, combined with neem cake (250 kg/ha). The strategy also includes soil drenching with humic acid (0.2percent), foliar sprays of zinc sulphate (0.5percent) and boron (0.2percent), the installation of yellow sticky traps (25 traps/ha), and the application of botanical pesticides like NSKE (5percent) or neem oil (3percent). This integrated pest management approach has been shown to reduce the incidence of mosaic disease in cucurbits, leading to higher fruit yields compared with conventional farming practices (Nagendran *et al.*, 2017) [64, 65].

10. Future Prospects

Future research and management strategies must adapt to the escalating threat of mixed infections in crops, driven by climate change and the genetic plasticity of viral genomes. These factors can increase the frequency and severity of synergistic virus interactions. To combat this, advanced diagnostic methods, including Next-Generation Sequencing (NGS), will be crucial for early virus detection and effective management, particularly to prevent the introduction of new pathogens through stringent quarantine measures. Promising technologies, such as SIGS-based RNAi, CRISPR/Cas, and speed breeding, offer significant potential for managing viral diseases. However, to fully realize their benefits, future efforts must focus on addressing technical challenges, mitigating off-target effects, and ensuring broader societal acceptance of these innovations.

11. Conclusion

As cucurbit production expands, the number of virus species infecting these crops has rapidly increased. Viruses from genera such as *Begomovirus*, *Potyvirus*, *Cucumovirus*, and *Tobamovirus*, including emerging threats like CGMMV and CABYV, as well as persistent viruses like CMV, PRSV, and ToLCNDV, pose significant risks to global cucurbit cultivation. These viruses are spread through various transmission methods, with the stability of some, such as CGMMV, contributing to their rapid emergence. However, human activities, particularly global trade, seed production, and the import-export of plant materials, are the primary drivers of virus spread. Climate change further exacerbates the situation by altering the epidemiology and transmission dynamics of these viruses.

Given the lack of curative treatments for viral diseases, an integrated management approach is essential. Preventive measures, such as maintaining clean fields, controlling weeds, eliminating alternative hosts, and using virus-free seeds, are critical in reducing the risk of infection. In addition to conventional breeding for resistance, novel strategies like RNA interference (RNAi) technology and CRISPR/Cas offer promising avenues for improved virus management. To safeguard cucurbit production, continuous research and the implementation of these integrated approaches are crucial for mitigating the impact of viral diseases on these essential crops.

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