

Biological Invasions of Begomoviruses: A Case Study of TYLCV and *Bemisia tabaci* in Oman

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ABSTRACT

This review article provides an in-depth analysis of the biological invasions of begomoviruses, focusing on a prominent case study involving the *Tomato Yellow Leaf Curl Virus* (TYLCV) and its vector, the whitefly *Bemisia tabaci*, in the unique agricultural landscape of Oman. Begomoviruses, known for their global impact on crop yields, have become a significant concern in Oman, posing a serious threat to the cultivation of various crops, particularly tomatoes. The review begins by exploring the molecular characteristics and ecological dynamics of TYLCV and *Bemisia tabaci*, shedding light on the intricate interactions between the virus, the vector, and the host plants. Through a comprehensive analysis of historical data and recent research findings, the article examines the patterns and pathways of invasion, elucidating the factors contributing to the successful establishment and spread of TYLCV in Oman. The impacts of TYLCV invasion on agricultural productivity and crop quality are critically evaluated, providing insights into the specific challenges faced by Omani farmers. Special attention is given to the socio-economic repercussions of TYLCV-induced crop losses, emphasizing the need for adaptive management strategies to mitigate the negative consequences on food security and rural livelihoods.

Furthermore, the review assesses the current state of knowledge regarding the management and control of TYLCV and *Bemisia tabaci* in Oman. It discusses the successes and limitations of existing strategies, ranging from conventional practices to innovative biotechnological approaches, providing a foundation for future research directions and the development of sustainable management practices in the context of biological invasions of begomoviruses in Oman. Overall, this review contributes to a nuanced understanding of the complex interplay between invasive begomoviruses, their vectors, and local agricultural systems, offering valuable insights for researchers, policymakers, and practitioners engaged in crop protection and biosecurity in Oman and beyond.

Keywords: begomoviridae, monopartite, whitefly, crispr/cas9, transgenic, vegetation

I. INTRODUCTION

Begomoviruses, a group of plant-infecting viruses transmitted primarily by the whitefly *Bemisia tabaci*, have emerged as a formidable threat to global agriculture, causing significant economic losses and jeopardizing food security. Among the begomoviruses, *Tomato Yellow Leaf Curl Virus* (TYLCV) stands out as a major pathogen affecting a wide range of crops, particularly tomatoes, and has become a focal point for research due to its global impact. The dynamic interaction between TYLCV and its vector, *Bemisia tabaci*, has led to the establishment of an intricate biological invasion scenario, with implications for crop production and ecosystem stability (Legg and Fauquet, 2004). This review aims to provide a comprehensive examination of the biological invasions of begomoviruses, using Oman as a case study to explore the specific dynamics between TYLCV, *Bemisia tabaci*, and the agricultural landscape. Oman, with its diverse agroclimatic conditions and unique crop cultivation practices, presents an interesting context for studying the invasion patterns and consequences of begomoviruses. By delving into the molecular aspects of TYLCV, the ecological interactions with its vector, and the impacts on agricultural systems in Oman, this review seeks to contribute valuable insights into the broader understanding of begomovirus invasions worldwide (Moriones and Navas-Castillo, 2000).

Recent advancements in molecular biology and ecological studies have deepened our understanding of the mechanisms underlying begomovirus invasions. Insights into the genetic diversity of TYLCV strains, the co-evolution with

Bemisia tabaci, and the adaptability of these pathogens to new environments have all added layers of complexity to the invasion dynamics. Furthermore, the review will critically assess the current state of knowledge on management strategies employed in Oman, ranging from conventional approaches to the integration of cutting-edge biotechnological interventions (Brown, 2007). As we delve into this case study, drawing upon the rich literature on begomoviruses, TYLCV, and *Bemisia tabaci*, this review aims to synthesize existing knowledge, identify gaps in understanding, and propose avenues for future research and management strategies to enhance global efforts in mitigating the impact of begomovirus biological invasions (Moriones and Navas-Castillo, 2008).

Biological invasions are one of the primary causes of planetary change. They typically have negative effects on the economy and biodiversity, and they commonly link to new diseases. This is especially true for Oman ecosystems where rapid evolution is possible and invasion-related impact is more obvious. To address agricultural problems, this makes the study of species introduced in insular habitats extremely intriguing. Numerous non-native species have been unintentionally or intentionally introduced by humans kinds as plants and animals in Oman. A species must complete a sequence of essential phases, including introduction, establishment, population growth, and geographic spread, to become invasive in a new location. SERC is a global leader in exploring biological invasions. In this review, we focus on the introduction of begomovirus as well as biological invasions in agricultural contexts, particularly the *Tomato Yellow Leaf Curl Virus* (TYLCV) and the whitefly *Bemisia tabaci* in Oman (Pérefarres et al 2019).

In the past 30 years begomoviruses and whiteflies have become a serious threats to the cultivation of a diversity of vegetable crops of excessive importance in different parts of the world especially in the tropics and sub-tropics and The Sultanate of Oman experiences extremely hot and muggy weather, as well as a subtropical desert environment. We also examine the global spread of invasive biotypes of *B. tabaci* and TYLCV following a brief assessment of historically recent examples of successful biological invasions of geminiviruses in agricultural settings and their corresponding causes. We also discuss the essential function of endosymbionts in the ecology and development of their whitefly hosts, as well as their potential impact on viral acquisition and long-term persistence. Finally, we discuss what happened in Oman, where the agricultural environment was significantly altered by the invasion of *B.tabaci* and TYLCV strains.

And Agriculture in Oman and transmission of begomovirus. Begomoviruses are a collection of plant viruses that have recently become significant hazards to the production of numerous vegetable, root, and fiber crops in temperate, tropical, and subtropical climates around the world (Navas-Castillo et al., 2021). Begomoviruses are transmitted by whiteflies, have monopartite or bipartite genomes, and can be found in both the Old and New Worlds (mainly bipartite genomes, with a small number of monopartite genome viruses). Currently, it is believed that the whitefly vector, *Bemisia tabaci* (Genn.), is a group of cryptic species. The viral coat protein's particular amino acid sequences are linked to whitefly vector specificity. Only dicot hosts are infected by begomoviruses. Monopartite begomoviruses only encode five to six proteins, but bipartite begomoviruses encode between seven and eight proteins. (Brown et al., 2019). Betasatellites, alphasatellites, and deltasatellites are three kinds of circular ssDNA satellites that have been linked to begomoviruses (Zhou 2022, Lozano et al., 2022). The replication-associated protein (Rep)-encoding elements of nanovirids are related to alphasatellites. With the exception of a 5'-TAATATTAC-3' sequence found in the loop of a putative stem-loop structure within the intergenic region (IR), beta- and delta-satellites contain sequences that are not similar to viruses. For movement in plants and transmission by *B. tabaci*, alphasatellites require the helper begomovirus and betasatellites and deltasatellites also depend on these viruses for replication. In many cases, betasatellites control virulence by preventing host gene silencing. Alphasatellites, on the other hand, are unclear as to how they affect the begomovirus infection cycle. Although deltasatellites are not protein-encoding genes, some of them have an impact on viral DNA accumulation and symptomatology (Ferro et al., 2021).

Genome Organization and Replication

Bipartite begomoviruses have genomes made up of two parts, each measuring 2.5–2.6 kb. These parts are referred to as DNA-A and DNA-B. The bipartite begomoviruses' DNA-A component can replicate independently and create virions, but systemic infection needs the DNA-B component. Approximately 200 b of sequence are shared by cognate DNA-A and DNA-B components in the intergenic region, also known as the "common region" (CR), which includes the conserved stem-loop and the 5'-TAATATTAC-3' sequence at the ori (Hanley-Bowdoin et al., 2000, Navas-Castillo and Fiallo-Olivé 2021).

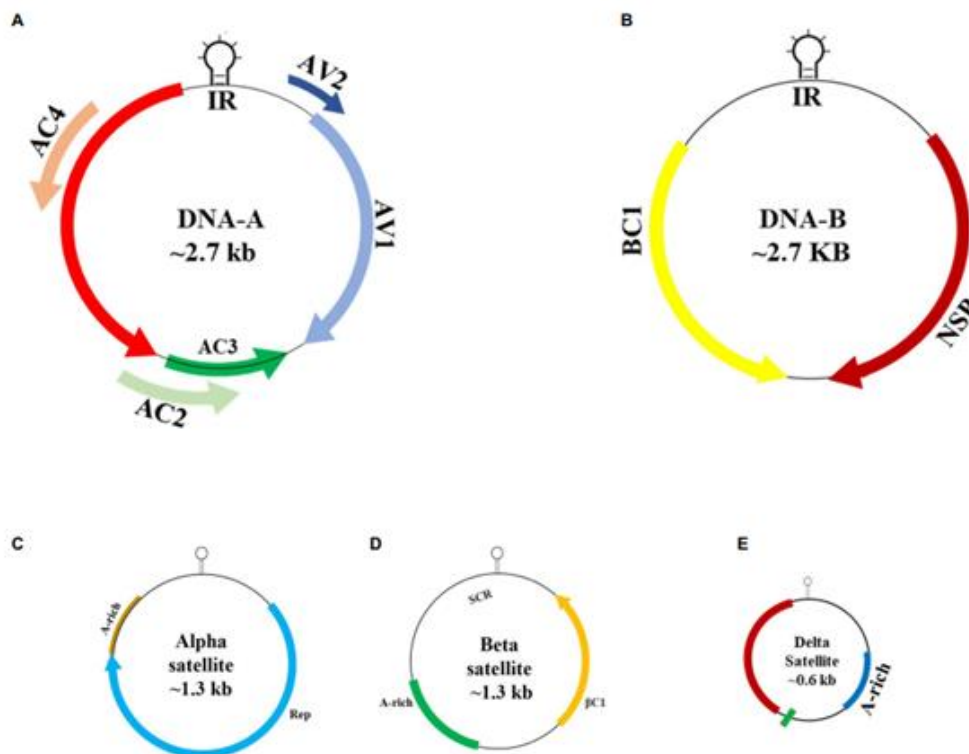


Figure 1: Begomovirus genome: (A) DNA-A segment of begomovirus. (B) DNA-B segment found in bipartite begomovirus along with DNA-A. (C) Alphasatellite, (D) betasatellite and (E) deltasatellite associated with monopartite begomoviruses (Qureshi et al., 2022).

Both the coat protein (ORF AV1/V1), which encapsidates the virion-sense ssDNA and may be important in virus movement, and the AV2/V2 protein (ORF AV2/V2), which has also been linked to virus movement, are encoded by the DNA-A (and the monopartite genome) virion-sense strand.

The AV2/V2 ORF is absent in New World begomoviruses. The replication-associated protein (ORF AC1/C1), a transcriptional activator protein (ORF AC2/C2), a replication enhancer protein (ORF AC3/C3), and the AC4/C4 protein (ORF AC4/C4) are all encoded on the DNA-A complementary-sense strand (Hanley-Bowdoin et al., 2000).

By attaching to iterated motifs (iterons) in the intergenic region and causing a nick into the conserved 5'-TAATATTAC-3' sequence, Rep starts viral DNA replication (Laufs et al., 2020, Fontes et al., 2020). To control cell cycle progression, Rep interacts with the plant homolog of retinoblastoma protein (Rb). This alters the environment of terminally differentiated cells by supplying host factors that facilitate viral DNA replication. (Arguello-Astorga et al., 2020)

TrAP suppresses transcriptional and post-transcriptional gene silencing in addition to transactivating the expression of virion-sense genes from DNA-A and DNA-B. Effective viral DNA replication needs REn. Involved in cell-cycle control, AC4 is a key symptom determinant, and C4 may block a host response to Rep expression. (Hanley-Bowdoin et al., 2019) A movement protein (ORF BC1) and a nuclear shuttle protein (ORF BV1) are both encoded by the DNA-B on the complementary-sense strand and the virion-sense strand, respectively. It has been shown that the begomovirus *Tomato yellow leaf curl virus* replicates in *B. tabaci's* salivary glands in addition to its host plants. (He et al., 2020)

II. DISCUSSION

2.1 Emergency of Begomovirus Diseases in an Agriculture Setting in Oman

Over the past two decades, begomoviruses (family *Geminiviridae*) have drastically decreased Oman's tomato production, particularly in the Al-Batinah region, the nation's main agricultural region. In the years 2012 and 2013, surveys of farms in the Al-Batinah area were carried out from January through March, November through December, and January through February. Leaf samples from tomato plants displaying the typical signs of leaf curl disease were collected to test for begomoviruses Oman *Tomato yellow leaf curl virus* (TYLCV-OM), Oman chili leaf curl virus (ChLCV-OM), and Oman

tomato leaf curl virus (ToLCOMV), all of which have been previously demonstrated to exist in Oman, were found in seven of the fifteen begomovirus clones. A novel species called "*Tomato leaf curl Al Batinah virus*" (ToLCABV) has been proposed for the four sequences that were shown to have the highest percentage identity (86%) to isolates of the pepper leaf curl Lahore virus. The *Tomato leaf curl beta satellite* (ToLCB; seven full-length sequences have been discovered) was present in certain isolates of ChLCV-OM, TYLCV-OM, and ToLCOMV, but not in any of the isolates of ToLCABV. Analysis of their genomes revealed that the TYLCV-OM and ToLCOMV isolates discovered here did not significantly diverge from previously known isolates of these viruses. The three ChLCV-OM isolates were found to have a distinctive recombination pattern from previously described isolates. We have demonstrated that ToLCOMV and ChLCV-OM underwent recombination to become ToLCABV. When a clone of ToLCABV was exposed to *Nicotiana benthamiana* and tomato by an agrobacterium, it became contagious and manifested symptoms similar to those seen in field-grown tomatoes. Furthermore, it was found that, despite the beta satellite not appearing to influence viral DNA levels, ToLCABV and ToLCB may interact in planta, changing the phenotype of the symptoms.

Transmission of Begomovirus

The cryptic species complex of whiteflies called *Bemisia tabaci* is the carrier of begomoviruses. Different species of the *B. tabaci* complex differentially transmit a large number of begomoviruses. Some begomoviruses can be experimentally transmitted by mechanical inoculation, but the majority require either biolistic delivery of cloned genomic DNA or *Agrobacterium*-mediated transfer (agro inoculation) from partly or tandemly repeated cloned genomic DNA for their experimental transmission. (Fiallo-Olivé et al., 2020)

2.2 Agriculture in Oman

Oman has long maintained commercial ties with numerous countries, particularly those in Asia and Africa, due to its non-agricultural character and geographic location. Oman imports agricultural products, in particular from Iran, India, Pakistan, Egypt, Lebanon, and other countries. Oman's agricultural products are typically grown for local consumption during the winter, with a few exports to nearby countries like the UAE. Oman's main agricultural cultivation regions are in the south, in Dhofar, and the north, in Al Batinah.

According to MAF (2019) (www.maf.gov.om), even though the majority of the planting supplies are imported from other countries, Oman has 67,000 ha of land that is used for agriculture. Different begomoviruses have invaded Oman through the importation of planting materials for industrial farms as well as through travelers and workers. Exchanges of planting materials between farmers and the local replication of imported planting materials tainted with viruses both contributed to the local spread of viruses.

2.3 The Omani Cassava Mosaic Disease Pandemic

The most serious disease affecting the subsistence crop cassava (*Manihot esculenta*) across Africa and the Indian subcontinent is cassava mosaic disease (CMD). There are now seven species of viruses in the family *Geminiviridae*'s genus *Begomovirus* that cause the disease. The Sultanate of

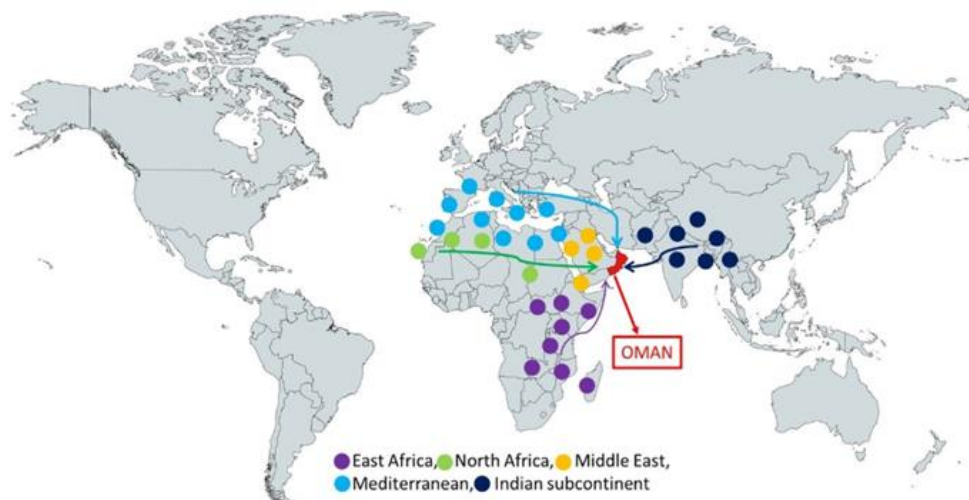


Figure 2: The world depicts possible origin and migration routes of begomoviruses identified in Oman, mainly from East and North Africa (purple and green arrows), the Middle East (Brown arrow), Mediterranean (blue arrow), and Indian subcontinent (dark blue arrow). (Shahid, M. S., & Al-Sadi, A. M. (2021).

Oman grows cassava on a smaller scale for domestic use than other Arab countries. During a recent examination, cassava plants in the A'Seeb wilayat of the Muscat governorate, Oman, displayed symptoms of CMD. Infected plants contained a begomovirus known as East African cassava mosaic Zanzibar virus (EACMZV). The only places where this virus was supposed to exist were Kenya and Zanzibar. During the 19th century, Zanzibar was administered by Oman, and the island was so important that the Sultan of Oman moved his capital from Muscat to Zanzibar. After gaining independence from colonial rule in the 1960s, the reigning Arab elite was overthrown, and many Omanis who had resided abroad returned to their home nation. It seems that having learned to like the indigenous Zanzibar cuisine, returning Omanis did not want to do without dishes made from one specific favorite, cassava. They brought planting supplies with them to Oman so they could use them in their kitchen gardens.

The data points to the presence of EACMZV in this medication. Recent research has revealed that Oman is the location of a cluster of geminiviruses and the satellite viruses connected to them from various geographic sources. Their capacity for recombination, a crucial mechanism for geminivirus growth, and the fact that Oman (and several other Arab countries) are significant hubs for trade and international air and sea travel raise concerns about the possibility of future dissemination. (Khan et al.,2019)

Viruses infecting cassava (Adapted, with modifications from Thottappilly et al., 2023).

| Viruses | Genus/Family | Symptoms | Vector | Distribution |
|------------------------------------------------------------|-----------------------------------|---------------------------------------|----------|------------------------|
| <i>African cassava mosaic virus (ACMV)</i> | <i>Begomovirus, Geminiviridae</i> | Mosaic, leaf distortion, and stunting | Whitefly | Africa and India |
| <i>East African cassava mosaic Zanzibar virus (EACMZV)</i> | <i>Begomovirus, Geminiviridae</i> | Mosaic, leaf distortion, and stunting | Whitefly | Zanzibar, Madagascar |
| <i>Indian cassava mosaic virus (ICMV)</i> | <i>Begomovirus, Geminiviridae</i> | Mosaic, leaf distortion, and stunting | Whitefly | India, Sri Lanka, Togo |



One of the most significant economic risks to regions that farm cassava is the cassava mosaic virus. Over time, numerous virus species have been discovered and demonstrated to be capable of infecting cassava in a variety of locations, including India, Africa, South America, and even Oman. The geminivirus family includes the cassava mosaic virus, which spreads persistently by whiteflies feeding on infected plants for up to many hours at a time. Before the virus may infect healthy plants, it must circulate in the adult whitefly after absorption. In other words, the virus requires a long, measured in hours, amount of time for its vector to acquire and transmit. Other than adult whiteflies, contaminated planting materials, and occasionally mechanical means are responsible for the spread. Whiteflies are drawn to fresh greenery and soon occupy it. Young leaves can be infected in just ten minutes of feeding time by a single whitefly that has the virus. A plant has a far increased possibility of contracting the disease when several infected whiteflies feed on it.

2.4 The Worldwide Emergence of a Whitefly Pest and Plant Virus Vector

The *Bemisia tabaci* Species Complex, *Bemisia tabaci* (Gennadius, order Hemiptera, family Aleyrodidae) is the only vector of the entire genus of Begomoviruses, as opposed to just being a vector of CMD viruses. This viral genus has recently developed, making it the most varied plant virus in terms of species known. It has become challenging to identify whether begomoviruses are a (Navas-Castillo-2019) intrinsically successful viral species or if this success is largely or mostly owing to the success of *B. tabaci* as a more complete understanding of the *B. tabaci* species has been achieved. *B. tabaci* is a member of a group of genetic species that were once known as biotypes. Although only a few numbers of biotypes have been described until recently, it is now clear that many different biotypes exist and that some of them are extremely aggressive. Even though they are morphologically identical, the biotypes have been identified using genetic and behavioral differences (isozyme profiling, barcoding based on conserved genes, life history traits), and up to 28 "putative" cryptic species are now proposed to be part of the *B. tabaci* species complex. [Despite having a pan-tropical origin, *B. Tabaci* is widespread throughout the world's warmer regions, including greenhouses with temperate temperatures. *B. tabaci* is currently listed as one of the top 100 invasive species in the world by the Global Invasive Species Database. In open fields or protected crop production, it is also one of the most devastating pests in the world. *B.tabaci* not only spreads viruses (such as the begomovirus, but also the criniviruses, carlaviruses, ipomoviruses, and torradoviruses;), but also directly damages crops by devouring phloem, excreting honeydew, and inducing phytotoxic illnesses.

2.5 Shifts in Whitefly Populations

The main factor restricting Oman's tomato production is begomoviruses, particularly in the Al-Batinah region, which is the country's largest agricultural region. Between January and March 2013, the commercial farms in the Al-Batinah area were assessed. We gathered and examined tomato samples that had leaf curl, a condition linked to begomovirus. Full-length sequences from five clones were found to have the highest level of identity (88.6%) with begomovirus isolates. The tomato leaf curl beta satellite (ToLCB) was found to be associated with four isolates of ToLCBrV. The five isolates of ToLCBrV identified in this investigation were discovered to be recombinants, with a Croton yellow vein virus (CrYVV) fragment spanning 3' half of the replication-associated protein serving as the major parent and ToLCOMV serving as the secondary parent. These findings' relevance is looked at.88.6% of the isolates of the begomovirus Tomato leaf curl Oman virus (ToLCOMV), which was previously described in Oman, have this percentage identity. This finding supports the theory that these clones are members of a recently identified species known as the *Tomato leaf curl Barka virus* (ToLCBrV) (Paredes-Montero et al.2022).

Symptoms produced in *Nicotiana benthamiana* and susceptible tomato plants by the ToLCSDV-OM isolate Mir1 (JN591385) of the *Tomato leaf curl Sudan virus*. mock-inoculated tomato (D) and *N. benthamiana* (A) plants. A tomato plant that has been inoculated with ToLCSDV-OM (E) and an *N. benthamiana* plant (B). The resolution of the photos was 25 dpi. A tomato affected in the field with classic leaf curl disease signs (C). *N. benthamiana* and tomato plants that had been inoculated were found to have ToLCSDV-OM by Southern blot (F). DNA was extracted from an *N. benthamiana* plant that had not been inoculated (lane 1), an undigested plasmid clone of ToLCSDV-OM (200 ng; lane 2), symptomatic young tomato plant leaves (lane 3), and an *N. benthamiana* plant (lane 4) that had been inoculated with ToLCSDV-OM. In each instance, 10 g of DNA that had been isolated from plants was loaded in almost equal proportions. ToLCSDV-OM fragment that was DIG-labeled was used to probe the blot. Super-coiled (sc), open-circular (oc), and single-stranded (ss) are the three viral DNA types that have been identified.

2.6 Begomovirus Research in Oman

The detection and characterization of begomoviruses in Oman (originating from diverse countries) have been the subject of numerous investigations recently. Studies on begomoviruses have made use of the polymerase chain reaction (PCR), rolling circle amplification (RCA), cloning, restriction endonuclease analysis, and next-generation sequencing technology (NGS). In terms of their sequence analysis, phylogeny, pathogenicity, interactions with plants and other viruses, pathogen-derived transgenic resistance, and characterization of DNA satellites, begomoviruses have been thoroughly explored. There

have been numerous begomoviruses and DNA satellites discovered so far from Oman's 16 different crops. In this study, the main Omani crops affected by begomoviruses are identified. (Shahid, M. S., & Al-Sadi, A. M. (2021).

| Disease | Virus (es) identified | Suggested origin | Detection method | Strain in Oman | Host |
|--------------------------|------------------------------------------------|-------------------------------------|------------------|----------------|---------------------------|
| Tomato leaf curl disease | <i>Tomato yellow leaf curl virus</i> | Middle East and Mediterranean | PCR\RCA | TYLCVOM | Tomato basil, radish |
| Leaf curl disease | <i>Chili leaf curl virus</i> | Indian subcontinent | PCR\RCA | ChiLCVOM | Tomato, paper, watermelon |
| Tomato leaf curl disease | <i>Tomato yellow leaf curl Albatinah virus</i> | Middle East and Indian subcontinent | PCR | ToLCABV | Tomato basil |

The mint plants displayed rus-like signs, such as leaf yellowing and stunted growth. Mint plant young symptomatic leaves were gathered for begomovirus identification.

Using the NCBI-BLAST program (<http://blast.ncbi.nlm.nih.gov/Blast.cgi>) to analyze the entire genome sequences of begomovirus, it was confirmed that the yellowing and stunting symptoms of mint were caused by an infection with a ChiLCV strain that is distinct from the ones previously described from tomato and pepper. Mint begomovirus had a significant degree of nucleotide sequence similarity to isolates of the "Oman" strain of ChiLCV-OM, with a maximum nt identity of 94.9% (Muhire et al., 2014) (Figure 2A), according to the SDT comparison of ChiLCV sequences with known begomovirus sequences. Phylogenetic research, which demonstrated that mint begomovirus is distinct from other ChiLCV strains and separated from ChiLCV isolates, provided additional evidence to support this result Table. According to Shahid et al. (2019c), *Mentha beta* satellite infection was likewise linked to the ChiLCV. According to Shahid et al.'s 2017a study, the SDT analysis revealed 98.2% nt identity with a ToLCB isolate (KX452222) that was recently discovered in *Phaseolus vulgaris*. ToLCB clustered with earlier ToLCB isolates discovered from the Arabian Peninsula, which are distinct from isolates from South Asia, in a phylogenetic investigation.

2.7 Whitefly Population Differentiation Based on Endosymbionts

The relationship that arachnids have with their endosymbionts is another important aspect of their existence, and it has greatly aided in their evolutionary success. Depending on how they are passed down from one generation to the next, endosymbionts for the host may be required or facultative. Facultative endosymbionts are not necessary for host development or reproduction, in contrast to obligatory endosymbionts. In addition to *Portiera aleyrodidarum*, an essential endosymbiont, *B. tabaci* is known to host the facultative endosymbionts *Cardinium*, *Arsenophonus*, *Rickettsia*, *Hamiltonella*, combinations that have been described in the literature, mostly according to preceding biotypes, suggests that endosymbionts may be involved in the biology of *B. tabaci* and its development into biotypes. It has been clear over the last 10 years that endosymbionts have a significant influence on the ecology and evolution of their hosts. Among these outcomes include modifications to host reproduction and increases in host survival or fecundity. *B. tabaci* may have a role in cryptic species' ability to regulate sexual reproduction. The detoxification of chemical substances by some endosymbionts, according to the current study, can make pest insects resistant to insecticides. (enkataravanappa et al.,2023).

2.8 Factors Affecting the Beg Virus's Prevalence and Transmission in Oman

The whitefly vector is a significant contributor to the propagation of begomoviruses. Only *B. tabaci* MEAMI, which can only move a small distance, has been found in Oman, even though it may actively help several virus species propagate. Nevertheless, we must not ignore international trade in agricultural goods, whether it occurs by air, sea, or land, as these actions may help the insect vector spread to new places.

However, other factors may contribute to the emergence and spread of viruses, such as virus mutation, recombination, the vector's polyphagous nature, stringent agricultural practices like the cultivation of a single crop or plant cultivar, cultivation of cultivars that are susceptible to infection, and the global transportation of agricultural products. So begomoviruses pose a serious threat to the safety of the world's food supply. To stop plant-infecting viruses from causing persistent crop failures and from being transported and spreading to new places (where environmental circumstances promote a high population density of

the whitefly vector), policies must be put in place. Environmental factors play a significant role in plant-virus interactions, and the proper temperature can have an impact on the start, severity, and/or incidence of disease.

According to Mangrauthia et al. (2019), the optimal temperature range for papaya ringspot virus replication, infection, and transmission to papaya plants is 26 °C to 31 °C. Cassava mosaic virus, a member of the begomovirus family and the Geminiviridae genus, increased symptoms and viral titers in cassava plants at 25 °C as opposed to 30 °C (Chellappan et al., 2019). According to Robson et al. (2019), the banana bunchy top virus, which is spread by the aphid *Pentalonia nigronervosa*, can actively develop and is least lethal at 25 °C. Viral illness severity is also impacted by heat and drought. For instance, in Arabidopsis, heat, drought, and the turnip mosaic virus collectively inhibited plant development more so than each element acting alone (Prasch et al., 2019). Trade routes are thought to have initially brought the diseases into the nation. Therefore, Oman has to establish a phytosanitary facility outfitted with the most recent viral detection and discovery technologies to prevent further trade of Geminiviruses.

III. CONCLUSION

Despite the existence of numerous viruses and DNA satellites with Oman as their origin, there is no proof that these begomoviruses are spreading outside of Oman. To stop the spread of these illnesses, improved phytosanitary controls could be applied to trade products. For instance, to remove the insect vectors, a stringent quarantine should be put in place for various import commodities arriving at the port of Sohar, notably for containers containing wood products. The same security measures ought to apply to imports crossing the land border into Saudi Arabia, Yemen, and the United Arab Emirates. Plant propagation materials and nursery stocks should receive extra attention during inspections for disease or insect infestations. For instance, in 2012 Oman imported a million tons of plant material for propagation, which may have been contaminated with pathogens like begomoviruses and their vectors. One recent example is the growth of the cotton begomovirus disease in China, which has been linked to inadequate quarantine protocols when ornamental plants were imported (Sattar et al., 2013). Furthermore, we must take into account the possibility of the emergence of novel and recombinant begomoviruses as well as DNA satellite strains that could arise in one place and spread along the same trade channels that are believed to have first brought the illnesses into the country. Therefore, to stop the continued trade of Geminiviruses, Oman must set up a phytosanitary center equipped with the most up-to-date viral detection and discovery methods.

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COMPETING OF INTEREST

There is no competing of interest declared.

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