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Tomato Leaf Curl and Tomato Yellow Leaf Curl Disease and Its Management in Oman

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Abstract: The tomato (*Solanum lycopersicum*) is one of the most significant food crops in the tropics and subtropics. In recent years, invasive pests and diseases have severely damaged tomatoes in the Middle East. Begomoviruses are a plant pathogen spread by the whitefly (*Bemisia tabaci* gen.) with a circular single-stranded DNA (ssDNA) genome belonging to the family *Geminiviridae*. Oman is a source of legume viruses, which cause significant yield loss in various Omani crops, particularly tomatoes. In this review, we discuss outbreaks of tomato leaf curl disease (TLCD) and tomato yellow leaf curl disease (TYLCD) caused by the *tomato leaf curl virus* (TLCV) and *tomato yellow leaf curl virus* (TYLCV) in Oman and their controls.

Keywords: *Solanum lycopersicum*, tomato leaf curl disease, begomoviruses, geminiviruses, whitefly.

1. INTRODUCTION

Begomoviruses carried by the whitefly cause severe diseases with symptoms of yellow mosaic and leaf curl in several plant types globally [1]. On the Arabian Peninsula, begomoviruses are one of the most destructive viral pathogens of several nurtured and uncommonly significant crops, such as tomatoes, spinach, chili peppers, and papaya, producing significant crop damage fluctuating from 10% to 100% [2,3]. Viral infection strongly affects tomato production [4]. In addition to affecting nurtured plant and fruit species, leguminous viruses also distress some wild hosts, including barren poinsettia [5].

Begomoviruses contain circular ssDNA with either one segment (DNA-A) or a binary genome (DNA-A and DNA-B), each nearly 2.7 kb, making a genome of approximately 5.2 kb [Figure-1, 2]. Each genomic element is modeled with an oblique icosahedron. Geminiviridae is currently divided into nine genera: Begomovirus, Mastrevirus, Curtovirus, Topocuvirus, Becurtovirus, Turncurtovirus, Capulavirus, Eragrovirus and Grablovirus [6]. Begomovirus is transmitted only by whiteflies (*Bemisia tabaci* Genn.) [7]. Single-stranded segments of viral DNA are associated with one or more satellites, often referred to as beta (~1.4 kb) or alpha (~1.3 kb) (formerly DNA 1) satellites. Both satellites entail “helpers” for trajectory spread and host plant infection. However, beta satellites rely on the helper begomovirus to reproduce in the host plant. Alpha satellites either

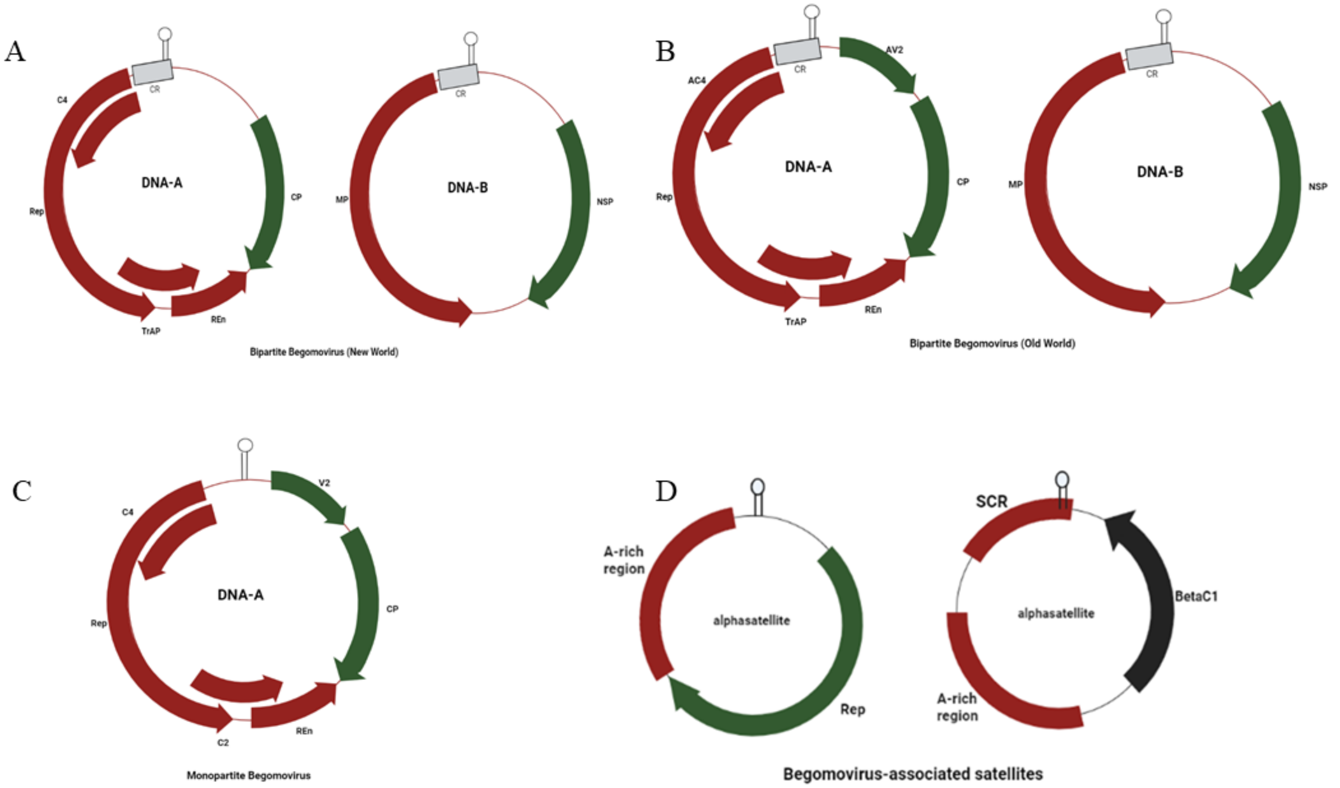

Figure 1. Genome organization of begomoviruses [37]

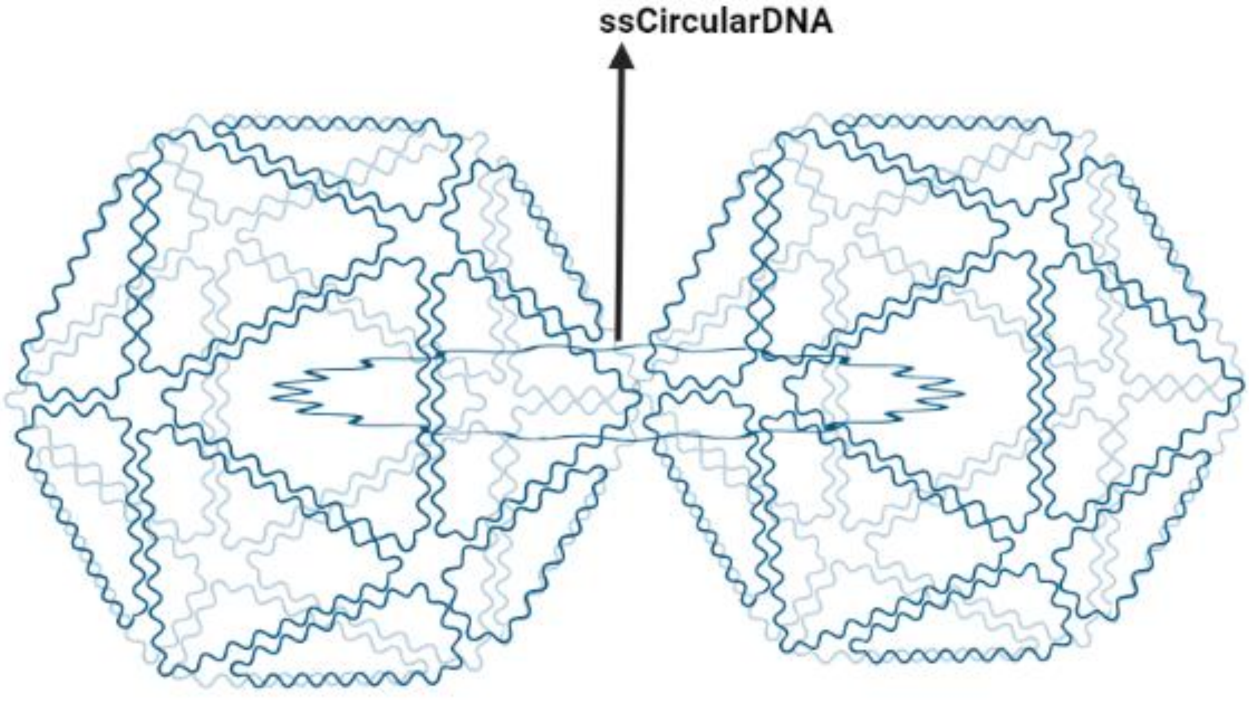

Figure 2. Non-enveloped, about 38 nm in length and 22 nm in diameter, twinned (geminate) incomplete T=1 icosahedral symmetry capsid that contains 22 pentameric capsomers made of 110 capsid proteins (CP). Each geminate particle has only a single circular ssDNA.

Self-replicate or resemble nano viruses but require a helper virus for systemic infection [5]. The Arabian Peninsula and Southeast Asia are diverse centers of five or more monosomal begomoviruses that infect tomatoes. Currently, at least five strains of TYLCV have been reported in Iran [8]. At least one has emerged as an economically important viral pathogen of tropical vegetables and fruit crops, including tomatoes. At least one strain of TYLCV has been reported in the Al-Batina region of Oman, Iran, Saudi Arabia [3], and Sudan [9]. Here we discuss the etiology and management of TLCD and TYLCD in Oman.

1.1. Agriculture in Oman

There are five (5) different agricultural regions in Oman. They range from north to south and comprise the Musand, the Al-Batinah coast, the valleys and plains of the eastern region, and the Dhofar region, along the narrow coastal strip from the border with Yemen to the mountains to the north. Rainfall is higher inland than on the coast, but it is not enough to grow vegetables and fruits. A slightly slanted shaft is excavated under these wells to drain the water and allow the water to drain below the surface, either into an aboveground tank or an underground tank, where it can drain.

The cool climate of the Al Jabal Al Akhdar Plateau allows for the cultivation of vegetables, grapes, peaches, and nuts. The coastal lands of Al-Batinah cover about two-fifths of Oman’s agricultural land. Although the annual rainfall is less along the coast, water vapor from the mountains penetrates the porous layers of the beach. This forms underground springs two meters below the surface. The cultivated area is 57,814 ha, an increase of about 18% between 1985 and 1990. During 1989–1990, harvested fruits were grown on 64% of the cultivated area or 36,990 ha. Dates are cultivated on 45% of the total area and 70% of the fruit area. Of the total cultivated area, cereals such as barley, wheat, and corn are cultivated at 19.2% (11,092 ha), and vegetables at 16.8% (9,732 ha). In the same five-year period, total agricultural production increased by 3% to 699,000 tonnes. Field crops, especially pulses, accounted for more than half of the total output, at 354,300 tonnes, an increase of 40% in five years. Fruit production (including dates and limes) increased from 154,500 tonnes to 182,400. Vegetable production increased by nearly 50% to 162,300 tonnes.

1.2. Outbreaks of TLCV and TYLCV in Oman

Oman has become a linkage of begomoviruses of various topographical ancestries [10]. The tendency for mixing, the primary tool for developing this virus, and the potential for transmission are increasing as Oman (and several other Arab nations) are vital centers of air and sea trade and travel [11,12]. Significant income losses and socio-economic improvements require efforts to study and develop long-term strategies to combat this devastating virus to ensure sustainable and cost-effective results without the heavy use of pesticides. Leaf curl of begomovirus is the central lethal infection of many significant crops in Oman, together with tomatoes, peppers, chilies, pumpkins, melons, and cucumbers [Figure-3] [4]. Subject to controlling applies, profit harms of these harvests can range from 0% to 100% and have been reported in Nizwa, Al Bateen, Musandam, Buraimi, Salalah, and inside Oman. Over the previous eight years, several begomoviruses have been categorized in Oman, containing numerous sparingly significant crops [Table 1]. Study in Oman is currently focused solely on the molecular classification of these viruses, which is only the first step towards developing strategies to control these essential plant viruses. Therefore, further research needs to be done on topics such as viral protein function, viral host interactions, resistance to viral-derived transformation, and related satellites. This chapter reviews the importance of begomoviruses for Omani agriculture, research on begomoviruses done in Oman over the previous 8 years, and possible future directions for more efficient and effective control and management of this viral disease.

So far, begomoviruses have been reported in nine crop groups in Oman. Only preliminary studies of begomoviruses, such as molecular replication, characterization,n, and phylogenetic analysis, have been performed [13]. In winter, tomatoes are grown on a big scale in the Albatina area of Oman. Leaves showing symptoms were collected, total nucleic acid was isolated, and the complete viral DNA was cloned and sequenced. Sequencing results indicated it to be closely related to TYLCV-IR (an Iranian unimolecular begomovirus species) with 91% nt identity. The Omani isolate was nominated TYLCV-OM and was reflected as a TYLCV-IR isolate. The satellite DNA sequence showed 88.5% similarity to the Pakistani beta DNA molecule. It was the first statement of beta satellite DNA (sat DNA) associated with TYLCV species. Alphasatellites and related betasatellites have been described for TYLCV-Om and therefore characterize a begomovirus intricate for Asia and the Middle East [Figure-4] [14,13]. This alpha satellite has the same 90%

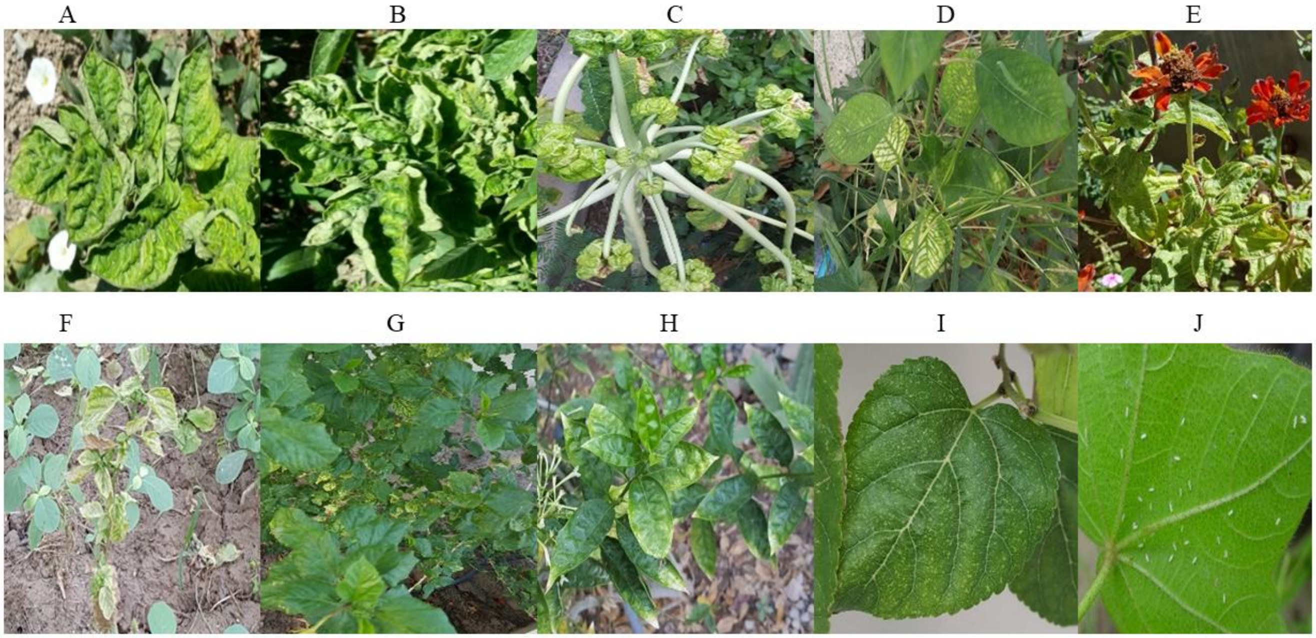

Figure 3. Symptoms of leaf curling and yellow mosaic diseases in the infected crops in the Al-Dkhliya region of Oman in different hosts and the vector (whitefly). (A) tomato (*Solanum lycopersicum*), (B) tomato (*Solanum lycopersicum*), (C) papaya (*Carica papaya*), (D) wild poinsettia (*Euphorbia heterophylla*), (E) common Zinnia (*Zinnia elegans*), (F) Common false mallow (*Malvastrum coromandelianum*), (G) tropical hibiscus (*Hibiscus rosa sinensis yellow*), (H) night-blooming jasmine (*Cestrum nocturnum*), (I) shahtoot (*Morus alba*), and (J) the vector whitefly (*Bemisia tabaci*) on the leaf of cotton (*Gossypium*) plant.

Table 1. List of all mono and bipartite begomoviruses and DNA satellites infecting different crops in Oman [36]

Disease	Viruses	Origin	Acronym	Host	Symptom	Detection Method	Stain in Oman	Association Satellite
				Monopartite				
Bean yellow mosaic disease	Tomato yellow leaf curl virus	Middle East/Indian subcontinent	TYLCV	Common bean	YM, Cr, LC	RCA	TYL-CV-IR	TolCB
Leaf curl disease	Chili leaf curl virus	Indian subcontinent	ChiLCV	Chili, tomato, radish, mint, basil	Y, LC, S	RCA/PCR	ChiL-CV-Om	ToLCB
Okra leaf curl disease	Okra leaf curl virus	North Africa	OLCV	Okra	VC, Y, RLA, RFZ	PCR/RCA	ToLCS-DV-OM	TolCB
Tomato leaf curl disease	Tomato yellow leaf curl virus	Mediterranean/ Middle east	TYLCV	Tomato Basil	Y, LC, S	PCR/RCA	TYL-CV-OM	ToLCB
Tomato leaf curl disease	Cotton leaf curl Gezira virus	North Africa	CLCuGV	Tomato, Papaya	SC, VT, VD	RCA	CLCuGV	ToLCB

Disease	Viruses	Origin	Acronym	Host	Symptom	Detection Method	Stain in Oman	Association Satellite
Tomato leaf curl disease	Tomato leaf curl Al-Batinah virus	Indian subcontinent/middle east	ToLCABV	Tomato	VC, S, Y	RCA	ToLCABV	ToLCB
Tomato leaf curl disease	Tomato leaf curl Braka virus	Indian subcontinent/Middle east	ToLCBrV	Tomato	VC, S, Y	RCA	ToLCBrV	ToLCB
Tomato leaf curl disease	Tomato leaf curl Liwa virus	Indian subcontinent/Middle east	ToLCL-wV	Basil Tomato	Y, VC, S	RCA/PCR	ToLCLwV	ToLCB and AYVSGA
Tomato leaf curl disease	Tomato leaf curl Sudan virus	North Africa	ToLCS-DV	Tomato	VC, S, Y	RCA/PCR	ToLCS DV-OM	ToLCB
Bipartite								
Casava mosaic disease	East African cassava mosaic Zanzibar virus	East Africa	EAC-MZV	Cassava	YM	RC	EACMZV	ToLCB
Mung bean yellow mosaic virus	Mung bean yellow mosaic India virus	India	MYMIV	Mung bean	Y, LC, S, YM	NGS/RCA/PCR	MYMIV	ToLCB
Squash leaf curl virus	Squash leaf curl virus	Mediterranean/middle east	SLCV	Squash	SC, Y, S	RCA	SLCV	ToLCB
Water melon leaf curl disease	Watermelon chlorotic stunt virus	Africa/Middle east	WmCSV	Water melon Cucumber Squash	LC, C, S	PCR/RCA	WmCSV	ToLCB
DNA Satellites								
Okra leaf curl disease	Tomato leaf curl yellow satellite	Middle east	ToLCB	Tomato	V, C, SY	NGS/PCR/RCA	ToLCB	
Okra leaf curl disease	Okra leaf curl Oman alpha satellite	Middle east	OLCA	Okra	VC, Y, RLA, RFZ	RCA	OLCO-MA	

Disease	Viruses	Origin	Acronym	Host	Symptom	Detection Method	Stain in Oman	Association Satellite
Tomato leaf curl disease	Tomato leaf curl beta satellite	Middle east	ToLCB	Tomato	VC, S, Y	NGS/PCR/RCA	ToLCB	
Tomato leaf curl disease	Ageratum yellow vein Singapore alpha satellite	South East Asia/Indian subcontinent	AYVSGA	Tomato	Y, VC, S	RCA	AYVSGA	

Y: yellowing, LC: leaf curl, YM: yellow mosaic, S: stunting, LC: leaf chlorosis, Cr: Crumpling, SC: severe curling, VD: vein deformation, VT: vein thickening, VC: vein clearing, RFZ: reduction fruit size, RLA: reduction leaf area, PCR: polymerase chain reaction, NGS: next-generation sequencing, RCA: rolling circle amplification.

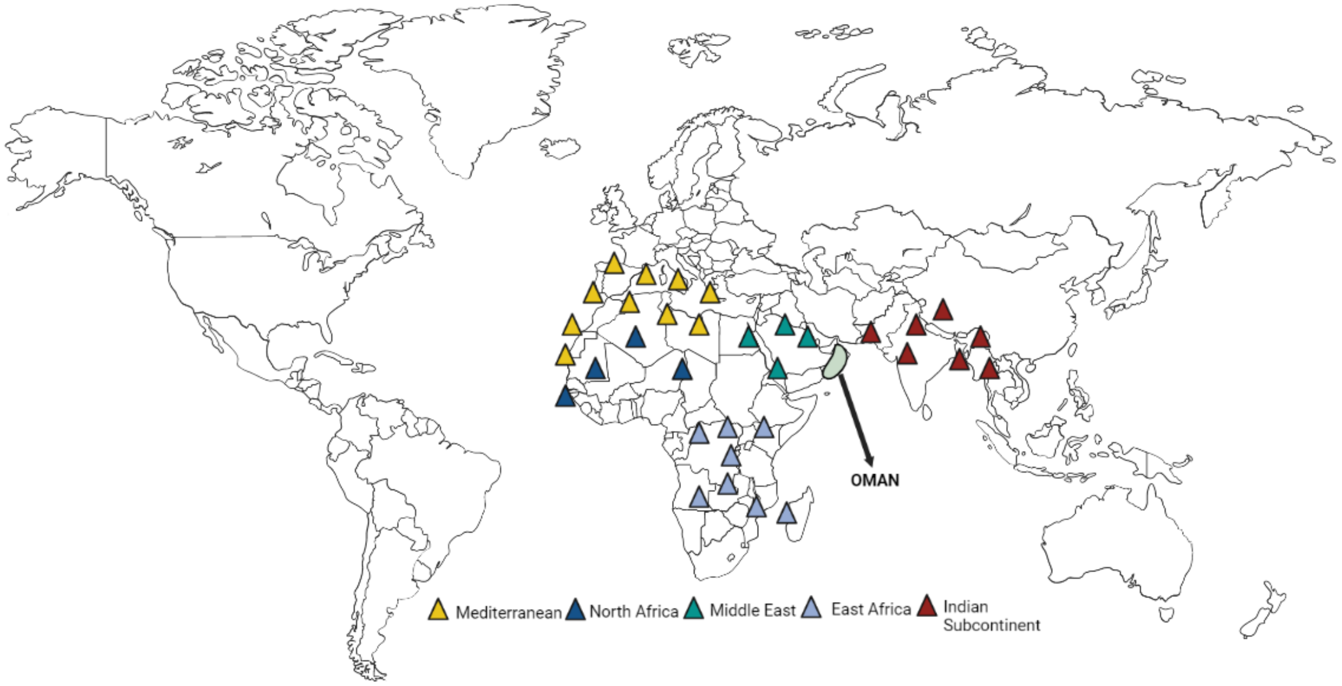

Figure 4. The world is depicting the possible origin and migration routes of begomoviruses identified in Oman, mainly from East and North Africa (purple and green arrows), the Middle East (Brown arrow), the Mediterranean (blue arrow), and the Indian subcontinent (dark blue arrow) [36]

Nucleotide identity as the unusual Ageratum Yellow Vein Singapore Alphasatellite (AYVSGA) DNA-2. Holcomb was established to contain recombinant TYLCV-OM and *Papaya leaf roll virus* (PLRV) from the Indian subcontinent [Figure-4]. Begomovirus is a foremost danger to Omani tomato crops. The four sequences were new species named *Tomato leaf curl Albatina virus* (ToLCABV). ToLCABVise is a recombination of ChiLCV-OM and ToLCOMV [10]. Plant inoculation studies have shown that ToLCABV interacts with ToLCB in plants [12].

Over the past 15 years, several begomoviruses were studied in Oman, including several significant crops. Recent studies in Oman have focused solely on the molecular characterization of this virus, which is only the first step in developing strategies to control this vital plant virus and its resulting resistance. Therefore, further work, such as viral protein function, molecular interactions between begomoviruses and hosts, and the natural and experimentally induced transformation resistance of viruses and related satellites, must be performed to understand molecular crosstalk better. They revealed features of their biology and new methodologies to switch and control.

The *Bemisia Tabaci* whitefly taxa consist of many morphologically identical genetic variants, only a few of which, including B, have an invasive haplotype [15]. This haplotype has reproductive potential for pest and plant-irrigated agroecosystems worldwide. Although unprecedented outbreaks associated with B variants were reported worldwide in the 1980s, the exact origin of the invasive haplotype has not been determined. The present study investigated available models for conserved single nucleotide alteration (SNP) patterns [15]. Whitefly sequence records show North African and Middle Eastern habitats, proposed centers of origin for variant B, and remote areas recently invaded by haplotypes of variant B. Analysis revealed eight SNP groups (haplotypes,) indicating that the genetic structure of Mitotype B is more complex than previously known. Moreover, the distribution patterns of the eight B haplotypes are closely related to well-defined ecological regions, suggesting that the different groups varied through geographic isolation. Contrary to claims that variant B is collectively invasive, only two of the eight haplotype clusters were established in geographic locations outside the uniqueness domain [15].

Begomovirus research primarily involves molecular characterization of viruses, phylogenetic investigation, infectivity in host plants, DNA replication, resistance to transformation, analysis of promoters, and expansion of vectors. Virus-based gene silencing. In this review, diseases caused by TLCV and TYLCV in tomatoes and other crops in Oman over the past 15 years have been discussed and focus on future research on begomoviruses that require more attention. Considering the importance of begomoviruses TLCV and TYLCV in Omani agriculture, notable scientific accomplishments associated with begomoviruses conducted in Oman over the past 15 yrs or so and possible directions for efforts are reviewed here.

1.3. Manner of transmissible

TLCV and TYLCV are not naturally spread by the species complex of the whitefly *B. tabaci* but consist of several secretly circulating species [16,17]. The status of *B. tabaci* was determined by the phylogenetic relationship of the nucleotide sequence of the mitochondrial cytochrome c oxidase subunit I gene (cox1). At least 24 species have been identified. The powder is separated from diseased cassava leaves. Altogether they were categorized as *B. tabaci* Asia II 1 [18,19].

Since tomato plants fall into the category of vegetative propagation, tomato stems infected with TLCV and TYLCV begomoviruses can also carry and expand diseases. In contrast, the whitefly acts as a disease vector in short-distance transmission (within a 20 m radius) [20], meaning that ensuring insecticides reduces whiteflies' density-message missions. However, pesticide abuse may accelerate the transfer of existing *B. tabaci* species to Mediterranean *B. tabaci* (biotype Q), which is resistant to the pesticides currently used against this pest [21]. Therefore, the development of integrated pest management is highly suggested to control whiteflies in the field and stop the growth of pesticide-resistant species that can be transmitted to areas where tomatoes and cassava are grown.

1.4. Factors Affecting Begomovirus Distribution and Spread in Oman

Tomato plantations represent vegetable crops grown mainly in Al-Batinah. Begomovirus is a major biological factor limiting tomato production in Oman [22]. Based on the whole nucleotide sequence of binary DNA-A and the complete single-component DNA of single-part begomoviruses, the International Commission on Virus Taxonomy (ICTV) recommended classification and nomenclature for the genus Begomovirus; a 91% sequence identity to complete DNA-A is required. The name of each virus includes the host plant, and symptoms, reflecting at the same time and place of collection [23,24].

Viral infection triggers a series of defense responses in plants, invading viral Rdegraded explicitly graded into small fragments (siRNA), a reaction known as RNA interference (RNAi). It is now believed that successful viral infection only occurs when this defense response is inhibited by specific viral proteins called RNAi repressors. RNAi inhibitory activity has been found in many begomovirus gene products reviewed [25]. Monopartite begomoviruses are mainly related to one or many beta-DNA satellite DNAs (about 1.4 kb in size). Two types of satellite DNA are known: alpha satellites and beta satellites sites code their own replication-associated proteins and are presumably derived from nano viruses use. In contrast, beta satellites do not encode replication-associated proteins and have one ORF (?C1). Alpha and beta satellite replication and reduced symptoms often produce viral helper components (DNA-A and DNA-B) [26]. Beta satellites depend on the A-DNA component plant replication, encapsulation, and migration ants [27,28,29].

Transformational resistance against begomoviruses has been achieved in many plants using a variety of approaches, including the expression of proteins of viral origin (CP, Rep and derivatives, and TrAP), expression of non-viral proteins with antiviral effects (toxic proDantinantin, antibodies against CP virus), damaged viral DNA, and DNA or RNAi transcripts (reviewed in [30]. In recent years, new resistance methods have been developed, such as the expression of the chaperone protein GroEL from bacterial endosymbionts that protect begomovirus particles from degradation that whitefly vectors produce in the phloem tissue of tomato plants by trapping viral particles in plants [31]. The new danger of viruses belonging to the genus Begomovirus has been discussed previously and extensively by Varma and Malathi [32]. The magnitude of yield loss due to multiple geminiviruses was estimated to be 100% by Dasgupta et al. [33]. Yield losses of up to 96% have been reported for the *Bhendi yellow vein mosaic virus* [34], while yield losses for legumes are estimated at approximately $300 million per year when chickpeas, green beans, and soybeans are combined.

Oman, a major center of trade and air trade center1], has become a link of begomoviruses of diverse geographical origins. Their tendency to recombine increases the likelihood of transmission, a principal evolutionary mechanism, since the viruses produce new virulent strains by recombination. The region of the Middle East has extensive trade and travel connections with the rest of the world, so the virus is very likely to spread. Significant socio-economic damages and subsequent improvement interventions require research and different approaches to manage the virus and provide sustainable and cost-effective results devoid of main pesticide contributions. Leaf curl, transferred by whitefly, is one of the deadly viral diseases of crops such as tomatoes, peppers, pumpkins, melons, cucumbers, and other essential crops in Oman [4]. Yield losses for this crop can range from 0% to 100% depending on recorded control efforts (e.g., shelter, use of pesticides to avoid white vectors) in Nizwa, AlBatinah, Musandam, Bureimi, Salalah, and remote areas of Oman.

2. CONCLUSION AND FUTURE PERSPECTIVES

There is still an urgency to investigate the variety of TLCV and TYLCV begomoviruses present in Oman and recognize the viruses that infect crucial food and medicinal plants and their molecular properties [35]. To date, Only several begomoviruses have been described in Oman. The prevalence of this virus may be in part due to the warm tropical climate favoring the annual survival of whitefly vectors and various types of crops. The serious severe it causes to food crops is certainly undoubtedly reason for further research.

An essential characteristic of Oman's begomoviruses is their intersecting host range. A recent example is the characterization of novel resistance traits of pepper against two Mexican begomoviruses, the golden mosaic virus, and the *Hu,asteco yellow vein virus*, as inhibition of RNAi by begomoviruses may play an important role in this synergy. Further investigation of the RNAi inhibition mechanism by begomoviruses prevalent in Oman is required. The recent emergence of many begomovirus-associated beta and alpha satellites in Oman is also essential.

Therefore, the interdependence of satellites and their begomoviruses is a critical area of investigation and promises significant benefits by introducing new methods of disease control that are not only scientifically interesting but also challenging for human disease. This is also true for the begomovirus of Oman. Begomovirus infection control strategies in various plants are increasing, with promising reports of successful control of begomovirus with viral and other transgene derivatives. Some genes that evolve resistance to begomovirus and can be used for introgression into popular plant cultivations have been identified. More studies are needed to find wild plant varieties resistant to the naturally occurring begomovirus and identify their resistance traits.

The communication between whitefly vectors and begomoviruses plays an essential role in the transmission of begomoviruses and needs to be carefully studied. These milestones, combined with the advances in the research of plant-virus interactions, suggest that the action mechanisms of begomoviruses may be unlocked shortly. This is urgent for the Sultanate of Oman to protect plants from massive losses due to begomovirus infection.

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Competing of interest

There is no competing of interest declared.

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