Geminivirus Occurrence in Australia, China, Europe, and the Middle Eastern Countries

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Abstract

Geminiviruses (family: Geminiviridae) are plant pathogenic viruses with single-stranded DNA (ssDNA) genome. Geminiviruses are classified into nine genera: Begomovirus, Mastrevirus, Curtovirus, Becurtovirus, Topocuvirus, Turncurtovirus, Capulavirus, Grablovirus, and Eragrovirus. Begomoviruses constitute the largest number of viruses in Geminiviridae family infecting most economically important crops in Australia, China, Europe, and the Middle East countries. Crops that have been infected with begomoviruses belong to the families, Malvaceae (cotton and okra), Cucurbitaceae (melon, watermelon, squash, and gourds), Euphorbiaceae (cassava), Solanaceae (tobacco, potato, tomato, and pepper), and Fabaceae (soybean, cowpea, common bean, and mungbean). Mastreviruses infect chickpea and pepper crops in Australia, Oman, Yemen, Jordan, Syria, and Iraq. Becurtoviruses infect some crops like sugar beet and tomato in Iran. Capulaviruses have been recorded in France and Finland infecting Alfalfa and *Plantago* plants, respectively. The geminiviruses pose a great challenge to the countries by their fast spread and infecting economic crops. Cooperation among these countries in exchanging information and adopting the most up-to-date system in quarantine can prevent further introduction of new viruses into new geographic regions.

1 Introduction

The viruses can be defined as "entities whose genomes are elements of nucleic acid that replicate in living cells using cellular synthetic machinery and causing the synthesis of specialized elements that can transfer the viral genome to other cells"

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(Luria et al. 1978). The International Committee on Taxonomy of Viruses (ICTV) has approved 3 orders, 73 families, 9 subfamilies, 287 genera, and ~1950 species of viruses (Briddon et al. 2008). Out of these, the plant viruses constitute 20 families, 88 genera, and around 750 species. More than 90% of plant viruses have ssRNA genomes and the remaining have DNA genomes, including both ssDNA and dsDNA. Caulimoviruses (family *Caulimoviridae*) are dsDNA viruses, whereas nanoviruses (*Nanoviridae*) and geminiviruses (*Geminiviridae*) are ssDNA viruses. The viruses show a wide range of genome sizes: the largest genomes of known virus are the mimiviruses and the smallest are the circoviruses. The family Geminiviridae has a worldwide impact on agricultural production that is ongoing. The diseases caused by geminiviruses represent serious constraints to agriculture. The name of geminivirus was derived when virus particles, which have a unique twinned quasi-isometric morphology, were isolated from maize which had streak symptoms and beet which showed curly top symptoms (Bock et al. 1974; Mumford 1974). This attribute provided the name geminivirus, symbolizing twins (Harrison 1977).

Because of the great losses caused by geminiviruses, they have become the subject of concern worldwide (Briddon et al. 2001). These viruses encode a few genes for their replication and depend mostly on their host proteins for their replication (Hanley-Bowdoin et al. 1999). The geminivirus was established as a group in 1979 (Matthews 1979). It was upgraded to the family *Geminiviridae* in 1995 (Murphy et al. 1995). They infect both monocots, such as wheat and maize, and dicots, such as tomato and cassava (Hanley-Bowdoin et al. 1999). It was reported that geminivirus has emerged in the Middle East and subsequently extended to the Mediterranean basin, Asia, Africa, and America (Czosnek and Laterrot 1997; Freitas-Astua et al. 2002; Varma and Malathi 2003). Several theories have been proposed for the recent distribution of geminiviruses around the world. One theory implicates the import of ornamental plants (Polston et al. 1999); another proposes that geminivirus was spread due to the introduction of infected nonsymptomatic tomato plants from the Eastern Mediterranean region into the Dominican Republic of the Caribbean islands (Brown and Bird 1992). In this chapter, I discuss about the geographic distribution of different geminiviruses in Australia, China, and some European and Middle East countries.

1.1 Geminiviruses

There are more than 199 recognized species of geminivirus in which 181 belong to the genus *Begomovirus* and more than 670 complete sequences are deposited in databases (Fauquet et al. 2008). Based on their host range, genome organization, and insect vector, geminiviruses are classified into nine genera: Begomovirus, Mastrevirus, Curtovirus, Becurtovirus, Topocuvirus, Turncurtovirus, Capulavirus, Grablovirus, and Eragrovirus (Stanley et al. 2005; Fauquet et al. 2008; Brown et al. 2012; Adams et al. 2013). Begomoviruses constitute the largest group of geminiviruses (Briddon et al. 2001; Mansoor et al. 2008). Based on their genomes, they are divided into two groups: monopartite (single component of size 2.8 kb) and bipartite (two components of about the same size known as DNA-A and DNA-B; (Stanley et al. 2005; Fig. 1). Bipartite begomoviruses include *Tomato golden mosaic virus* (TGMV), *Tobacco yellow crinkle virus* (TbYCV), *Tomato leaf curl New Delhi virus* (ToLCNDV), *African cassava mosaic virus* (ACMV), and (Padidam et al. 1995). Monopartite begomoviruses include *Tomato yellow leaf curl virus* (TYLCV), *Tomato leaf curl virus* (ToLCV), and *Tomato yellow leaf curl Sardinia virus* (TYLCSV); even they lack DNA-B but they can induce disease in plants due to the differences in their gene functions (Briddon and Stanley 2006).

Two subgenomic molecules are associated with monopartite begomoviruses: betasatellite and alphasatellite. Betasatellite is defined as a satellite that has no sequence homology to monopartite begomovirus (helper virus) and is entirely dependent on it for replication (Mayo et al. 2005). The first DNA satellite isolated from tomato crops was infected with the monopartite begomovirus, *Tomato leaf curl virus* (ToLCV), which has no open reading frame (ORF) (Dry et al. 1997; Behjatnia et al. 1998). DNA-βs are widely distributed in the Old World (OW) and absent in the New World (NW) (Briddon et al. 2008; Fig. 1). Alphasatellites are the second group of DNA molecules that have a conserved structure and genome size of ~1380 nt. These molecules are associated with monopartite begomoviruses along with betasatellites in the same host (Mansoor et al. 1999; Saunders and Stanley 1999; Briddon et al. 2004; Fig. 1).

The *Mastrevirus* genus includes leafhopper-transmitted viruses, which have monopartite genomes infecting both monocotyledonous and dicotyledonous plants (Boulton 2002; Nahid et al. 2008). *Maize streak virus* (MSV) and W*heat dwarf virus* (WDV) are two well-studied members of the genus. The *Curtovirus* genus includes leafhopper-transmitted viruses, which have monopartite genomes and infect dicots. The curtovirus genome consists of circular ssDNA molecule of about 3.0 kb (Hur et al. 2007). *Beat curly top virus* (BCTV) is a well-studied member in this genus. The *Topocovirus* genus contains treehopper-transmitted viruses which have monopartite genomes. The only known topocuvirus is *Tomato pseudo-curly top virus* (TPCTV), which was isolated from Florida (Briddon et al. 1996). Becurtoviruses have close similarities to the *Curtovirus* genus in terms of their biological properties. An example is *Beet curly top Iran virus* (BCTIV). *Eragrovirus* genus has a single member *Eragrostis curvularia streak virus* (ECSV). The CP of this virus is very close to the CP of viruses in *Mastrevirus* genus. *Turncurtovirus* genus has only one virus, *Turnip curly top virus* (TCTV). The genome organization of geminivirus genera and the genes they encode are clarified in Fig. 1.

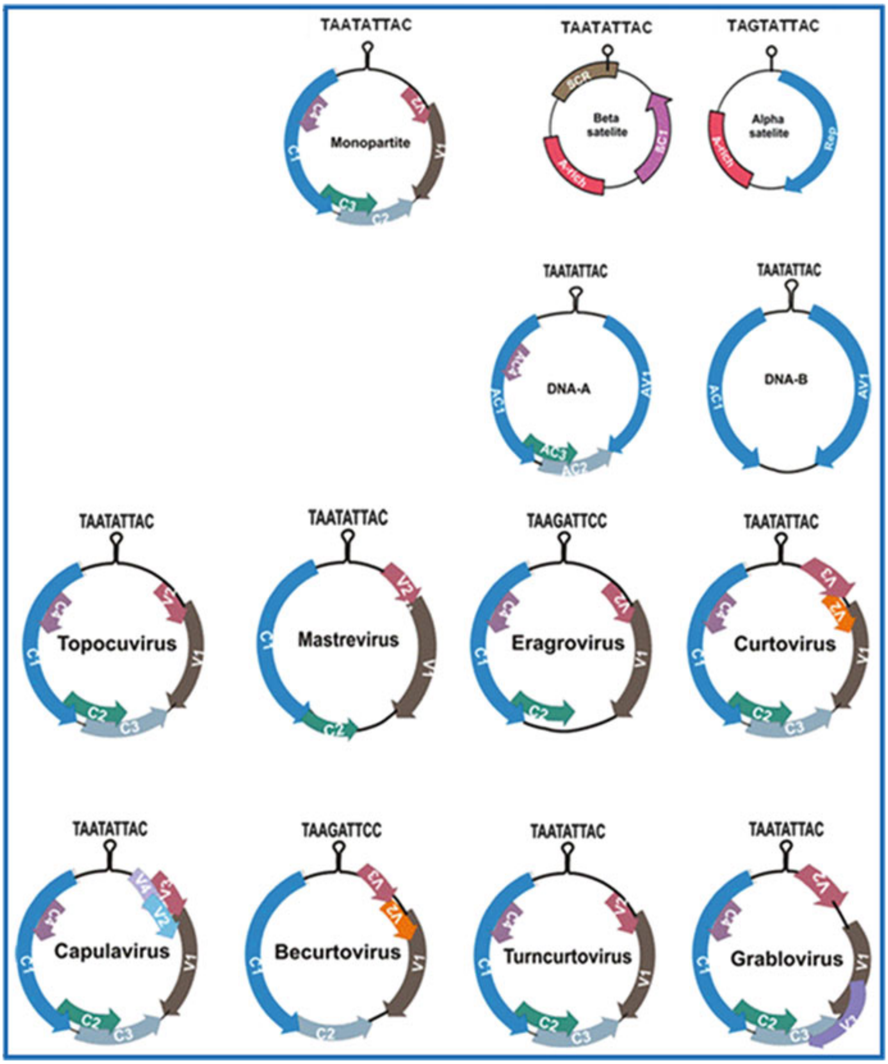

Fig. 1 *Genome organization of different geminivirus genera*. The ORFs (V1, V2, V3, C1, C2, C3, C4.) are coded according to the function of their genes (C1, replication associated protein; C2, transcriptional activator protein; C3, replication enhancer protein; C4, symptom determinant; V1, capsid protein; V2, movement protein;V3, a protein involved in regulating the ss/ds DNA ratio; AV1, nuclear shuttle protein; AC1, movement protein). The position of the stem-loop containing the conserved sequence located in the intergenic region is shown (TAAGATTCC sequence for Becurtoviruses and Eragoviruses; TAATATTAC for other genera). Genome map of Beta satellite consist of Adenine rich sequence (A-rich), sequence common region (SCR) and hairpin structure having the nonanucleotide sequence TAATATTAC. Genome map of Alphasatellites consists of one large gene in the virion-sense (Rep), adenine rich sequence (A-rich) and a hairpin structure containing, the nonanucleotide sequence TAGTATTAC

1.2 Geminivirus Evolution

Genetic variation can arise in the genome of geminiviruses through mutation, recombination, and pseudorecombination (Seal et al. 2006). The rate of mutation is very low in DNA as compared to RNA viruses. Isnard et al. (1998) reported that mutation in *Maize streak virus* (MSV) has occurred at frequencies of about 10^{-4}–10^{-5} throughout their genome. Pseudorecombination has been reported to occur among begomoviruses in different countries. It describes the exchange between the genome components of DNA-A and DNA-B (Pita et al. 2001; Ramos et al. 2003; Idris and Brown 2005). Experimentally, it was reported that the exchange between components of *Tomato mottle Taino virus* (ToMoTV) pseudorecombines with *Potato yellow mosaic virus* (PYMV) but not with *Tomato mottle virus* (ToMoV) (Ramos et al. 2003). The DNA-A component of some geminiviruses can form association with some DNA-B of other viruses and can cause infection when co-inoculated with each other (Karthikeyan et al. 2004). Recombination is the process by which the segments of one nucleotide strand are incorporated into segments of other nucleotide strands during replication process. Recombination is common under natural field conditions among geminiviruses (Zhou et al. 1997; Padidam et al. 1995; Al Shihi et al. 2014). Recombination has been reported to occur between DNA-A molecules of different begomoviruses. For example, Zhou et al. (1997) reported that *Cassava mosaic virus* (CMV) is a recombinant between *African cassava mosaic virus* (ACMV) and *East African cassava mosaic virus* (EACMV). In addition, Monci et al. (2002) stated a recombinant between *Tomato yellow leaf curl Sardinia virus* (TYLCSV) and *Tomato yellow leaf curl virus* (TYLCV). Similarly, Al Shihi et al. (2014) reported a recombinant between *Tomato leaf curl Oman virus* (ToLCOMV) and *Croton yellow vein mosaic virus* (CroYVMV) and hence the name *Tomato leaf curl Barka virus* (ToLCBrV).

1.3 Disease Symptoms

Yield losses due to infection by TYLCD have become a major threat to crop production in the Middle East, Southeast Asia, and Europe (Czosnek and Laterrot 1997; Moriones and Navas-Castillo 2000). Fiallo-Olive et al. (2013) reported that about 40 different countries (about seven million hectares) are subjected to the attack by geminiviruses. There are different types of symptoms resulting from geminivirus infection. Up-curling of leaves and reduction of upper leaf size is common when hot pepper, okra, and papaya plants are infected with geminivirus. Leaf curling, mosaic-like pattern, and general stunting of plant can be seen on plants like squash, radish, and tomato when infected with geminiviruses. The disease symptoms can vary from slight to severe depending on several factors such as plant stage, time of infection, type of virus strain, and type of vector (Fig. 2).

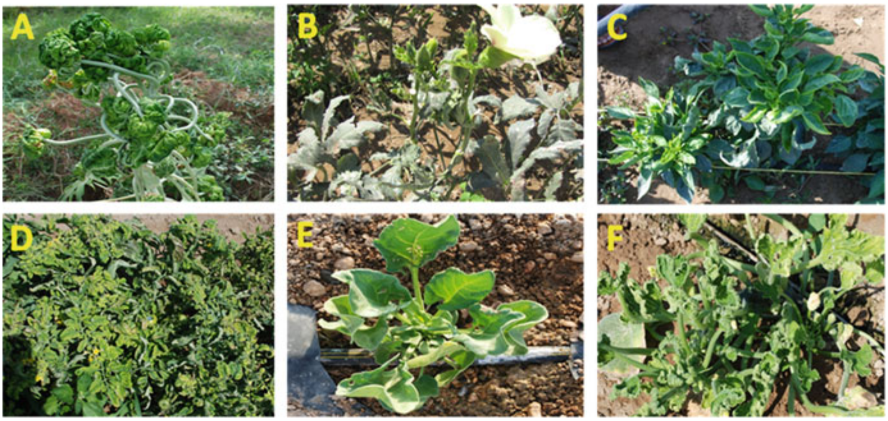

Fig. 2 *Geminivirus disease symptoms*. (**a**) Papaya infected with TYLCV and ChLCV; (**b**) Okra infected with OLCOMV; (**c**) Hot pepper infected with ChLCV; (**d**) Tomato infected with ToLCBrV and; (**e**) Radish infected with TYLCV and ChLCV, and (**f**) Squash infected with TYLCV (Source: Adel Al Shihi)

2 Geminiviruses Occurrence in Australia, China, Europe, and the Middle East Countries

2.1 Geminiviruses in Australia

Geminiviruses (*Geminiviridae*) are economically important pathogens which lead to serious losses in food crops worldwide. Agriculture in tropical and subtropical regions is mostly under danger, especially those growing crops such as tomatoes, beans, peppers, cucurbits, and cassavas (Brown 1994). *They* limit crop production in several regions in the world, including Australia (Behjatnia et al. 1998).

In Australia, a monopartite *Begomovirus*, *Tomato leaf curl virus* (TLCV), was reported in 1970 in the Northern Province of the country causing severe losses to tomato crops (Behjatnia et al. 1998). It is having a ssDNA genome of 2766 nt encoding six open reading frames (Dry et al. 1997). The whitefly (*B. tabaci* biotype B) was recorded in Australia for the first time since 1994 (Gunning et al. 1995). In addition to their high efficiency in begomovirus transmission, they cause significant damage through direct feeding on some crops such as soybeans, sunflowers, tomatoes sweet potatoes, cotton, cucurbits, and eggplants.

Areas infected with TLCV have till now been away from intensive horticultural areas being located on the east coast of Queensland and currently crop losses are limited to a relatively small area around Darwin (Stonor et al. 2003). Whitefly inoculation was done to a group of plants and weed species common in northern Australia to test their susceptibility to TLCV. Out of 58 species tested, only 11 species showed symptoms typical to begomovirus infection, but 47 species failed to show symptoms, and when tested molecularly using probe hybridization, no TLCV DNA was detected (Stonor et al. 2003). This screening by whitefly inoculation might suggest that TLCV may have a narrow host range. The area where TLCV (Northern area) occurs is separated from southern areas by a distinct climatic region. This region is represented by a long dry period extending from April to November (Anonymous 1988).

Another virus in *Mastrevirus* genus is named as *Tobacco yellow dwarf virus* (TYDV) which is recorded only in Australia and causes significant diseases in bean (*Phaseolus vulgaris*) (Hill 1937) and tobacco (*Nicotiana tabacum*) (Ballantyne 1968). It occurs in all states of Australia and transmitted by the leafhopper vector (*Orosius argentatus*) or by grafting 30 species in seven dicotyledonous families (Helson 1951; Hill and Mandryk 1954; Thomas and Bowyer 1979). The common symptoms that result from TYDV infection on bean (*Phaseolus vulgaris*) are reduction in the growth rate of the first trifoliolate leaf, down-curling of the trifoliolate leaf margin, and vascular necrosis of the stem. In tobacco, the symptoms which are seen when plants are infected with TYDV are down-curling of the tips and margins of the youngest leaves, chlorosis, and stunting of the whole plant. TYDV can be distinguished from other viruses by its geminate particles and leafhopper vector. Other geminiviruses, like *Tobacco leaf curl virus* (TbLCV) and *Beet curly top virus* (BCTV), have many hosts in common with TYDV. However, TbLCV is transmitted by the whitefly (*Bemisia tabaci*). BCTV causes similar symptoms to TYDV in several hosts and is also transmitted by leafhoppers, so the two viruses can be distinguished easily by using serological tests. In addition to the recognized species (TYDV), two more distinct species of mastrevirus are known to infect dicotyledonous crops in Australia including *chickpea Chlorosis virus* (CpCV-A, CpCV-B) and *Chickpea red leaf virus* (CpRLV; Thomas et al. 2010). These mastreviruses infect chickpea, bean, and tobacco crops. The dicot-infecting mastreviruses, biologically, serologically, and phylogenetically, constitute a distinct group in comparison to monocot-infecting mastreviruses (Brown et al. 2012). The important strains of dicot-infecting mastreviruses from eastern Australia are TYDV, CpCV-A, CpCV-B, and *Chickpea red leaf virus* (CpRLV) (Thomas et al. 2010). It was believed that Australia could be the hotspot of dicot-infecting mastrevirus diversity and more mastrevirus diversity could exist in chickpea and maybe other cultivated host species in Australia. Schwinghamer et al. (2010) suggested that the geographical distribution of distinct dicot-infecting mastreviruses is overlapping broadly in eastern Australia.

2.2 Geminiviruses in China

In China, geminiviruses have been emerging as serious plant pathogens in many areas in recent years, and several begomovirus species and strains have been reported infecting tomato, squash, tobacco, and *Malvastrum coromandelianum*. Some of these viruses were found to be associated with betasatellite molecules. Begomovirus–DNAβ complex was found to be associated with tomato leaf curl disease in Guangxi province, China. Monopartite begomoviruses that have been associated with betasatellite are *Tobacco leaf curl virus* (TbLCV), *Tomato leaf curl*

China virus (ToLCCNV), *Tobacco leaf curl Yunnan virus* (TLCYNV), and *Tobacco curly shoot virus* (TbCSV) (Meng et al. 2012). In China, there are three types of whitefly biotypes, *Bemisia tabaci* biotype B, biotype Q, and Biotype Cv. Biotypes B and Q are well known for their high efficiency in transmitting viruses (Cui et al. 2004). Infectivity assay showed that *Tomato leaf curl China betasatellite* (ToLCCNB) is required for inducing disease symptoms in the tested plants. This role coincides with DNA-β species associated with *Cotton leaf curl Multan virus*, *Ageratum yellow vein virus* (AYVV), and TYLCCNV (Briddon et al. 2001; Cui et al. 2004).

Zhou et al. (2003) reported that begomoviruses isolated from some crops including tobacco, tomato, and weed species in China (Yunnan) were found to be associated with DNA betasatellites, and the complete nucleotide sequences were found to be 1333–1355 nt. DNA betasatellites associated with begomoviruses from the same region are clustered closely, but begomovirus isolates from different regions were more distantly related. *Ageratum yellow vein China virus* (AYVCNV) retained more concentrations in infected leaves in the presence of DNA betasatellites. It was suggested that DNA betasatellites may have a direct effect on viral DNA replication, probably by providing proper cellular functions (Liu et al. 1999; Nagar et al. 1995). Another hypothesis is that they may facilitate the systemic movement of viral DNA within the plant, hence enhancing the level of viral DNA in infected tissues (Xiong et al. 2007).

Alphasatellites were identified in begomovirus-infected plants in Yunnan and all crops (tobacco, tomato, and squash) infected with alphasatellites also have been found to be infected with betasatellites (Xie et al. 2010). They were divided into three types based on phylogenetic tree of the complete nucleotide sequences. The first type was associated with *Tomato yellow leaf curl China virus* (TYLCCNV)/*Tomato yellow leaf curl China betasatellite* (TYLCCNB) complex. The second type was associated with *Tobacco curly shoot virus* (TbCSV)/*Tobacco curly shoot betasatellite* (TbCSB) complex. The third type was associated with TbCSV/*Ageratum yellow vein betasatellite* (AYVB) complex (Xie et al. 2010). It was confirmed that unlike betasatellites, alphasatellites are self-replicating in host plants because they encode a rolling-circle replication initiator protein; however, they require helper begomoviruses for movement in plants and insect transmission as well. They may play an important role in the epidemiology of begomovirus and betasatellite complexes, but more studies need to be conducted to clarify this role.

In China, geminivirus species has obvious geographical characteristics, that is different regions have different virus strains. The geminiviruses occur in high incidence in Yunnan, but due to the isolated mountain valleys, its distribution is discontinuous rather than continuous (Jing et al. 2016). After amplifying the whole genome of DNA-A, cloning, and sequencing analysis, the results revealed the presence of a number of begomoviruses such as *Malvastrum yellow vein Yunnan virus* (MYVYnV), *Chinese squash leaf curl virus*, *Squash leaf curl China virus*, (SLCCNV), *Sweet potato leaf curl virus* (SPLCV), *Tomato yellow leaf curl China virus* (TYLCCNV), Yunnan chilli leaf curl virus (Pepper leaf curl Yunnan virus (PeLCYnV), *Crassocephalum yellow vein virus* (CYVV), *Yunnan Tobacco leaf curl virus, and Tobacco leaf curl Yunnan virus* (TbLCYnV) (Meng et al. 2012).

The distribution of geminiviruses has showed the dominance of some strains in some regions more than others. For instance, in northern district, there are four geminivirus species, of which *Tomato yellow leaf China curl virus* (TYLCCNV) is the most dominant type; in South Central of Yuanjiang, there are four geminiviruses, of which the dominant species is TYLCCNV, followed by *Pepper leaf curl Yunnan virus* (PeLCYnV); in the western district where climate is humid, four geminiviruses species have been identified of which the dominant species is *Sweet potato leaf curl virus* (SPLCV); and in the southern of Lancang River Basin four geminiviruses have been identified as well, among them *Tobacco curly shoot virus* (TbCSV) and *Tobacco leaf curl Yunnan virus* (TLCYnV). The occurrence of begomoviruses in some regions like Sichuan is increasing more. The mixed infection of several begomoviruses like TYLCCNV/TYLCCNB and *Papaya leaf curl China virus* (PaLCuCNV) was identified in tomato (Jing et al. 2016).

2.3 Geminiviruses in Europe

Over the past years, surveys in the main tomato production area of Sicily Ragusa province in Italy confirmed the presence of TYLCV (Accotto et al. 2000). Tomato (*Solanum Lycopersicon*) crops in Sardinia and Sicily have been severely affected by yellow leaf curl disease. Accotto et al. (2000) reported that TYLCV has spread quickly in an area where the other viral species like *Tomato yellow leaf curl Sardinia virus* (TYLCSV) causes yellow leaf curl disease. In Portugal (Algarve), disease symptoms on some vegetable crops include plant stunting, leaf curling, and yellowing. Louro et al. (1996) reported that up to 100% of tomato crops were affected and yield was severely reduced due to TYLCV infection. In Spain, severe leaf yellowing has occurred in tomato (*Solanum Lycopersicon*) crops in southern Spain, and this outbreak was associated with high populations of the whitefly *Bemisia tabaci*. Symptoms including leaf interveinal yellowing that developed initially on lower leaves and then progressed to the upper leaves of tomato have been seen (Moriones et al. 1993). In Spain, sweet potato (*Ipomoea batatas*) and *Ipomoea indica* plants were found to be infected with sweepoviruses. They comprise a monophyletic group of begomoviruses which have been known to infect sweet potato (*Ipomoea batatas*) and other species of the family Convolvulaceae (Lozano et al. 2016). Lozano et al. (2016) reported that sweepoviruses infecting *Ipomoea* sp. in Spain were associated with small molecules named as deltasatellites (ToLCV-sat). In September 2013, in the province of Almeria, Spain symptoms including leaf chlorotic mottling and vein distortion on middle leaves were seen in tomato (*Solanum lycopersicum* L.) growing in a greenhouse. Nearby greenhouse having zucchini squash plants (*Cucurbita pepo* L.) showed leaf curling symptoms and chlorotic mottling on intermediate leaves. The results revealed the presence of ToLCNDV, which has been known to infect tomato crops in India for the last two decades, in both samples of tomato and zucchini squash crops (Padidam et al. 1995). Recently, ToLCNDV was reported to infect zucchini squash crops in Italy (Panno et al. 2016). Pepper plants infected with begomoviruses like symptoms exhibiting light mosaic leaf distortion, interveinal and leaf chlorosis, and upward curling of leaf margins combined with large population of the whitefly *Bemisia tabaci* were observed in Basilicata region in Italy. The molecular analysis confirmed the presence of *Tomato yellow leaf curl Sardinia virus* (TYLCSV) in the infected pepper plants (Fanigliulo et al. 2008). In France, TYLCV was reported to infect tomato in a single field in the Camargue district in 1999 (Dalmon et al. 2005; Lefeuvre 2010). *Alfalfa leaf curl virus* (Genus: *Capulavirus*), which is transmitting through *Aphis craccivora* (Roumagnac et al. 2015), was isolated from alfalfa crop showing leaf curl disease in France (Varsani et al. 2017). In Greece, tomato crops grown in greenhouses in several places in Crete, Attiki, and southern Peloponnese showed severe symptoms of TYLCV. Infected plants were infested with high populations of *Bemisia tabaci*. Partial sequencing indicated the identity of TYLCV strain (Avgelis et al. 2001). In Finland, the sequence analysis confirmed the presence of *Plantago lanceolata latent virus* which was infecting flowering plant called *Plantago lanceolata*; this virus belongs to the genus *Capulavirus* (Varsani et al. 2017).

2.4 Geminiviruses in the Middle East Countries

Geminiviruses have emerged as a problem for agriculture in some Middle East countries such as Oman, Iran, Saudi Arabia, Yemen, Jordan, Syria, Kuwait, and Iraq. Generally, begomoviruses constitute the largest number of geminiviruses spreading in the Middle East countries infecting many economically important crops then mastreviruses coming in the second rank in their distribution.

In Oman, the presence of geminivirus was detected first in 1993, when symptoms of tomato leaf curl disease were seen on some tomato and papaya crops (Ministry of Agriculture and Fisheries, Government of Oman). Begomoviruses constitute the largest number of isolated geminiviruses in Oman and affect the most economically important crops in the country. Both types of begomoviruses either with a monopartite or bipartite genome are present in Oman. Most monopartite begomoviruses are associated with DNA satellites. Most begomoviruses that have been identified in Oman are not native to the region. Till now, two betasatellites have been identified in Oman: *Tomato leaf curl betasatellite* (ToLCB) and *Okra leaf curl Oman betasatellite* (OLCOMB) (Al Shihi 2017). The distribution of geminiviruses in Oman is concentrated mostly in Al Batinah Governorate, which constitutes about 85% of agricultural area in Oman. The geminiviruses that have been isolated and characterized in this region belong to begomovirus genus including *Tomato leaf curl Al Batinah virus* (ToLCABV; Khan et al. 2014), *Tomato leaf curl Oman virus* (ToLCOMN; Khan et al. 2008), *Chilli leaf curl virus Oman* (ChLCV-OM; Khan et al. 2013), *Tomato leaf curl Barka Virus* (ToLCBrV; Al Shihi et al. 2014), and *Cotton leaf curl Gezira virus-Al Batinah* (CuLCGV-Al Batinah; Al Shihi et al. 2017). All these begomoviruses were isolated from tomato crops plus ChLCV-OM, which infect both tomato and pepper crops. *Tomato yellow leaf curl virus* (TYLCV-OM) was identified in most regions in Oman including northern part of Oman, Musandam Governorate. This virus constitutes high identity to the Iranian strain (TYLCV-IL) (Khan et al. 2008). Most of these viruses are monopartite begomoviruses and are associated with betasatellites (ToLCB). In the Southern region of Oman, Dhofar Governorate, two monopartite begomoviruses have been identified, *Chilli leaf curl Multan virus* (ToLCMuV) and *Tomato leaf curl Sudan virus* (ToLCSDV) infecting tomato and pepper (Al Shihi 2017). Some bipartite begomoviruses have been seen in some crops such as watermelon, cassava, and bean. *Watermelon chlorotic stunt virus* has been isolated from watermelon (Khan et al. 2012), *East African cassava mosaic virus* isolated from Cassava (Khan et al. 2013), and *Mungbean yellow mosaic Indian virus* from bean (Shahid et al. 2017). One mastrevirus named as *Chickpea chlorotic dwarf virus* (CpCDV) had been isolated from pepper which was collected from Al Sharqia Governorate (Akhtar et al. 2014). This wide distribution of begomoviruses in Oman refers to several factors such as presence of whitefly (*Bemisia tabaci* Genn; Al Shihi and Khan 2013) biotype B which is known as highly aggressive in transmitting begomoviruses worldwide (Brown et al. 2012). In addition, internal transport of plants and plant products among different governorates without proper inspection help to spread pests and diseases. The global movement of agricultural products plays a major role in introducing geminiviruses, and this was indicated to the virus origin. Most begomoviruses that have been identified in Oman have their origin outside the country (Al Shihi 2017). Farmers mostly use F1 tomato hybrid seeds which can offer moderate protection against begomoviruses, and they can get a good protection if floating row cover (AGRYL) is used from the seedling till flowering stage. Al Shihi et al. (2016) stated that covering tomato crops with floating row cover for 6–7 weeks can minimize tomato leaf curl disease and maximize the yield.

The geminivirus infection was detected on several crops in Saudi Arabia. The first report of infection was published in 1957 in tomato crops which showed mosaic-like symptoms grown under field condition (Talhouk 1957). The most important crops that have been infected with begomoviruses in Saudi Arabia are tomato, beans, okra, squash, and cucumber (Idris et al. 2012; Alhudiab et al. 2014). In Jeddah, Sohrab et al. (2016b) reported that *Tomato leaf curl Sudan virus* and *Tomato yellow leaf curl virus* cause leaf curling and yellowing. Okra (*Abelmoschus esculentus* L.) crops showing disease symptoms like leaf curling and whole plant stunting have been reported in Hofuf and Al-Hassa Governorates. Molecular analysis confirmed the presence of *Cotton leaf curl Gezira virus* (CLCuGV) which shares 89% identity with CLCuGV-Egypt isolate (Idris et al. 2014). Bean (*Phaseolus vulgaris* L.) crops showed disease symptoms such as dwarfing, leaf malformation, and vein yellowing, grown under field conditions in Al-Hassa, Hofuf, Eastern Province of Saudi Arabia (Ghanem et al. 2003). The serological analysis confirmed the presence of begomoviruses which has been named as *Bean dwarf mosaic virus* Saudi Arabian isolate (BDMV-SA) (Ghanem et al. 2003). Recently, TYLCV was isolated from cucumber (*Cucumis sativus*) crops which showed mosaic-like symptoms on the leaves (Sohrab et al. 2016b). Weeds can act as alternative hosts for begomoviruses; just recently the natural occurrence of begomovirus on a weed called Corchorus has been reported from Saudi Arabia (Sohrab 2016a).

Iran is one of the main countries growing all kinds of vegetables in the world. The total area harvested with vegetable accounts for about 811,616 hectare (Ha) and yield 264,367 hectogram Hg/Ha. Recently, geminiviruses cause significant losses to many vegetable crops and most of these viruses belong to the genus begomovirus (Farzadfar et al. 2002; Ayazpour 2014). Some begomoviruses like *Tomato yellow leaf curl virus* (TYLCV) infect important crops such as potato, tomato, and cucurbits and can cause significant yield losses. TYLCV was first reported in 1996 from tomato crops grown in the southern provinces of Iran (Bushehr, Khuzestan, Hormozgan, Sistan-va- Baluchestan, and Kerman) (Hajimorad et al. 1996). TYLCV virus was also detected in other plant species such as cucumber (*Cucumis sativus*), pepper (*Capsicum annuum*), alfalfa (*Medicago sativa*), cowpea (*Vigna unguiculata*), cantaloupe (*Cucumis melo* var. cantalupensis), and red pepper (*Capsicum sp.*) (Hosseinzadeh and Garivani 2014; Azadvar et al. 2016; Bananej 2016). Five strains of TYLCV have been identified in Iran including TYLCV-IL, TYLCV-IR, TYLCV-Bou, TYLCV-Ker, and TYLCV-OM. Among these strains, TYLCV-IL is considered the most damaging strain worldwide, and it is present in different provinces of Iran (Lefeuvre et al. 2010; Pakniat et al. 2010). *Tomato Leaf Curl Palampur Virus* (ToLCPMV) is a bipartite begomovirus which was isolated from tomato fields located in the southern region of the country in 2006 (Hormozgan Province). *Tomato Leaf Curl New Delhi Virus* (ToLCNDV) is another destructive bipartite begomovirus species infecting melons in Iran (Yazdani-Khameneh et al. 2013). ToLCNDV is also infecting other crops including tomato, potato, pepper, and cucurbit plants (Hussain et al. 2005). *Tomato Yellow Leaf Curl Iran Virus* (TYLCIRV) is another strain of TYLCV infecting tomato crops which showed typical yellow leaf curl symptoms in the following provinces: Iranshahr, Sistan, and Baluchestan. *Okra Enation Leaf Curl Virus* (OELCuV) was isolated from papaya crops showing leaf curl disease in Bahu Kalat, Zarabad in Sistan-va-Baluchestan. Therefore, papaya was listed as a new species in the natural host range of OELCuV (Bananej et al. 2016). *Watermelon Chlorotic Stunt Virus* (WmCSV) was first identified in Yemen and then in Sudan (Bedford et al. 1994). In 1998, watermelon was found to be severely infected with begomovirus-like symptoms in the south of Iran; the virus was isolated and characterized from plants through molecular analysis. The sequence analysis confirmed the presence of *Watermelon chlorotic stunt virus* (Bananej et al. 1998). *Beet curly top Iran virus* (BCTIV) is a major geminivirus (Genus: *Becurtovirus*) of sugar beet in Iran. Nine genomes of new BCTIV isolates were characterized and sequenced. These genomes were isolated from crops such as cowpea, bean, tomato, and sugar beet showing leaf curling, yellowing, and swelling of veins. The BCTIV is distributed in some fields in north-eastern Iran (Khorasan Razavi, Northern Khorasan), north-western Iran (East and West Azerbaijan), and southern Iran (Fars) provinces (Kardani et al. 2013). The presence of *Bemisia tabaci* in different parts of Iran combined with different climatic conditions seems to encourage the potential spread of these viruses in many new areas of the country (Shahbazi et al. 2010).

Anfoka et al. (2016) reported that tomato plants in Jordan were infected with new begomovirus strain named as *Tomato yellow leaf curl Axarquia virus*. Another virus, *Chickpea chlorotic dwarf virus* (*Mastrevirus* genus), was reported to infect some crops like chickpea and pepper in Yemen, Jordan, Iraq, and Syria (Akhtar et al. 2011; Kumari et al. 2006). In Kuwait, TYLCV is widespread in tomato fields causing a devastating disease since 1993 (Montasser et al. 1999). In Yemen, TYLCV is increasing in tomato-growing regions since the 1970s. It is present in the Abayan and Hadramaut Governorates. Based on partial sequencing, the results indicated that TYLCV from Yemen (TYLCYV) is distinct from other TYLCV isolates (Bedford et al. 1994) (Fig. 3).

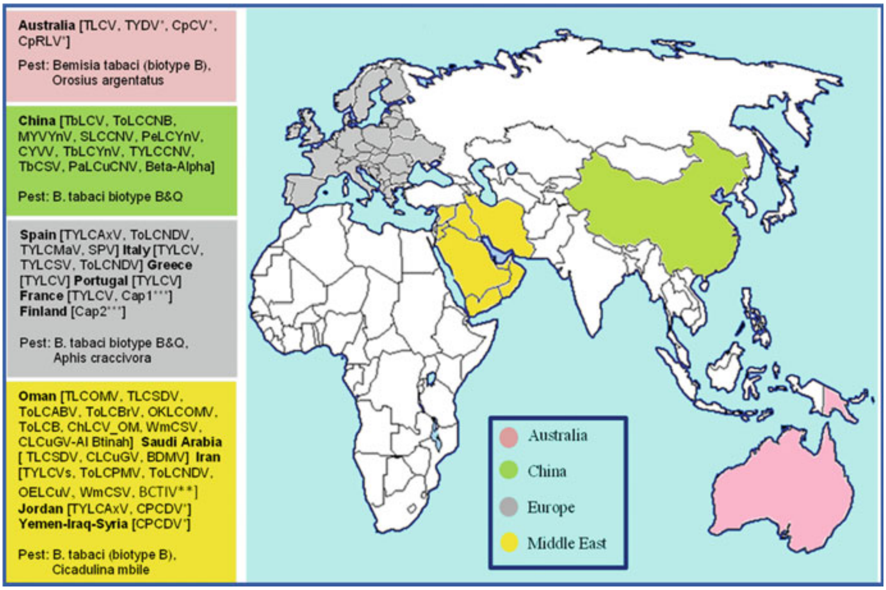

Fig. 3 *World map along with colored boxes showing the geminivurs species and strains in Australia, China, Europe and Middle East countries*. *TLCV Tomato leaf curl virus*; *TYDV** Tobacco yellow dwarf virus, *CPCV** Checkpea chlorosis virus, *CPRLV** Checkpea red leaf virus, Bemisia tabaci biotype B. *TbLCV* Tobacco leaf curl virus, *ToLCCNB* Tomato leaf curl China beta satellite, *MYVYnV* Malvastrum yellow vein Yunnan virus, *SLCCNV* Squash leaf curl China virus, *TYLCCNV* Tomato yellow leaf curl China virus, *PeLCYnV* Pepper leaf curl Yunnan virus, *TbLCYnV* Tobacco leaf curl Yunnan virus, *PaLCuCNV* Papaya leaf curl China virus, *CYVV* China yellow vein virus, *SPV* Sweet potato leaf curl virus, *TYLCV* Tomato yellow leaf curl virus, *TYLCAxV* Tomato yellow leaf curl Axarquia virus, *TYLCSV* Tomato yellow leaf curl Sardinia virus, *TYLCMaV* Tomato yellow leaf curl Malaga virus, *ToLCNDV* Tomato leaf curl New Delhi virus, Cap1***Alfalfa leaf curl virus; Cap2*** Plantago lanceolata latent virus; *ToLCABV* Tomato leaf curl Al Batinah virus, *ToLCBrV* Tomato leaf curl Barka virus, *ToLCSDV* Tomato leaf curl Sudan virus, *CpCDV** Chickpea chlorotic dwarf virus, *ChLCMuV* Chilli leaf curl Multan virus, *ChLCV* Chilli leaf curl virus, *CLCuGV* Cotton leaf curl Gezira virus, *OLCOMV* Okra leaf curl Oman virus, *ToLCPMV* Tomato Leaf Curl Palampur Virus, *BDMV* Bean dwarf mosaic virus. *OELCuV* Okra enation leaf curl virus, *WmCSV* Watermelon chlorotic stunt virus, *BCTIV*** Beet curly top Iran virus, *Mastrevirus, **Becurtovirus, ***Capulavirus, No star means Begomoviruses (Source: Adel Al Shihi)

3 Future Aspects

Available information reveals that these disease complexes are expanding rapidly in terms of their geographical distribution and host range. For instance, ToLCNDV was originally a major problem in India but now it is spreading and causing extensive damage in Spain, Italy, and Iran. In some countries in Europe and the Middle East, new virus strains are emerging and their host range is expanding to other new crops. The presence of such a diverse population of geminiviruses in some regions, combined with the ability of these viruses to exchange their genetic material by recombination, will increase the probability of evolution of new viruses which may emerge and cause epidemics in new unaffected crops. Geminiviruses have a strong impact on most economically important crops which in turn affects the economy value for some crops in most countries. The continual growth in international trade, the movement of infected plants, and the widespread of the whiteflies and leafhoppers will facilitate the spread of geminiviruses. Under any circumstance, identifying and characterizing geminiviruses will help countries in determining the diversity of geminiviruses which later can aid to apply proper quarantine procedures either within the country regions or with other countries. Computer-based databases will offer an excellent choice for obtaining information about geminivirus strains and species present in each country. This can be applied in each quarantine where exchange of information can be provided easily.

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