

Emerging Threats of Begomoviruses to Cultivating Vegetables, Fruits, and Medicinal Plants and their Management Strategies in Oman.

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ABSTRACT

Begomoviruses, a group of plant-infecting viruses transmitted by whiteflies, have emerged as a significant threat to agricultural productivity in Oman. This comprehensive review examines the escalating challenges posed by begomoviruses to the cultivation of vegetables, fruits, and medicinal plants in the Omani agroecosystem, while also scrutinizing the various management strategies employed to mitigate their detrimental effects. The review begins by elucidating the molecular and ecological aspects of begomoviruses, providing an in-depth understanding of their diversity, evolution, and host interactions. A critical analysis of the impact of begomovirus infections on key crops in Oman follows, exploring the nuances of symptomatology, yield reduction, and economic consequences. Emphasis is placed on the unique agroclimatic conditions in Oman that contribute to the increased vulnerability of crops to begomovirus outbreaks. Subsequently, the review synthesizes the existing knowledge of management strategies, encompassing both traditional and cutting-edge approaches. The efficacy of breeding for resistance, cultural practices, biological control, and emerging biotechnological interventions is evaluated in the context of Omani agriculture. Special attention is given to the socio-economic implications of begomovirus-related crop losses, highlighting the need for integrated and sustainable management practices to safeguard food security and farmer livelihoods.

By synthesizing the latest research findings and identifying knowledge gaps, this review serves as a valuable resource for researchers, policymakers, and practitioners involved in agricultural development in Oman. It sets the stage for future research directions and underscores the importance of a multidisciplinary approach in addressing the emerging threats of begomoviruses to the diverse and vital crops cultivated in the Sultanate.

Keywords: CRISPR/Cas9, Transgenic, Vegetation, Begomoviridae, Monopartite, Whitefly

INTRODUCTION

Most of the viruses in this family belong to the Begomoviridae family. The only insect that carries them is the whitefly (*Bemisia tabaci*). Few single-genome begomoviruses are occasionally related to satellite viruses found in the Old World. Most begomoviruses have a two-part genome and are common in tropical and subtropical America (Alshihi, 2017). (OW) are unipartite (with a single genome component homologous to the DNA A of bipartite begomoviruses), whereas a few New World (NW) and some Old World (OW) begomoviruses have a bipartite genome (2 I have two) genomic components known as DNA A and DNA

B). stunting and severe yield loss are symptoms caused by the virus, primarily affecting watermelon crops (*Citrullus* spp.). Most cucurbitaceous plants, including melons, cucumbers, squash, and squash, belong to the host range of the virus. including test tube plants *Nicotiana benthamiana* and *N. glutinosa*.

Begomoviruses have a genome consisting of one or two circular single-stranded DNA components, known as DNA-A and DNA-B, each approximately 2.6-2.8 kb in size. New World begomoviruses have a bipartite genome, while those from the Old World have either bipartite or monopartite (DNA-A) genomes. Monopartite begomoviruses, such as the Tomato yellow leaf curl virus from Israel and Sardinia, have only a single component similar to DNA-A in genome organization. DNA-A is essential for replication and encapsidation, while DNA-B plays a role in systemic movement and symptom production. Begomovirus replication cycles rely on DNA intermediates and occur within the nucleus of the infected cell through two basic stages: conversion of ssDNA to dsDNA intermediates and rolling circle replication (RCR). DNA-A of all begomoviruses has five ORFs, with one (AV1) on the virion DNA strand and four (AC1, AC2, AC3, and AC4) on the complementary strand. The proteins encoded by the ORFs on the complementary strand are involved in viral DNA replication and are translated from spliced and unspliced versions of the same mRNA. Begomoviruses from the Old World have an additional ORF (AV2) not found in New World begomoviruses. DNA-A has two ORFs in the virion sense or rightward direction and four ORFs in the complementary sense or leftward direction. DNA-B has one ORF each in the virion strand or rightward direction and one in the complementary strand or leftward orientation.

DNA-A and DNA-B sequences differ except for an approximately 200 bp intergenic region (IR), also known as the common region (CR). CR is the only region with significant sequence similarity between DNA-A and DNA-B components of the same virus, and it has many regulatory elements, including two TATA motifs for ORF AV1/AV2 and another for ORF AC1/AC4 (Snehi *et al.*, 2015).

Has the effect of begomovirus reached the crops of Oman? the answer is yes, According to previous studies, *Tomato leaf curl Oman virus* (TYLCOM) and *Tomato yellow leaf curl virus* (TYLCV) are found in the northern regions of the country. (Khan *et al.*, 2013) A bipartite begomovirus called *Watermelon chlorotic stunt virus* (WmCSV) was first detected in Yemen in 1988 and has since been reported in several countries in the Middle East and North Africa (Khan *et al.*, 2012). Plant diseases belonging to the Geminiviridae family are characterized by twin icosahedral particles, each with a circular single-stranded DNA (ssDNA) genome (Zerbini *et al.*, 2017). Based on genome organization, host range, and insect vectors, the *Geminiviridae* family is divided into seven genera. Becurtovirus, Begomovirus, Eragrovirus, Mastrevirus, Curtovirus, Topocovirus, and Turncurtovirus. (Brown *et al.* 2015).

Commercial farms in Oman rely on monocultures and social practices, with farmers sometimes exchanging planting materials. Returning Omanis and migrant workers (mainly from the Indian subcontinent) grow herbs and vegetables in their gardens, increasing the risk of introduction and spread of begomovirus. (Alshihi, 2017). Emergence of most begomoviruses in Oman that have been found in Oman are monopartite and mostly connected with DNA satellites; they are not local species. Only two beta satellites—the *Tomato leaf curl beta satellite* (ToLCB) and the *Okra leaf curl Oman beta satellite* (OLCOMB)—have been found in Oman, despite the Middle East and Africa having a diverse range of beta satellites (Akhtar *et al.* 2014).

REVIEW OF LITERATURE

Begomovirus-infesting whiteflies pose a serious threat to agricultural crops everywhere, but especially in Oman these viruses are the subject of studies focused on virulence testing, recombination analysis, molecular characterization, and phylogenetic relationships. It has become. The recent discovery of begomovirus in Oman and the discovery of DNA satellites have changed agricultural practices and consequently advanced virus detection techniques. Furthermore, tomato cultivars with multiple Ty genes

express resistance to the TYLCD complex (Shahid, Al-Sadi, 2021). Begomoviruses cause severe crop diseases worldwide, affecting agriculture and human activities. Management options include agricultural practices, cultural control, insecticide control, and breeding-resistant cultivars. Transgenic resistance is limited due to rapid evolution. Modern biotechnology focuses on engineering resistance through transgenic approaches and antisense RNA and RNAi technology (Snehi *et al*, 2015). A previous report from Oman described a *Tomato yellow leaf curl virus* (TYLCV-OM) strain and its beta satellite ToLCB. The same plant samples also revealed his To LCOMV, his second begomovirus closely related to the rare DNA type 2 ageratum yellow vein Singapore alpha satellite (AYVSGA). Plants vaccinated with TYLCV-OM showed more severe symptoms than those infected with ToLCOMV. In *N. benthamiana* infected with both beta satellites and helper virus, alpha satellites reduced the accumulation of beta satellite DNA and alleviated symptoms. According to this finding, specific DNA-2 alpha satellites may be able to control begomovirus beta satellite infection by interfering with the assembly of beta satellite DNA (Idris *et al*, 2011). Evidence of leaf curl was found in February 2016 in a *Cucurbita maxima* plant in Albatina, Oman. Symptoms of begomovirus infection were leaf curling, yellowing, and discoloration. *Tomato leaf curl beta satellite* (ToLCB) and *chili pepper leaf curl virus* (ChLCV) were identified by RCA as unidentified causative agents. This study provides the first concrete evidence that ToLCB and ChLCV caused leaf curl in his *Cucurbita maxima* plants in Oman (Shahid, 2020). Tomato plants were collected in AlBatinah, Oman to determine the cause of widespread disease caused by whitefly infestations. Total nucleic acid was extracted from tomato leaves and used as a template for U29 DNA polymerase amplification. The virus from Oman most closely resembled TYLCV-IR, a single-part begomovirus species previously identified in Iran. An isolate from Oman, known as TYLCV-Om, is believed to be a TYLCV-IR isolate. At the border of Asia and the Middle East, TYLCV-Om and related sat DNA form a characteristic begomovirus complex (Khan *et al*, 2008). A serious viral disease called *Okra leaf curl* (OLCD) affects okra plants in tropical and subtropical regions. Begomoviruses and beta satellites were found to be present in symptomatic okra plants from Barqa, Oman. Analysis revealed a novel begomovirus closely related to the African begomovirus *Cotton leaf curl Gezira virus* (CLCuGeV). This novel virus, called OLCOMV, resulted from the recombination of the Omani *Tomato yellow leaf curl virus* (TYLCV-OM) and a CLCuGeV isolate. The same plant samples also generated alpha and beta satellites, but the beta satellites were more closely related to the South Asian alpha satellites. This is the first report that an Omani-specific begomovirus satellite complex infects okra (Akhtar *et al*, 2014). Over the past two decades, begomovirus has posed a major challenge to tomato cultivation in Oman, especially in the Al-Batinah region. A survey of farms in the region showed that 7 of 15 begomovirus clones were *Tomato yellow curl virus Omani strain* (TYLCV-OM) and 3 were *Chilean leaf curl virus Omani strain* (ChLCV-OM) and were found in the *Oman Tomato curl virus strain Oman virus* (ToLCOMV). Four sequences showed low percent identity values to known Begomoviruses, with the highest value (86%) being *Pepper leaf curl Lahore virus*. These sequences should be included in a new species called *Tomato leaf roll Albatina virus* (To LCABV). Several isolates of ChLCV-OM, TYLCV-OM, and his To LCOMV have been identified in the beta satellite *Tomato Leaf curl beta satellite* (To LCB), but are not related to any of the To LCABV isolates (Khan *et al*, 2013). *Tomato leaf curl disease* (ToLCD) is a major constraint on tomato production in Oman and is caused by the single begomoviruses tomato yellow leaf curl virus and tomato leaf curl oman virus. The disease is caused by these two viruses and often carries beta satellites that enhance symptoms. This study analyzes viruses isolated from tomatoes showing his To LCD symptoms in southern and central Oman. Three clones of unipartite begomoviruses were obtained, one of which was found to infect tomato and *Nicotiana benthamiana* and cause symptoms typical of To LCD. Analysis of the cloned sequences revealed that they corresponded to isolates of *Tomato leaf Sudan virus* (ToLCSDV), a virus found in Sudan and Yemen. However, these sequences share less than 93% nucleotide sequence identity with previously characterized To LCSDV isolates, indicating that they are a distinct strain of this species, the 'Omani' strain (ToLCSDV-OM). was shown. A more detailed analysis revealed that the divergence of the 'Omani' and 'tobacco' strains may be due to recombination. Interestingly, unlike other To LCSDV strains, To LCSDV-OM was not associated with beta satellites. We discuss the significance of these results and possible reasons for the different geographical distribution of tomato-infecting

begomoviruses in Oman (Khan *et al*, 2013). Begomovirus, a member of the Geminiviridae family, causes extreme yield loss in economically important crops such as Medicinal and aromatic plants (MAPs). Global trade, modern cultivation techniques, and new varieties all contribute to these problems. This study provides both conventional and state-of-the-art management techniques for begomovirus and its vectors in MAP. We also provide an overview of current research on begomoviruses that affect MAP (Saeed, Samad, 2017). Vegetables are crucial for the rural poor in Africa, but diseases caused by begomoviruses hinder global production. In West and Central Africa, begomoviruses infect crops, and *B. tabaci* is associated with infections in various vegetable and weed species. Weeds are important reservoirs of begomoviruses, and their potential recombination and transmission pose a serious threat to crop production (Leke *et al*, 2015). Whiteflies carry 141 viruses, of which *Bemisia tabaci* carries 111 and *Trialeurodes Vaporariorum* and *T. abutilonia* carry 3. These viruses are found in the European Mediterranean region and belong to 90% Begomovirus, 6% Crinivirus, and 4% Closterovirus, Ipomovirus, or Carlavirus genera. Other names for whitefly-borne viruses have also been documented (Jones, 2003). Geminiviruses have been present in Brazil since the 1950s, with eight new strains first appearing in the early 1990s. Recombination and pseudo-recombination between these novel viruses were caused by the transmission of natural viruses to tomatoes by insect vectors. Effective control of tomato geminivirus requires a comprehensive strategy that includes a tomato-free period of at least 30 days, virus-free transplantation, and logical chemical control of the vector. An example of a new method is to use tomatoes genetically engineered using RNA silencing to target the viral genome or host genes required for viral replication (Zerbini *et al*, 2017).

The structure of begomovirus

Small, circular, single-stranded DNA genomes that are encapsidated inside twinned icosahedral particles define the structure of begomoviruses. Their structure's main pillars are as follows: First, the begomovirus genome consists of single-stranded DNA molecules, typically 2.6-2.8 kilobases (kb) in size. The ends of the DNA molecule are covalently bound to form a continuous circle, hence the name "closed circular" genome. Multiple overlapping open reading frames (ORFs) encoding different viral proteins are found in the genome. Second, capsid: The capsid is a protein shell that surrounds the viral DNA. The coat protein (CP) is a single viral protein found in many copies throughout the capsid and is what makes up the capsid. CP divides its 30 units into 12 pentamers and 20 hexamers to build an icosahedral symmetric capsid. Third, viral protein: the genome-encoded begomovirus also produces a number of other proteins. These include proteins involved in regulating host defenses, locomotion within plants, and replication. Rep (replication-associated protein), TrAP (transcriptional activator protein), and C4 (host defense repressor) are some of the key proteins. Fourth, complex replication: In infected plant cell nuclei, begomovirus copies its DNA. During the replication process, a specific replication complex consisting of viral proteins, host factors, and viral DNA is formed. The Rep protein is essential for the initiation and promotion of viral DNA replication. Fifth, Symmetry: Begomoviruses have a twin icosahedral symmetry represented by an icosahedral lattice with 60 subunits (T=1). Each subunit is composed of CP monomers.

Genome of begomovirus

Their genome consists of one or two circular segments. DNA-A and DNA-B are single-stranded DNA, each approximately 2.6-2.8 kb in size. Begomovirus infection source. The Old World genome is either two-part or one-part (DNA-A), whereas the New World genome organization is two-part (DNA-A and DNA-B). DNA-B is involved in systemic mobility and symptom generation, while DNA-A is required for replication and encapsulation. Conversion of ssDNA to dsDNA intermediates and rolling circle replication (RCR), two fundamental steps of the begomovirus replication cycle, occurs in the nucleus of infected cells. All begomoviruses have DNA-A with 5 ORFs. One of these, AV1, also known as AR1, is on the virion chain, and the other four, AC1, AC2, AC3, and AC4 (also known as AL1, AL2, AL3, and AL4, respectively), are on the virion chain. It is on the virion chain. complementary strand. Both the coat protein and the proteins

required for the cell-to-cell movement of the virus are encoded by the viral strain's ORF. Both spliced and unspliced forms of the same mRNA are used for the translation of the protein encoded by the ORF on the complementary strand, and both are involved in viral DNA replication. Old World begomoviruses have an additional ORF (AV2) that is not present in New World begomoviruses. DNA-A has four ORFs [AC1/AL1 replication initiator protein (Rep), AC2/AL2 transcriptional activation protein (TrAP), AC3/AL3 replication enhancer protein (REn), AC4 /AL4 and AC5/AL5] and two virion-sense or right-hand ORFs [AV1/AR1 coat protein (CP) and AV2/AR2 precoat protein]. DNA-B has a complementary strand or left ORF [BC1/BL1-Movement Protein (MP)] and a virion strand or right ORF [BV1/BR1-Nuclear Shuttle Protein (NSP)]. The sequences of DNA A and DNA B differ from each other, except for the 200 bp intergenic region (IR), also known as the common region (CR). A CR highly specific for the virus is located in the intergenic region between ORFs AV1 and AC1 in DNA-A and ORFs BV1 and BC1 in DNA-B. The only region where the DNA A and DNA B components of the same virus share significant sequence similarity is the CR. Two TATA motifs (one for ORFs AV1/AV2 and one for ORFs AC1/AC4) are among the many regulatory elements found in CR. (Snehi *et al.*, 2015). The role of each ORF (Gene) in the DNA-A and DNA-B components of begomovirus is shown in Table 1.

Table 1: Lists the ORF (Gene) order and functions of the DNA-A and DNA-B components of begomoviruses.

ORF	Function
AV1	Encapsidation
AV2	cellular communication protein(cell movement)
AC1	beginning of replication
AC2	Transcriptional activator of right-handed ORF, repressor of PTGS
AC3	Replication enhancement
AC4	PTGS suppressor, viral replication
AC5	virus reproduction
BV1	Nuclear trafficking
BC1	Movement between cells and factor determining pathogenicity

Ways of transmission of begomovirus

Begomoviruses are transmitted through different methods, including:

First, whiteflies: The most common mode of transmission is through whiteflies, which feed on infected plants and then carry the virus to healthy plants. Whiteflies transmit the virus in a persistent manner, meaning they retain the virus in their mouthparts and can infect multiple plants over an extended period. (Jones, 2003). Second, grafting: Begomoviruses can also be transmitted through grafting infected plant tissues onto healthy plants. This method is commonly used in laboratory settings to infect plants with specific begomovirus strains. (Venkataravanappa *et al.*, 2013). Third, seed transmission: Some begomoviruses can be transmitted through infected seeds. However, this mode of transmission is rare and usually occurs at very low rates. (Fortes *et al.*, 2023). Begomoviruses cannot be transferred by soil, air, or water, it is vital to remember this. They can only spread through contact with sick plant tissues or by an insect vector.

Long-distance spread of geminiviruses Increased international trade in seeds, seedlings, propagation material, and agricultural products We have pioneered new ways to transport agricultural products between countries and around the world. It has also led to a dramatic increase in the long-distance spread of geminiviruses and their viruses. Insect vectors. additional elements Contributing to the spread and

establishment of infections include (a) relaxation of quarantine regulations; (b) Intensification and diversification of agriculture due to changes in cultivation (c) cultivation of crops in new areas; Climate change is another factor in the successful spread of the Gemini virus to hitherto disadvantaged areas virus or vector. All these circumstances combine to facilitate the long-range spread of Geminivirus establishment on a global scale (Rojas *et al*, 2018).

Impact of begomovirus on Oman Farms vegetables

The term “impact” is used to describe the broad consequences or consequences of a particular action, event, or phenomenon. Especially when the resources of the problem are invisible to the human eye, like a virus.

Impact of begomovirus on the environment

Begomovirus has multiple adverse environmental impacts as it can seriously damage agricultural systems. Below are some of the main impacts of begomovirus on the environment:(a) Ecosystem destruction: Begomovirus can cause disruption to natural ecosystems by altering wild plant populations. Some begomoviruses have the ability to infect weed species, which can act as reservoirs of the virus and transmit the disease to neighboring crops. Spread of the virus between cultivated and wild plants can destroy local plant communities and reduce biodiversity. (b) Begomovirus can reduce the genetic diversity of plant populations. Farmers often use a few commercial plant species that are susceptible to these viruses. Prolonged cultivation of susceptible species can lead to loss of genetic diversity and increased plant susceptibility to disease and other environmental stresses. (c) Use of pesticides: Farmers often rely on chemical pesticides to control begomovirus infections and whitefly populations. Increased use of pesticides can lead to environmental destruction. Pesticides can upset the balance of ecosystems and harm beneficial insects, birds, and other species, as well as contaminate soil, water, and non-target organisms. (Saeed *et al*, 2017).

Impact of begomovirus on humans

In fact, Begomovirus does not infect humans directly. These viruses have a limited host range as they infect and multiply only within plant cells. As a result, begomoviruses primarily affect agricultural production and food security and indirectly affect human health. Moreover, the economic impact of begomovirus infection may indirectly affect human health. Declining crop yields can increase food costs and make it difficult for communities in need to obtain healthy food. Malnutrition and food insecurity can have serious health consequences, especially for children and low-income people (Wang *et al*, 2022).

Impact begomoviruses on the cultivation of crops in Oman

crops cultivation is an important industry in Oman, supporting the country’s agricultural economy and food security. Vegetable crops are at serious risk from begomovirus, which damages various crops such as tomatoes, cucumbers, peppers, and pumpkins. These viruses can affect plants and cause various symptoms such as leaf curling, yellowing, stunting, and poor fruit quality. Begomovirus could have devastating effects on vegetable production in Oman. Reduced vigor of infected plants can lead to lower yields and lower quality. In extreme conditions, whole crops can be devastated, causing financial difficulties for farmers and affecting the availability and price of vegetables in surrounding markets.

General impact of begomovirus on crops

Normally the vegetable will have the following effect:

Reduced crop yield: Begomovirus-infected vegetable crops can significantly reduce crop yields. These viruses interfere with the normal growth and development of plants, resulting in reduced growth, reduced

fruit production, and lower overall production (Ghosh *et al*, 2007). Leaf curling and deformation are one of the characteristic signs of begomovirus infection. The leaves of infected plants are curled, creased, and warped. This can reduce the plant's ability to produce photosynthetic energy and hinder further development (Zhong *et al*, 2017). Chlorosis and mosaic patterns: Mosaic patterns, in which bright and dark green spots create an asymmetrical pattern on leaves, are also typical indicators of begomovirus infection. Another possibility is leaf yellowing or chlorosis. These symptoms are caused by impaired chlorophyll synthesis and distribution within the plant (Funayama-Noguchi, 2001). Fruit anomalies of infected vegetables are caused by begomoviruses. These abnormalities include deformation, shrinkage, and uneven maturation. In extreme cases, the fruit may become disfigured or degrade in quality, thus losing its commercial value (Singh *et al*, 2021). Begomoviruses have the ability to transmit from infected plants to their progeny through contaminated seeds, known as intergenerational transmission. This vertical transmission within crops can make the virus difficult to control and eradicate (Leke *et al*, 2015). Economic loss: Begging virus infections can result in significant economic losses for vegetable growers. For farmers dependent on vegetable production, lower crop yields, lower fruit quality, and increased spending on disease control strategies can cause financial hardships (Yadava *et al*, 2010).

General symptoms of begomovirus on crops and example of the impact of begomovirus on crops in Oman

The general symptoms of begomovirus on crops include

Leaf curling: The leaves of infected plants curl downwards, giving them a characteristic distorted appearance. Yellowing: The infected leaves may turn yellow, especially along the veins. Stunted growth: Infected plants usually have reduced growth and appear smaller than healthy plants. Mosaic patterns: Some begomoviruses cause mosaic patterns on the leaves, with light and dark green patches. (Riley *et al*, 2002).

Examples of Oman's crops impacted by begomovirus

First one, Okra: Okra farming is severely restricted in many tropical and subtropical areas of the OW by begomovirus infections (Figure 1). Unipartite begomoviruses associated with beta satellites are the main cause of these diseases, although bipartite begomoviruses are also thought to be implicated (Jose, Usha, 2003). *Okra yellow vein disease* (OYVD) and *Okra leaf curl disease* (OLCD) are two forms of begomovirus disease that affect okra (Venkataravanappa *et al*, 2015). a vegetable crop that is widespread in West Africa, is grown during the winter in the Al-Batinah region of Oman to meet the demand of the domestic market. *Okra leaf curl disease* (OLCD) is a major limiting factor causing stunted growth, leaf curl, skewing, mottling, and yellow mosaic. Several begomoviruses and begomovirus satellite complexes have been found to cause his OLCD, including *Cotton leaf curl Gezira virus* (CLCuGV), *Okra yellow crinkle virus* (OYCrV), and *Okra leaf curl Cameroon virus* (OLCuCMV). (Akhtar *et al*, 2014). Symptoms: Growth retardation, swollen veins, leaf yellowing, and slight curling are all signs of OYVD. Plants can exhibit both types of symptoms. Infected plants eventually develop severe stunting, reduced fruit size and quantity, and the majority of the fruit unfit for commerce (Shetty *et al*, 2013). The second one, cucurbita maxima: Leaf curl was observed during the February 2016 survey (Figure 2). At Al Batina commercial farm in Oman, Cucurbita maxima plants showed signs of disease. Symptoms: Curling, yellowing, and fading of leaves were signs of begomovirus infection, followed by mosaic patterns (Shahid *et al*, 2021). The third one, is tomato (Figure 3). One of the most important vegetables is the tomato, mainly grown in Albatina. The main biological factor limiting tomato production in Oman is begomovirus. MAF first noticed plants suffering from *Tomato leaf curl disease* (ToLCD) in the early 1990s. These plants exhibited various symptoms such as yellowing, upward curling, stunting, and a bushy appearance. (Khan *et al*, 2008). Fourth, In Oman, the radish (*Raphanus sativus*), a member of the cruciferous family, is an important and popular winter vegetable. Previous investigations found reddish plants in Al-Batina showing typical signs of begomovirus infection. Contaminated leaves were collected to learn more about the virus (Al-Shihi *et al.*, 2018a). last

one, *Nicotiana tabacum* or tobacco: Few farms grow tobacco in Oman. In 2015, tobacco plants in Sohar showed signs of leaf curl (downward), yellowing, raised veins, and stunted growth (Shahid *et al.*,2021).

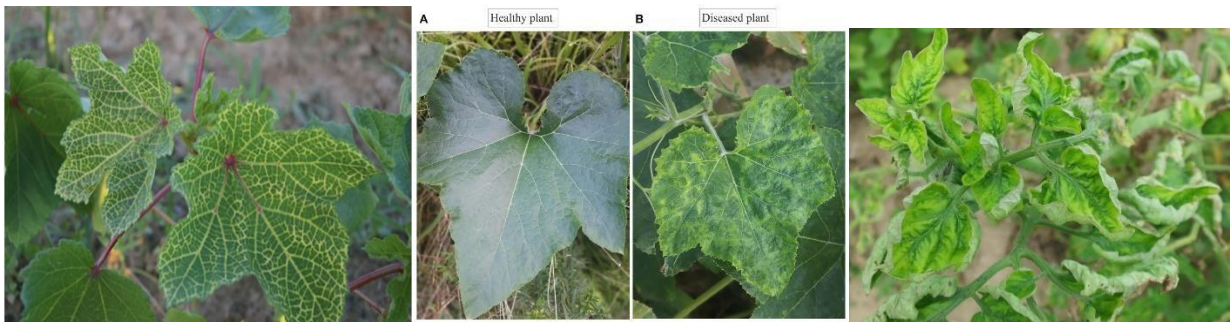


Figure 1

Figure 2, A

Figure 2, B

Figure 3



Figure 4

Figure 1: Okra infected by begomovirus (Sagar *et al.*, 2020).

Figure 2A: Healthy *Cucurbita maxima*

Figure 2B: *Cucurbita maxima* infected by begomovirus [1]

Figure 3: Infected tomato [2]

Figure 4: Infected Tobacco (Shahid, Al-Sadi, 2021)

Geminivirus diagnostics

This aids in confirming the existence of a certain geminivirus and is essential for creating a management regimen. Golden and yellow mosaic, leaf curling, deformation, enations, vein yellowing, swelling, and purpura are all signs of geminivirus infections. Striations and streaks are common signs of astrovirus infection in monocots. The presence of potential vectors like leafhoppers and whiteflies may also point to the genesis of the geminivirus. However, other viruses may also be responsible for the symptoms, therefore it's critical to determine which virus is at fault. Due to its speed, sensitivity, and accuracy, PCR has emerged as the method of choice for the detection and characterization of geminiviruses thanks to recombinant DNA technology. Rolling circle amplification (RCA) has been successful in locating and cloning new and uncharacterized geminiviruses, which helped to identify GRBV. For the purpose of finding unidentified geminiviruses and mixed infections, high-throughput sequencing has gained popularity. Geminivirus detection techniques have also been developed, including recombinase polymerase amplification and loop-mediated isothermal amplification assays for TYLCV and *Squash leaf curl virus* (SLCuV). Once the geminivirus causing an illness has been identified, it is feasible to ascertain the state of our understanding of

the virus' biological characteristics and make the best management decisions (Rojas *et al*, 2018).

General geminivirus management actions

A general strategy for dealing with the Geminivirus is described in three points Growing stages: before, during, and after.

Before season of growing

cultivar selection prior to the growing season, especially if it is resistant. If resistant cultivars are not available, look for virus- or vector-free planting material, such as transplants or propagation material. Other measures include planting timing and field placement.

Choosing the right variety and seed source is a critical factor for successful geminivirus management. Ensure availability of horticulturally desirable cultivars with traditional resistance (dominant, semi-dominant, recessive, etc.) to geminiviruses. These genes are found in wild and landrace species but can be difficult to introduce into commercially acceptable strains. If commercially available, it is highly recommended to grow cultivars that are resistant to geminiviruses or vector insects as they provide complete protection against geminivirus disease. Examples of crops with effective geminivirus resistance include tomatoes, cotton, and cassava. Planting material free of viruses and mediators. When resistant cultivars are not readily available, planting virus-free explants and propagation material is important to reduce primary inoculum and delay the onset of geminivirus disease. Transplants of vegetable crops such as cucumbers, peppers, and tomatoes should be grown in quality greenhouses or screen houses, not in open nurseries. To prevent the vector from transmitting the geminivirus to the explants, open-field nurseries should be covered with at least a net when growing in areas where the vector is present. Virus-free mother plants are selected because plants produced from cuttings (such as cassava) are asymptomatic, preferably molecularly symptomatic. These sections should be obtained by testing (eg PCR). Selection of planting date and location of field., Choosing the planting date and field location is critical to the successful cultivation of your crop. Plant annual crops when the number of vectors and sources of inoculum is lowest to delay infection and protect young plants. This is most effective when the host is absent or away from the infected field. Later plantings should be done upwind of the previous ones. Barrier crops such as maize should be planted between fields to reduce vector transmission (Rojas *et al*, 2018).

Protected culture. Protected culture allows for effective treatment of geminivirus disease, eliminates insect vectors, and improves the efficiency of other means. in extreme cases. In some cases, crops are protected throughout the growing season. B. Contained in vegetables grown in greenhouses and screen houses. It is important that these structures have a double-door airlock system to prevent the entry of insect vectors. By using UV-absorbing ingredients, Plastic or mesh covers increase vector rejection by hindering vector orientation and landing (Antignus, 2014). Protective culture significantly reduced losses due to geminivirus (begomovirus) disease Protects outdoor-grown vegetable crops throughout the growing season. A row cover (such as a ribbon or grill) can be used here to protect the seedlings (figure 5). The biggest loss of revenue is due to the Gemini virus disease occurs when plants are infected when young. Protected with row covers. Protects young plants from early infestations. Additionally, in high-yielding areas, row covers can be removed and then combined with other means to achieve economically acceptable yields (Rojas *et al*, 2018). Improves plant and soil health. This is especially true when plants are infected in the late stages of growth. Plant health can be improved in a number of ways, some of which can help reduce the incidence of geminivirus disease. Mulch is a surface soil cover that helps retain moisture in the soil, improve soil fertility and health, and reduce weed numbers (figure 6). There are many different types of mulch. Synthetic mulch is usually a type of plastic, more expensive and commonly used in intensive farming systems. Organic mulch includes a variety of materials. B. Leaves, bark chips, field hay, straw, and live vegetation, more common in cheap and subsistence farming. Reflective plastic mulches can work through reflected UV and

visible light disorientation and reduced landing rates, preventing vectors from detecting crops (Lapidot *et al*, 2014).



Figure 5 (Rojas *et al*, 2018)



Figure 6 (Rojas *et al*, 2018)

Through growing season.

After crops are established, these are the controls that can be used to prevent geminivirus disease. Insecticide-based vector control is the most widely used defense. The use of this measure in an IPM program that includes vector population monitoring and using thresholds to initiate pesticide applications will maximize its efficacy and safety. Additionally, it is advisable to use insecticides in conjunction with other strategies that can delay the onset of Geminivirus disease during the growing season (conventionally resistant).

Vector control with pesticides

In IPM, pesticides should only be used if: The vector population reaches a threshold that must be determined for each region. Threshold levels and the types of pesticides required will vary depending on the crop, local disease pressure, and other factors. Options include continued use of systemic insecticides, such as neonicotinoids and cyadipir, as well as contact insecticides (such as bifenthrin, fenprothrin, and lambda-cyhalothrin) and insect growth regulators (ibuprofen, pyriproxyfen, spiro). (e.g., mesiphene). environmentally friendly alternative is the use of herbal pesticides such as neem oil. These materials are applied to leaves and roots. B. By drip irrigation. Furthermore, to effectively limit the spread of geminivirus disease, pesticides must act quickly or the virus will be transmitted before the carrier is killed. In fact, most pesticides take hours to take effect, but viruses can take 5-15 minutes to infect. Therefore, for the most effective control, insecticides should act quickly and be applied when vector populations are relatively low. Another problem is the emergence of insect vector populations that are resistant to various pesticides (Nauen, Denholm, 2005).

Roguing: During the growing season, removing virus-infected plants is referred to as tampering (figure 7). This method lessens the inoculum that helps the virus spread secondarily in fields and crops that are protected. It works best when applied early in the growing season (up to 30-45 DAT), in protected crops, and in open fields where the prevalence of disease is low. To prevent the release of toxic vectors, infected plants should be sealed in a plastic bag and thrown away right away. In protected crops and open fields, routine inspections (weekly or biweekly) and the eradication of plant symptoms are advised (Sisterson, Stenger, 2013).

Biological regulation: Insect vectors and geminivirus illnesses, particularly *B. tabaci* and begomovirus diseases, can be controlled in protected agricultural areas via biological management. Here, biocontrol agents can be kept and result in significant parasitism and predator invasion rates. Predators, parasites, and

fungi are the three active components that have been successfully employed to control the biological activity of *B. tobacco*. IPM programs can effectively employ these agents (Stansly *et al*, 2004).



Figure 7: Roguling [3]

Following the growth season

Several steps should be made to lessen the source of viral transmission in a specific geographic area following harvest and before to planting the following crop. Harvested crops should be quickly removed, burned, or deeply tilled since they constitute a significant source of inoculum. In contrast to covered crops, where vegetation is neither removed nor damaged, cultivation is frequently done on open ground. Although difficult to administer and enforce, host-free times are successful at lowering viral inoculum and vector populations. The viral inoculum must be reduced at this time in order to prepare for the next harvest.

Sanitation: Any procedure known as sanitation aims to eliminate or drastically reduce the amount of geminivirus inoculum on and surrounding the field. It is crucial to remove and destroy the crop after harvesting since it might act as an inoculum source. For annual crops like gourds, peppers, and tomatoes, this is rather simple; however, it can be more challenging for other crops like cassava and vines. Weed management in and around fields should also be a part of hygiene precautions, particularly when the weed host of a virus that infects plants is identified. Therefore, it is crucial to perform hygienic measures between harvest and the following growing season (Andersson *et al*, 2011).

Host-free time frame. In certain areas, host-free intervals interrupt the ongoing production of annual crops. A host-free time of two to three months is necessary for various begomovirus illnesses to allow for geminivirus cleaning and numerous generations of whitefly vectors. None of them are capable of reproduction, and there is no transovarial exchange. The viral inoculum may be reduced or eliminated as a result, and the number of vectors may also decline. The host's free time should give the freshly formed cultures (for example, 4–8 weeks) a respite from intense viral pressure. Some begomovirus illnesses can be effectively treated by a host-free interval. This is due to the fact that (a) crops constitute the most significant inoculum, (b) the host range of these viruses is frequently limited, and (c) the majority of begomoviruses do not spread. Winter is a naturally host-free time of year in temperate countries. Host-free times should be implemented locally in tropical and subtropical areas where continuous plant culture is feasible. Farmers may choose to voluntarily designate host-free intervals, or the legislation may require it. Some hostless era characteristics. Depending on the crop, cultivation technique, and host-virus vector interactions, different seasons, lengths, cultures, and geographical locations are involved (Hilje *et al*, 2001).

New technologies that show promise

To create crops resistant to geminiviruses, a variety of transgenic techniques have been investigated. Some of them, particularly the ones that used RNA silencing (intervention), have been quite successful.

Transgenic vegetation. Some transgenic plants with high degrees of resistance have been created to start transcriptional gene silencing after begomovirus infection. This method entails modifying a portion of a virus or insect's vector genome in a plant to create a double-stranded RNA structure. As a result, the target virus/insect vector genome is precisely degraded or methylated by plant RNA silencing. Despite the fact that Geminiviruses are ssDNA viruses, this method of methylating promoters and other sequences has proved successful in producing transgenic plants with great resistance (Hagen *et al.*, 2008). For instance, the transgenic common bean (*Phaseolus vulgaris*) was created to benefit from RNA silencing by expressing intron-containing hairpin RNA that is a part of the Rep (AC1) gene of BGMV (Bonfim *et al.*, 2007). This cultivar exhibited a high level of BGMV resistance (Aragao *et al.*, 2013). Gene transfer techniques utilizing pathogen-derived genes and transgenic methods, particularly viral gene-derived resistance, now have a better chance of success thanks to the first coat of protein-derived resistance against the *Tobacco mosaic virus* (TMV) (Sagar *et al.*, 2020). this pathogen-derived resistance is very useful in the control of RNA viruses. such as faulty interfering genes, satellite RNAs, antagonist RNAs, replication genes, movement proteins, envelope proteins, and so on. The use of pathogenic gene derivatives. However, transgene-based resistance is most frequently derived from the coat protein, followed by mobility protein and replicase gene. The first begomovirus resistance was attained for ToLCV expressing capsid protein genes although the initial effort was mostly directed toward RNA viruses (Kunik *et al.* 1994). By including the RNAi construct in the common seed, the viral AC1 gene was rendered inactive (Bonfim *et al.* 2007). Both a copy-associated transgene (AC1) and a shortened gene (AC1) resistant to ToLCV were used to produce an anti-ACMV virus (Noris *et al.*, 1996). An RNA antagonist of the rep protein gene was used to create resistance to *Tomato yellow mosaic virus* (TGMV) (Day *et al.*, 1991). Rep. ToLCV-resistant tomato lines have been successfully created utilizing Agrobacterium-mediated tomato gene transfer using the ToLCV envelope protein gene (Raj *et al.*, 2005a). ToLCV in tomatoes has been effectively silenced utilizing a hairpin RNA-mediated method employing the AC-1 and AC4 genes (Ramesh *et al.*, 2007). Singh demonstrated how to use transactive siRNAs to fight TOLCNDV. The use of chimeric vectors containing partial fragments of the AC-2 and AC-4 allowed for the targeting of multiple genes. Plants that had been infiltrated accumulated less of the target virus and showed no symptoms. In proportion to the degree of resistance, siRNA was produced against AC-2 and AC-4. An RNAi strategy was used to achieve host resistance in the case of potato apical curl caused by ToLCNDV. The creation of transgenic plants that ultimately result in the expression of pathogen-derived resistance was made possible by the replication-associated gene (AC-1). After the challenge, completely asymptomatic plants were isolated (Tomar *et al.*, 2018).

CRISPR/Cas9

The most potent genome editing tool currently in use by molecular biologists to target host susceptibility factors and create resistant strains is CRISPR/Cas9 (Jiang and Doudna, 2017). This system specifically processed the AC2 and AC3 genes. The most successful site for editing begomoviruses to confer TYLCV resistance was found to be the stem loop of the intergenic region (IR) of the origin of replication (Ali *et al.*, 2015). Tobacco rattle virus used the short guide RNA (sgRNA) of TYLCV to create *N. benthamiana* that overexpressed Cas9. The next step was agroinfiltration to inject harmful TYLCV clones into *N. benthamiana* plants. The TYLCV genome accumulated relatively little in the IR mutant, according to their observations. The effectiveness of coding and noncoding regions as CRISPR/Cas9 targets in the multibegomovirus genome was examined in one research. While noncoding area mutants were more effective at creating viruses that could cause systemic infection and replication and provided interference activity, coding region mutants were still able to make movement proteins and reproduce (Ali *et al.*, 2016). To combat the threat posed by begomovirus, the same research team focused on the TYLCV coat protein and the replicase gene. The TYLCV DNA genome accumulates relatively slowly as a result of the target region's considerable effect on viral replication (Tashkandi *et al.*, 2018). Off-target Cas9 activities in the plant genome, however, have only sometimes been found. Recent research has also shown Cas9 enzymes that have fewer off-target effects, further lapping this worry in plants. Utilizing CRISPR/Cas9 technology to create plant pathogen-resistant viral pathogens also creates the opportunity to address fundamental issues in

virus infection and plant host resistance. By analyzing the genomes of viruses that are not recognized by the CRISPR/Cas9 system, for instance, the CRISPR/Cas9 platform might be used to study how the viral genome has evolved to combat plant immunity. To find host variables that regulate plant resistance and susceptibility to viral infection, the CRISPR/Cas9 platform might potentially be employed for targeted mutagenesis. As a result, the CRISPR/Cas9 technology presents a viable strategy for comprehending and engineering plant resistance to both single- and multi-viral infections (Fondong *et al*, 2016).

CONCLUSIONS AND RECOMMENDATIONS

This study completed the discussion of the Emerging threats of begomoviruses to the cultivation of vegetable, fruits, and medicinal plants and their management strategies in Oman with an extensive discussion about it. As far as we have read in our research, the most important information and theories of modern and ancient times are related to the topic of emerging threats of begomoviruses to the cultivation of vegetable, fruits, and medicinal plants and their management strategies in Oman, and the key points that I discussed the structure of begomovirus and transmission methods of begomovirus, and impact begomovirus on the environment and human, and I mentioned some Oman's crops that impacted by begomovirus. Finally, the Geminivirus diagnostics and ways of management of Begomovirus. All information mentioned and on which we rely has been obtained from reliable sources and references. We have also confirmed that everything presented in this paper is supported by sufficient evidence.

This study aims to understand and control the begomovirus in vegetable and medical plants.

Several points are very necessary:

1. Protecting crops is very important. The study of crop viruses helps scientists understand their biology, transmission patterns, and host range, enabling effective disease prevention, early detection, and control measures to reduce crop damage and economic losses. can be minimized. food Security. To ensure a stable supply, crop virus research can develop resistant cultivars through breeding programs and genetic engineering. These resistant cultivars are resistant to viral infections, ensuring stable crop production and food security.
2. Sustainable agriculture focuses on conserving natural resources and protecting the environment. Crop virus research is essential for integrated pest management (IPM) strategies using biopesticides, resistant crop varieties, crop practices, and insecticide use. This approach reduces reliance on chemical treatments and develops a targeted and environmentally friendly approach to controlling crop diseases.
3. Researchers can develop early warning systems, predictive models, and risk assessment tools to predict and mitigate the economic impact of viral diseases, helping farmers and policymakers to make informed decisions to help implement measures to minimize losses.

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Competing of interest

There is no competing of interest declared.

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