Plant Viruses Affecting Major Vegetable Crops of the Families *Solanaceae* and *Cucurbitaceae* in Jordan: A Review

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Abstract

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Jordan is a country that has limited water resources and agricultural land. Food security is currently one of the major issues that is getting special attention to overcome hunger. Among the one million hectares that are used for crop production, 40,000 hectares are used for vegetable crops of the family *Solanaceae* (potato, tomato, pepper and eggplant) and *Cucurbitaceae* (squash, cucumber, watermelon and melon) and considered the most important vegetables cultivated in Jordan, and their production is affected by different diseases. Viruses among other pathogens infect vegetables and seriously affect both the quantity and quality of these crops. During the past few decades, many surveys were conducted in Jordan to investigate the occurrence of different viruses that attack important vegetable crops using different biological, serological, and molecular techniques. Many viral pathogens were identified and reported to threaten the production of these crops, and consequently food security in Jordan. The results obtained from these surveys could be used to develop effective strategies for controlling the viruses of economic importance and ensuring the sustainability of the production of important vegetable crops to meet the demands of the growing Jordanian population.

Keywords: Jordan, virus diseases, vegetable crop, *Solanaceae, Cucurbitaceae*.

Introduction

In Jordan, agriculture contributes 5.6% of the country's gross domestic production in 2018 (World Bank, 2021). Jordan has a total area of about 9 million ha, with only around one million ha used for crop production (FAOSTAT, 2024). In 2023, approximately 41,000 ha were planted with vegetables (Annual Statistical Yearbook, 2023). Plants of the family Solanaceae: tomato, *Solanum lycopersicum* L., potato, *S. tuberosum* L.), eggplant, *S. melongena* L. and pepper, *Capsicum annum* L. and family Cucurbitaceae: squash, *Cucurbita pepo*; cucumber, *Cucumis sativus*; melon, *Cucumis melo*; watermelon, *Citrullus lanatus* are considered the most important vegetable crops according to the statistics issued by the Department of Statistics for the year 2023 regarding the cultivated area and production in Jordan.

In Jordan, tomato ranks first among important vegetable crop since its cultivated area is 7,733 ha with a total production of 591,726 tons. The potato cultivated area is 4,815 ha and the total production was 193,728 tons. For eggplant, the total cultivated area was 1,334 ha and the production reached 74,086 tons. The total cultivated area for pepper is 2,845 ha with an annual production of 118,880 tons. The estimated cultivated area for squash is 3,167 ha with an annual production of 86,302 tons and for cucumber was 1,867 ha with annual production of 160,758 tons. For melon, the cultivated area was 1,642 ha and the annual production was 64,756 tons. The cultivated area and the annual production for watermelon were 1,520 ha and 90,054 tons, respectively (Annual Statistical Yearbook, DOS, 2023).

The production of vegetable crops is highly affected by different biotic and abiotic factors (Duan & Lin, 2024). These stresses are estimated to cause a 50% annual yield loss for the major crops worldwide (Shelake *et al.,* 2024). Oraon *et al.* (2024) indicated that biotic stress such as viruses, bacteria, nematodes, and fungi pose a threat to the quantity and quality of agricultural products. It is worth mentioning that plant virus diseases constitute 47% of the worldwide pathogens that cause emerging and re-emerging epidemics of plant disease (Anderson *et al.,* 2004). So far, the International Committee on Taxonomy of Viruses (ICTV) approved more than 2,100 plant virus species (Tatineni & Hein, 2023; Walker *et al.,* 2021). Many of these plant viruses infect plants by producing mild or symptomless diseases. However, several viruses can develop severe disease symptoms threatening the productivity of important crops. In 2014, viral diseases caused an estimated annual yield loss of about 30 billion dollars worldwide (Sastry & Zitter, 2014; Tatineni & Hein, 2023). Since then, the economic impact of virus diseases increased as the global food demand increased because of population increase (Jones, 2021). In a recent review of plant viruses that are considered as pandemic or epidemic diseases, suggested three reasons for the rapid spread of new and severe virus diseases: (i) the trade globalization of plant material and intense international trade, (ii) The movement of the crops away from their domestication area into high plant-density monocrop cultures, and (iii) challenges imposed by climate change (Jones, 2021). Around 71% of the recorded new emergence

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of viruses is a result of new introduction, and almost 17% are caused by changes in the population dynamics of virus vectors. Recombination events of virus mutant strains resulted in 5% of emerging events (Hančinský *et al.,* 2020). In this context, many viruses have been reported to infect the crops in Jordan since the early 1960s until today. Thus, this review provides an up-to-date status of the plant viruses affecting some of the vegetables of economic importance from the families Solanaceae and Cucurbitaceae that were reported in Jordan during the last few decades.

Viruses of solanaceous crops

Around 16,727 ha were planted with solanaceous crops for the year 2023 in Jordan (Annual Statistical Yearbook, DOS, 2023). Crops from the family Solanaceae are used as a source of food and bioactive molecules (medicinal plants). In addition, members of this family can be used as ornamental plants. Many plant viruses were reported to infect solanaceous crops worldwide resulting in reduced yield and quality. In the genus Begomovirus alone, there are around 200 virus species reported to naturally infect Solanaceae species (Hančinský *et al.,* 2020). This section focuses on the viral diseases that have been reported on solanaceous crops in Jordan.

Tomato viruses

The viruses associated with the tomato tallow leaf curl disease (TYLCD) belong to the largest genus of plant viruses, *Begomovirus*, of the *Geminiviridae* family (Marchant *et al.,* 2023; Prasad e*t al.,* 2020). They are transmitted in a circulative, persistent non-propagative manner by the whitefly *Bemisia tabaci* (Gennadius) (Anfoka, *et al.,* 2009a; Yan *et al.,* 2021). Their genome is circular single-stranded monopartite DNA with size of about 2.8 kb (Cohen & Antignus, 1994; Yan et al., 2021). TYLCD symptoms on tomato plants include stunting, reduced leaf size accompanied by upward curling, chlorosis, leading to complete yield loss (Prasad *et al.,* 2020). Tomato yellow leaf curl virus (TYLCV), the major causing agent of TYLCD, was ranked third in the list of the top ten economically important plant viruses, recognized by its global spread, threatening tomato production worldwide (Marchant *et al.,* 2023; Rybicki, 2015; Scholthof *et al.,* 2011).

TYLCD-like symptoms were first observed in the Jordan Valley in the 1930s as cited by Marchant et al., 2023. The disease-causing virus was identified in the 1960s (Cohen & Harpaz, 1964). Later, it was known to be the first identified monopartite begomovirus as reported by Navot et al. (1991). The earliest report of TYLCV in Jordan was in 1978, which was identified in symptomatic tomato plants collected from nine sites in the Jordan Valley (Makkouk, 1978). At that time, this virus was the most broadly spread causing serious economic losses (Makkouk, 1978). On the other hand, one of the very earliest trials conducted in Jordan to control the virus spread was the use of a combination of pesticides against whiteflies combined with mineral oil as demonstrated by Sharaf & Allawi (1981).

In a survey that covered eight locations in the Jordan Valley from 1979 to 1980, it was shown that the incidence of TYLCD ranged from 0.0 to 13.2% in spring-grown tomatoes, whereas it reached 93-100% in fall-grown tomatoes (Al-Musa, 1982). It was estimated that when tomato plants are inoculated 10 weeks after sowing, significant yield loss of up to 63% can be obtained (Al-Musa, 1982). In addition, it was reported that when cucumber plants were planted in rows alternating with tomatoes one month before tomato transplantation, the disease was significantly hampered (Al-Musa, 1982). In another survey conducted nearly during the same period from 1979 to 1982, it was reported that TYLCV was the predominant plant virus affecting tomatoes in the Jordan Valley (Al-Musa & Mansour, 1983).

Al-Musa (1988) demonstrated that TYLCV is transmitted by whiteflies over the summer to wild weeds, tobacco plants, and some ornamental shrubs acting as a reservoir for the virus, which becomes a source of inoculum for infecting tomatoes in the fall. This was later confirmed by Anfoka *et al.* (2017), who characterized at the molecular level, that charlock mustard, *Sinapis arvensis* L. could be a host for the viruses associated with TYLCD.

In 1992, Mansour and Al-Musa determined the host range of the Jordanian isolate of TYLCV, where they demonstrated that *Datura stramonium* as well as tomatoes displayed severe virus symptoms. On the other hand, *Nicotiana glutinosa* and *N. tabacum* cvs. Samsun and Havana 423 did not show any symptoms despite their infection. Moreover, Mansour & Al-Musa (1992) demonstrated the role of *Bemisa tabaci* as a vector, where it was shown that the minimum acquisition time was 60 min and the minimum inoculation feeding period was 30 min. In addition, it was found that the latent period was 20–24 hours and the vector retained the virus for 11 days.

The first molecular characterization of the TYLCV strains infecting tomatoes in Jordan was carried out in a survey conducted during 2002-2003 (Anfoka *et al.,* 2005). In this study, symptomatic tomato leaves were collected from 58 farms in the Jordan Valley, Al-Mafraq, and Amman. The virus strains were characterized by dot blot hybridization, PCR, and sequencing and the strains detected were TYLCV-IL, TYLCV-Mild (TYLCV-Mld), and Tomato yellow leaf curl Sardinia virus-ES (TYLCSV-ES) (Anfoka *et al.,* 2005). During the period 2005-2007, multiplex PCR was used to detect TYLCV strains in tomato samples collected from the Jordan Valley, Madaba, Amman and Homret Al-Sahen (Anfoka *et al.,* 2009a). The most dominant strain was TYLCV-IL followed by TYLCV-Mld. TYLCSV-ES and for the first time TYLCSV-Sic was also detected (Anfoka *et al.,* 2009a). During this study the full-length sequence of TYLCV was determined and submitted to GenBank, and given the accession number EF054893 (Anfoka *et al.,* 2009a).

In 2013, severe TYLCD symptoms were detected on tomato plants infected with TYLCV in the field. Investigation with PCR using primers amplifying betasatellites revealed that the samples were co-infected with a betasatellite that has high similarity to Okra leaf curl virus (OkLCV) satDNA 10 and Cotton leaf curl Gezira betasatellite (CLCuGβ) in association with TYLCV (Anfoka *et al.,* 2014a). CLCuGβ was also detected in the weed reservoir Charlock mustard, Sinapis arvensis L. plants in Amman, Jordan (Anfoka *et al.,* 2017).

The TYLCAxV-Sic2 recombinant strain was first detected in symptomatic tomato plants in Homret Al-Sahen region in 2013 (Anfoka *et al*., 2016a). In this study, it was demonstrated that this recombinant strain might have originated from a recombination event between the Jordanian isolates of TYLCV and TYLCSV. A dimeric infectious clone was constructed from this isolate, which could successfully induce severe typical TYLCD symptoms (Anfoka *et al.,* 2016a).

Alfalfa mosaic virus (AMV) was reported to develop mosaic and stunting symptoms in tomato plant samples that were collected from Jordan Valley (Nienhaus & Saad, 1967). Cucumber mosaic virus (CMV) and Tobacco mosaic virus (TMV) were also reported by Nienhaus & Saad, (1967) to cause severe mosaic symptoms, shoe stringing, and necrosis in tomato plants collected from Jordan. A few years later, Al-Musa & Mansour, (1983) conducted a survey during the period 1979–1982 aiming to detect plant viruses infecting tomatoes in Jordan Valley and found that CMV, TMV, and Potato virus Y (PVY) are causing mosaic disease in tomato plants.

Anfoka *et al.* (2006) reported the occurrence of Tomato spotted wilt virus (TSWV) for the first time in Jordan. Tomato samples were collected from plants showing disease symptoms, and then the capsid protein of the virus was amplified by RT-PCR, sequenced, analyzed, and deposited in GenBank. Abu-Shirbi *et al.* (2012) indicated shortly later that TSWV has the highest incidence either in single or mixed infection together with other viruses detected in tomato plants collected from the Jordan Valley. In a survey conducted by Abu-Shirbi (2012) to detect viruses that infect tomato in the open fields of the southern Jordan Valley, Tobacco etch virus (TEV), Tobacco rattle virus (TRV), Tomato aspermy virus (TAV), Tomato bushy stunt virus (TBSV), and Tomato ring spot virus (ToRSV) were detected, in addition to TSWV, CMV, and PVY. TBSV and ToRSV that were reported later by Mansour *et al.* (2014) in tomatoes under greenhouse conditions during the fall growing season of 2011-2012 in the Jordan Valley. Few years earlier, ToRSV was detected in tomato plants that were grown close to two fruit orchards by enzyme-linked immunosorbent assay (ELISA) when Al-Nsour *et al.* (2010) tried to look for the virus in stone fruit trees and other hosts in different governorates of Jordan during the period 2000-2002.

In another study, testing tomato leaves showing interveinal and general yellowing led to the first detection of Tomato infectious chlorosis virus (TICV) by Anfoka and Abhary (2007) using RT-PCR. This detection was followed by a survey for the virus in the Jordan Valley using non-radioactive dot blot hybridization to discover a high incidence of the virus. In addition, TICV was detected in weed species such as *Chenopodium album* and *C. murale* that could serve as a source of the virus to initiate new infections. Haj Ahmad *et al.* (2013) detected other viruses that commonly cause virus disease in cucurbits such as Squash leaf curl virus (SLCV) and Watermelon chlorotic stunt virus (WmCSV) in tomato plants as a first record in Jordan. In 2015, Salem et al. reported the first incidence of Tomato chlorosis virus (TCV) in tomato plants showing interveinal yellowing, leaf downward rolling, and thickening symptoms in the Jordan Valley. The virus was found to be transmitted by whiteflies to healthy tomato plants, after an acquisition period of 48 hours.

Salem *et al.* (2016) reported the occurrence of an emerging plant virus disease that showed mild foliar symptoms and brown rugose fruits in 100% of symptomatic tomato plants. The virus was identified as Tomato brown rugose fruit virus (ToBRFV), after testing these samples for plant viruses that commonly infect tomato in Jordan. The Jordanian isolate of ToBRFV was identified by Salem *et al.* (2016) based on the full-length genome sequencing of the isolated virus, which has a single-stranded RNA genome of 6393 bases encoding for four open reading frame (ORFs): replication-related proteins (ORF1a and ORF1b), movement protein (ORF2), and coat protein (ORF3). Further experiments were carried out to investigate the seed transmission of ToBRFV. The virus was found to be located on the seed coat but this could initiate infection at a low rate (Salem *et al.,* 2022).

Pepper viruses

The first report of the incidence of plant viruses infecting pepper crops in Jordan refers to the year 1967. At that time, Nienhaus & Saad, (1967) detected AMV in the chili pepper *Capsicum frutescens*. During the winter seasons of 2015-2016, pepper plants, *Capsicum annuum* L. showing stunting, puckering, and yellow mottling of leaves symptoms were collected from plastic houses in the Jordan Valley by Salem *et al.* (2020a). Tobacco mild green mosaic virus (TMGMV) and ToBRFV were detected in the tested samples. The amplified fragment of RdRp gene and CP gene (accessions MK816313 to 16) of TMGMV shared 96% identity with the genome sequences of the virus already deposited in the Genbank. In the case of ToBRV, around 56% of 39 of the tested samples were positive for the virus when ToBRFV-specific primers were used to amplify RdRp and CP genes by RT-PCR. Results obtained by Salem *et al.* (2020a) were the first record of these two viruses infecting pepper crops in Jordan

Potato viruses

Several viruses have been reported to infect potatoes in Jordan until now. PVY and potato virus X (PVX) were identified in potato fields in Jordan Valley and highlands depending on host range, symptoms, transmission, serology, and electron microscopy in a survey conducted by Al-Mnayer (1985). In this survey, Al-Mnayer reported that PVY was dominant over PVX in most of the samples collected in winter during the growing season of 1984-1985. In the highlands, PVX infection occurred in 24% of the samples collected during the spring season, whereas PVY was predominant in the summer season of the same year. A few years later, Nimer (1993) reported that potato fields in Jordan had infections of PVY in addition to Potato virus A (PVA).
Viruses infecting potatoes have been spreading, as Mansour (1999) reported that potato fields in Jordan are facing serious problems caused by viral agents. Mansour (1999) performed a study to evaluate the role of quarantine regulations in eliminating viral infection of potatoes in Jordan Valley. Typical viral symptoms of PVY, PVA, and Potato leafroll virus (PLRV) were observed in about 66-94% of the potato

plants in the field. PLRV has the highest incidence, followed by PVY and PVA, respectively.

In a survey performed during the potato growing season 2006-2007 by Odeh (2007), 466 leaf samples showing viral symptoms such as necrosis, leaf rolling, chlorosis, etc. from different regions of Jordan (north and south Jordan Valley, Naur, Al-Baqaa, Al-Ramtha, Irbid, and AL-Mafraq) were collected and tested to detect the incidence of five potato viruses: PVY, PVY, PVX, PLRV, and Potato virus M (PVM). PVY had the highest relative incidence among tested potato viruses. Around 56% of the tested samples showed positive results for PVY when tested by ELISA, followed by PLRV (6.9%), then PVX (0.25%). In this study, PVA and PVM were not detected in potato fields in Jordan.

Odeh (2007) Characterized the potato viruses detected in Jordan at the molecular level by amplifying and sequencing the CP gene of the PVY, PVX, and PLRV, and the obtained sequences were deposited in the GenBank. Moreover, the PVY isolates collected were tested for the different PVY strains available in Jordan. The PVY strains that were detected are: EU-PVY$^{N/NTN}$, NA-PVY$^{N/\ NTN}$, PVY$^{N/NTN}$, PVY^{O,} and PVY^{N}. All surveyed regions showed around 85% infection with both PVY^{O} and PVY$^{N/NTN}$. Around 80% of the samples tested were identified as PVY$^{N/NTN}$, whereas around 39% of the samples were identified as PVY^{O}. All these isolates of the different PVY strains were identified by multiplex PCR and then uniplex PCR, sequenced, and the sequences were deposited in the GenBank.

Anfoka *et al.* (2014b) reported the occurrence of PVY recombinant strain PVY^{NTN} for the first time in Jordan from samples collected from potato plants showing symptoms of potato tuber necrotic ringspot disease (PTNRD) in Wadi Rum (South Jordan). PVY Strain N-Wilga was reported for the first time in Jordan's north and east parts by Anfoka *et al.* (2016b).

Eggplant viruses

Only two viruses were reported to infect eggplants in Jordan. One of these viruses is the Eggplant Mottled Dwarf Virus (EMDV), which was detected in eggplants showing stunting and vein yellowing by Al-Musa & Lockhart (1990), depending on the host range, aphid transmission, and serology. The other virus Cowpea mild mottle virus (CPMMV) was detected in 100 leaf samples of eggplants showing mild leaf mosaic symptoms in Jordan Valley in the growing seasons of 1986 and 1987 using ELISA (Mansour *et al.* 1998).

Viruses of Cucurbit crops

In Jordan, around 9,000 hectares were planted with cucurbits during 2023 (Annual Statistical Yearbook, DOS, 2023). Cucurbit crops are vulnerable to a wide range of plant viruses that have a great impact on the sustainability of these crops (Velasco *et al.,* 2020). Cucurbits all over the world have been reported to be affected by more than 90 viruses (Desbiez, 2020). In 2012, Lecoq & Desbiez reported the presence of 28 plant viruses infecting cucurbits in the Mediterranean region; some of these viruses cause serious crop losses such as Zucchini yellow mosaic virus (ZYMV). However, from 1977 until 2012, new viruses were detected, one every two years, on average (Lecoq & Desbiez, 2012). The emergence of a new virus disease infecting cucurbit crops resulted in great yield losses and threats to food security. Since virus diseases have been emerging for decades on cucurbits and other crops for the reasons described earlier in the introduction (Radouane *et al.,* 2021)., this section summarizes the viruses that have been reported on the important cucurbits (squash, cucumber, melon and watermelon) in Jordan

Melon and watermelon viruses

In Jordan, melons are considered important cash crops. They are planted twice during the year: in the winter in the southern Jordan Valley and in the summer in the highlands: the Madaba, Baqa, Mafraq, and Jerash regions (Al-Musa et al. 2011). Watermelon mosaic virus (WMV) is one of the most dominant viruses on cucurbit in Mediterranean countries and is the most prevalent cucurbit virus in the region (Lecoq & Desbiez 2012). One of its strains was watermelon mosaic virus- 2 (WMV-2), a strain which was isolated and first reported in Jordan in 1982 from squash and melon plants (Al-Musa & Mansour, 1982). Different aphid Species are recorded as vectors for this virus in a non-persistent manner: *Aphis gossypii, A. fabae and Myzus persicae*. Systemic infection is expressed as vein chlorosis, green mosaic deformation, and necrotic leaf spots in many melon cultivars followed by plant collapse. Severely discolored and distorted fruits are obtained following early plant infection (Kurowski *et al.,* 2015).

Cucumber vein yellowing virus (CVYV) was recorded in Jordan to infect cucumber. A host range study demonstrated that this virus can infect different cucurbitaceous plants including melon and watermelon (Al-Musa *et al.,* 1985), causing a range of symptoms from vein yellowing to chlorosis and necrosis depending on the cucumber cultivar and cucurbit variety (Mansour & Al-Musa, 1993). Infected melons show vein clearing, vein yellowing, necrosis, chlorosis, and plant stunting with a high reduction in yield. In watermelon, foliar symptoms are not clearly expressed, only fruit cracking was detected (Kurowski et al., 2015).

Cucurbit yellow stunting disorder virus (CYSDV) was detected in Jordan for the first time in 1995 (Duffus, 1995). After that, it was detected in 9 out of 31 commercial cucurbits collected samples from Jordan. CYSDV isolates showed 99% identity with isolates from Spain and Türkiye (Rubio *et al.,* 1999). In addition, this virus was reported to affect melon plants as well as watermelon plants in several areas in Jordan including Al-Mafraq, AL-Karak, Al-Tafila, AL-Balqa, and Jordan Valley. Sequencing revealed that Jordanian isolates of this virus were closely related to those from the Americas, suggesting low genetic diversity across regions (Sweiss *et al.,* 2007). The vector of this virus is Silverleaf whitefly, *Bemisia tabaci* biotypes B and Q. Infected melons show the most pronounced symptoms, which can be misleading for nutrient deficiencies or other yellowing viruses. Melon fruit may not display noticeable symptoms, but its sugar content can be significantly reduced. Symptoms begin on older leaves with interveinal mottling, which worsens over time and eventually affects the entire plant. While the veins stay relatively green, the rest of the leaf turns yellow. The leaves may curl upward and become brittle (Kurowski *et al.,* 2015). Viruses associated with TYLCD (TYLCSV, TYLCV-IL and TYLCV-Mld) were detected to infect melon and watermelon that are grown in the Jordan Valley adjacent to TYLCD-infected tomato fields (Anfoka *et al.,* 2009b).

WmCSV is a major pathogen transmitted by whiteflies *Bemisia tabaci*. It was first reported in Jordan by Al-Musa *et al.* (2011), detected in melon and watermelon samples collected from Jordan Valley and Al-Mafraq. Mixed infections of WmCSV with other viruses such as the SLCV can lead to more severe disease symptoms and increased yield losses. WmCSV isolated in Jordan shares high sequence homology (97.6–99.4%) with isolates from other countries, such as Sudan, Yemen, Lebanon, and Iran, indicating a close genetic relationship between these isolates. WmCSV causes severe symptoms in watermelon plants, including vein yellowing, chlorotic mottling, leaf curling, and stunting (Al-Musa *et al.,* 2011).

Recently, squash vein yellowing virus (SqVYV) was reported to infect melons in Jordan. Hussein et al (2024) highlighted SqVYV as a new threat to cucurbit production in Jordan. A total of 14 melon and 7 watermelon symptomatic leaves were collected for testing. Using molecular diagnostic tools, SqVYV was detected in combination with other viruses in 3 melon samples but not in watermelon samples. BLASTn analysis of four cloned amplicons of cylindrical inclusion (CI) gene confirmed the identification of SqVYV, with the highest identity of ~91% to an isolate from the USA (MW584342). cDNA library conducted from the total RNA of squash and melon pool to reconstruct the complete genome sequence of Jordanian isolate to generate 18,723,252 total reads. The deduced polyprotein sequence and complete genome sequence have over 99% similarity with SqVYV-IL (Hussein *et al.,* 2024). The symptoms observed on virus-infected watermelon appeared first as chlorotic leaves, followed by browning and collapse of the entire vine during few weeks. When fruits mature, symptoms develop rapidly with flesh discoloration and internal rind (Kurowski *et al.,* 2015).

Squash viruses

Nienhaus & Saad (1967) reported that squash plants were infected with CMV for the first time in Jordan. Later in 1976, Squash mosaic virus (SqMV) was first detected in squash by Mink in addition to CMV (Mink, 1976; Al-Musa & Mansour, 1982). Watermelon mosaic virus-1 (WMV-1) was identified in Jordan in a sample collected by Martelli and Russo in 1976. This isolate was initially characterized as WMV-2, and then identified as WMV-1 based on serological tests (Purcifull & Hiebert, 1979). WMV-1 is now considered as a strain of Papaya ring spot virus (PRSV). Whilst the first report of WMV-2 was in 1982, it was detected in squash and melon plants that showed deformed fruits, with mosaic and blisters on leaves (Al-Musa and Mansour, 1982). Furthermore, host range studies showed that squash can be a host for the CVYV that was isolated from cucumber in Jordan (Al-Musa *et al.,* 1985).

In addition to the previously mentioned viruses, ZYMV was detected in 68-100% of cucurbit samples collected during the years 1987-1988 (Al-Musa, 1989). CYSDV was reported on cucurbits collected from Jordan in 1999 (Rubio *et al.,* 1999), and later in another study, it was detected in 58.5% of 2344 collected samples from cucurbits throughout the years 2005-2006 (Sweiss *et al.,* 2007). SLCV was reported in Jordan infecting squash samples collected in 2005 from Jordan Valley and the highlands (Al-Musa *et al.,* 2008). Moreover, TYLCSV, TYLCV-IL, and TYLCV-Mld were reported to infect cucurbit crops including squash that are grown adjacent to tomato fields infected with TYLCD in Jordan (Anfoka *et al.,* 2009b).

During the period 2004-2006, around 909 squash samples were collected from the Jordan Valley for a study aimed to identify viruses that infect squash in Jordan Valley and Southern Syria using ELISA. The results reported the presence of 15 viruses infecting squash, with the most predominant viruses were in a decreasing order as follows: ZYMV (53.2%), SLCV (43.78%), Cucumber green mottle mosaic virus (CGMMV, 40%), WMV (30.47%), PRSV (25.63%), and CMV (23.65%). The less common viruses were: TSWV (4.46%), Tobacco ring spot virus (TRSV, 3.08%), SqMV (1.98%), Arabis mosaic virus (ArMV, 1.43%), Lettuce mosaic virus (LMV) (1.43%), AMV (1.1%), ToRSV (0.88%), Tomato black ring virus (ToBRV) (0.44%) and TBSV (0.39%). All these less common viruses were reported for the first time on squash in Jordan except the AMV and SqMV (Al-Tamimi et al., 2009). During the same period, squash samples were collected for molecular identification for the ZYMV using RT-PCR, and the isolate JOR-N3 showed 100% identity with ZYMV obtained from Japan with the accession number (AB004641) (Al-Tamimi et al., 2010). The molecular identification made for an SLCV from Jordan showed 95% identity with an isolate obtained from Syria, as well as with an SLCV isolate from Egypt (Al-Tamimi *et al.,* 2011).

An isolate of WmCSV from Jordan (WmCSV-JO) was molecularly characterized by genome sequencing. Among 1060 symptomatic samples collected, only 98 samples (9.4%) were found infected. Host range study confirmed that this virus can infect squash, cucumber, pumpkin, melon, watermelon, *Nicotiana benthamiana*, and *N. glutinosa* (Al-Musa *et al.,* 2011). In 2024, SqVYV was first detected in 10 out of 70 symptomatic cucurbit samples collected in 2022 from the Jordan Valley, highlands, and desert areas using RT-PCR with SqVYV-specific primers. SqVYV was detected in four squash samples, three cucumber samples, and three melon samples. Furthermore, the complete genome was sequenced using NextSeq 2000 instruments and deposited in GenBank under the accession number PP916052. The sequencing results showed 99% identity with SqVYV-IL. In addition to SqVYV, nine samples were infected with CGMMV, 34 samples with CYSDV, whereas CVYV, Cucurbit Chlorotic Yellows Virus (CCYV), and cucurbit aphid-borne yellows virus (CABYV) were detected in 18, 23, and 7 samples, respectively. On the other hand, among plant DNA viruses detected in 70 samples, 36 were infected with SLCV, and 30 were infected with WmCSV (Hussein *et al.,* 2024).

Cucumber viruses

In 1967, CMV was first reported in Jordan infecting cucumbers (Nienhaus & Saad 1967). After that, CVYV was reported to affect cucumbers in the Jordan Valley, and infected plants were stunted with vein yellowing of the leaves. In addition, it was reported that cucurbits were the only host for this virus (Al-Musa *et al.,* 1985; Qusus, 1983). In 2012, the full CVYV genome sequence of a Jordanian isolate with severe symptoms was published. The similarity for the complete genome between severe and mild isolates was 94%, and 96% for the amino acid sequence (Galipienso *et al.,* 2012). ZYMV was detected to predominantly infect cucurbits during 1987-1988 (Al-Musa, 1989). CYSDV, a whitefly-transmitted virus, was reported to affect cucumber crops in Jordan (Sweiss *et al.,* 2007). In 2005, SLCV was detected in 39% of cucumber samples collected from four fields in the Jordan Valley (Al-Musa *et al.,* 2008).

Viruses associated with tomato yellow leaf curl disease (TYLCD) including TYLCSV, TYLCV-IL, and TYLCV-Mld were reported to infect cucumber crops cultivated close to tomato fields that were affected by TYLCD (Anfoka et al., 2009b). In 2011, around 9.4% of the collected cucurbit samples were infected with WmCSV. An isolate from Jordan (WmCSV-JO) was molecularly characterized by genome sequencing. The virus has a bipartite genome (DNA-A and DNA-B), the sequences of the DNA segments were submitted to the GenBank under accession numbers EU561237 and EU561236. DNA-A had 99.42% nucleotide identity with WmCSV-IL (LEF201809), whilst DNA-B had the highest nucleotide identity (95.52%) with WmCSV-YE (AJ012082). The host range study showed that the virus could be detected in the following inoculated plants: cucumber, squash, pumpkin, melon, watermelon, *Nicotiana benthamiana*, and *N. glutinosa* (Al-Musa *et al.,* 2011). Cucurbit chlorotic yellows virus (CCYV) was first reported in Jordan by Salem *et al.* (2020b). When 185 symptomatic cucumber samples cv. Banan were collected in 2017 from the Jordan Valley, CCYV was detected in 82.1% of these samples using RT-PCR-specific primers. In addition, around 25.94% of the samples were infected with CYSDV, and 5.4% were infected with CVYV (Salem *et al.,* 2020b). SqVYV was first detected in 14.28% of 70 symptomatic cucurbit samples collected in 2022 from the Jordan Valley, highlands, and desert areas using RT-PCR, and the full genome of this virus was sequenced (Hussein *et al.,* 2024).

Conclusions

It can be concluded from the above that around 40 different viruses were detected on solanaceous crops (tomato, potato, pepper, and eggplant), and cucurbit crops (squash, cucumber, watermelon, and melon) in Jordan. Table 1 summarizes the detected viruses, their classification, and the hosts they infect. It is noteworthy that the Jordan Valley is a favorable environment for the occurrence of virus diseases as reported by several workers. The Jordan Valley is considered an important region for producing agricultural products for export, with tomatoes representing 85% of the exported products (Kool, 2016). Therefore, the high incidence of virus diseases in such a major agricultural region poses a negative impact on yield (quantity and quality) that seriously affects the food security of the country, especially because its population has been increasing rapidly over the last decade.

The epidemiology of plant viruses was greatly affected by climate change. The parameters of climate change influence the sustainability of viral resistance that can be broken under unfavorable environmental conditions and could be the reason for the emergence and evolution of new viruses. Likewise, climate change alters the population dynamics of the vectors of the viruses, which enhances the spread of virus diseases.

Plant viruses are spreading very fast in addition to the emergence of new viruses that magnify their impact on cultivated crops. For example, in the case of ToBRFV, after reporting the first incidence of this virus in tomato plants in Jordan by Salem et al. (2016), shortly thereafter, this virus was reported on peppers (Salem *et al.,* 2020a). The virus is now spreading in 37 tomato-producing countries in Asia, Africa, Europe, and North America leading to great economic losses and affecting the worldwide production of tomatoes (Caruso *et al.,* 2022; Zhang *et al.,* 2022). Most of the viruses reported in this study were also reported in the surrounding countries such as Syria, Iraq, Saudi Arabia, Egypt, and Palestine (Alhudaib *et al.,* 2018; Alkowni, 2017, Amer & Mahmoud, 2020; Ismaeil *et al.,* 2023; Khalifa *et al.,* 2024; Mohammed & Lahuf, 2023). To minimize the widespread of plant viruses, quarantine regulations should be adopted seriously within a single country and between different countries to minimize the spread of plant viruses from one country to another (Jones, 2021).

Certification programs that produce virus-free plants or seeds are considered an essential approach to guarantee that the starting planting material is virus-free before it is distributed to farmers. Meristem culture has been used effectively to obtain virus-free potato tubers for seed production (Naik & Buckseth, 2018). Lethal mutagenesis increases the mutation rate of the RNA genome of the virus resulting in the loss of infectivity of TMV in *N. tabacum*. (Díaz-Martínez *et al.,* 2018).

Plant viruses cannot be controlled by chemical treatment of the infected plant, making controlling plant diseases of viral origin a critical issue. However, chemical treatment and many other approaches of integrated pest management can reduce the vector populations and consequently hinder the infection cycle of the virus. Insecticides could be used to reduce the population of insect vectors such as whiteflies and aphids, which are considered the main vectors of most viruses.

Many of the above-mentioned reports indicated that viruses not only infect important solanaceous and cucurbit crops, but these viruses were also detected in neighboring weeds that act as a natural reservoir of the plant viruses and considered a good inoculum source for the virus (Al-Musa, 1988; Anfoka *et al.,* 2017; Anfoka & Abhary, 2007). These virus-harboring weeds could start new infections when planting the seedlings of the vegetable crop. It is recommended to remove such virus sources from the field before planting a new crop.

The most effective method to manage plant viruses is to use virus-resistant cultivars. Breeding programs that involve the introgression of resistance genes into susceptible varieties are successfully developed for different crops worldwide. The introgression of TYLCV resistance genes (*Ty-1*, *Ty-2, Ty-3, Ty-4, ty-5, Ty-6*) from wild relatives to susceptible cultivated tomatoes is a good example (Gill *et al.,* 2019; Hutton *et al.,* 2012; Lapidot *et al.,* 2015; Yan *et al.,* 2018). With advances in molecular biology, new approaches such as RNA interference and CRISPR-Cas have been used to enhance virus resistance in cultivated crops (Tatineni & Hein, 2023).

Finally, all these control approaches should be used combined to ensure effective virus diseases management. In addition to the methods mentioned previously; good cultural practices will improve the health status of the cultivated crops. Crop rotation for example will break the infection cycle of the virus when non-host crops are planted in the fields where high incidence of the target virus is common.

Table 1. Viruses reported to infect solanaceous and cucurbit crops in Jordan.

Virus	Abbreviation	Genus	Family	Host	Reference*
Alfalfa mosaic virus	AMV	*Alfamovirus*	*Bromoviridae*	Tomato, Pepper, Squash	11, 29
Arabis mosaic virus	ArMV	*Nepovirus*	*Secoviridae*	Squash	11
Cowpea mild mottle virus	CPMMV	*Carlavirus*	*Betaflexiviridae*	Eggplants	24
Cucumber green mottle mosaic virus	CGMMV	*Tobamovirus*	*Virgaviridae*	Squash	11, 22
Cucumber mosaic virus	CMV	Cucumovirus	Bromoviridae	Tomato, Squash, Cucumber, Melon	5, 11, 29
Cucumber vein yellowing virus	CVYV	*Ipomovirus*	*Potyviridae*	Squash, Cucumber, Melon	6, 20, 22, 23, 32, 37
Cucurbit aphid-borne yellows virus	CABYV	*Polerovirus*	*Luteoviridae*	Squash	22
Cucurbit chlorotic yellows virus	CCYV	*Crinivirus*	*Closteroviridae*	Squash, Cucumber	22, 37
Cucurbit yellow stunting disorder virus	CYSDV	*Crinivirus*	*Closteroviridae*	Squash, Cucumber, melon	33, 38, 39
Eggplant mottled dwarf virus	EMDV	*Nucleorhabdovirus*	*Rhabdoviridae*	Eggplants	3
Lettuce mosaic virus	LMV	*Potyvirus*	*Potyviridae*	Squash	11
Papaya ring spot virus	PRSV	*Potyvirus*	*Potyviridae*	Squash	11
Potato virus Y	PVY	*Potyvirus*	*Potyviridae*	Potato, Tomato	1, 2, 5, 26, 29, 30, 31
Potato virus X	PVX	*Potexviruses*	*Alphaflexiviridae*	Potato	2, 29, 31
Potato virus A	PVA	*Potyvirus*	*Potyviridae*	Potato	26, 30
Potato leafroll virus	PLRV	*Polerovirus*,	*Luteoviridae*	Potato	26, 29, 31
Squash leaf curl virus	SLCV	*Begomovirus*	*Geminiviridae*	Tomato, Squash, Cucumber	7, 11, 13, 21
Squash mosaic virus	SqMV	*Comovirus*	*Secoviridae*	Squash	4, 11, 28
Squash vein yellowing virus	SqVYV	*Ipomovirus*	*Potyviridae*	Squash, Cucumber, Melon	22
Tobacco etch virus	TEV	*Potyvirus*	*Potyviridae*	Tomato	1
Tobacco mild green mosaic virus	TMGMV	*Tobamovirus*	*Virgaviridae*	Pepper	36
Tobacco mosaic virus	TMV	*Tobamovirus*	*Virgaviridae*	Tomato	5, 29
Tobacco rattle virus	TRV	*Tobravirus*	*Virgaviridae*	Tomato	1
Tobacco ring spot virus	TRSV	*Nepovirus*	*Secoviridae*	Squash	11
Tomato aspermy virus	TAV	*Cucumovirus*	*Bromoviridae*	Tomato	1

Virus	Abbreviation	Genus	Family	Host	Reference*
Tomato black ring virus	ToBRSV	*Nepovirus*	*Secoviridae*	Squash	11
Tomato brown rugose fruit virus	ToBRFV	*Tobamovirus*	*Virgaviridae*	Tomato, Pepper	35, 36
Tomato bushy stunt virus	TVSV	*Tombusvirus*	*Tombusviridae*	Tomato, Squash	1, 11, 25
Tomato chlorosis virus	TCV	*crinivirus*	*Closteroviridae.*		34
Tomato infectious chlorosis virus	TICV	*Crinivirus*	*Closteroviridae*	Tomato	14
Tomato ring spot virus	ToRSV	*Nepovirus*	*Secoviridae*	Tomato, Squash	1, 10, 11, 25
Tomato spotted wilt virus	TSWV	*Tospovirus*	*Bunyaviridae*	Tomato, Squash	1, 11, 16
Tomato yellow leaf curl Axarquia virus	TYLCAxV-Sic2	*Begomovirus*	*Geminiviridae.*	Tomato	16
Tomato yellow leaf curl Sardinia virus (and its strains)	TYLCSV	*Begomovirus*	*Geminiviridae.*	Tomato, Cucumber, Squash, Melon	15, 17, 18
	TYLCSV-ES	*Begomovirus*	*Geminiviridae.*	Tomato	17
	TYLCSV-Sic	*Begomovirus*	*Geminiviridae.*	Tomato	17
Tomato yellow leaf curl virus (and its strains)	TYLCV	*Begomovirus*	*Geminiviridae.*	Tomato	1, 5, 9, 15, 18
	TYLCV-IL	*Begomovirus*	*Geminiviridae*	Tomato, Cucumber, Squash, Melon	17
	TYLCV-MID	*Begomovirus*	*Geminiviridae*	Tomato, Cucumber, Squash, Melon	15, 17
Watermelon chlorotic stunt virus	WmCVS	*Begomovirus*	*Geminiviridae*	Tomato, Squash, Cucumber, Melon, Watermelon	8, 21, 22
Watermelon mosaic virus-1 (a strain of PRSV)	WMV-1	*Potyvirus*	*Potyviridae*	Squash	27
Watermelon Mosaic virus (Watermelon mosaic virus-2)	WMV WMV-2	*Potyvirus*	*Potyviridae*	Squash, Melon	4
Zucchini yellow mosaic virus	ZYMV	*Potyvirus*	*Potyviridae*	Squash, Cucumber	9, 11, 12

* (1) Abu-Shirbi *et al.*, 2012; (2) Al-Mnayer, 1985; (3) Al-Musa & Lockhart, 1990; (4) Al-Musa & Mansour, 1982; (5) Al-Musa & Mansour, 1983; (6) Al-Musa *et al.*, 1985; (7) Al-Musa *et al.*, 2008; (8) Al-Musa *et al.*, 2011; (9) Al-Musa, 1989; (10) Al-Nsour *et al.*, 2010; (11) Al-Tamimi *et al.*, 2009; (12) Al-Tamimi *et al.*, 2010; (13) Al-Tamimi *et al.*, 2011; (14) Anfoka & Abhary, 2007; (15) Anfoka *et al.*, 2005; (16) Anfoka *et al.*, 2006 ; (17) Anfoka *et al.*, 2009a; (18) Anfoka *et al.*, 2014a ; (19) Anfoka *et al.*, 2016a; (20) Galipienso *et al.*, 2012; (21) Haj Ahmad *et al.*, 2013 ; (22) Huseein *et al.*, 2024; (23) Mansour & Al-Musa 1993; (24) Mansour *et al.*, 1998; (25) Mansour *et al.*, 2014 ; (26) Mansour, 1999; (27) Martelli & Russo, 1976; (28) Mink, 1976 ; (29) Nienhaus & Saad, 1967 ; (30) Nimer, 1993; (31) Odeh, 2007; (32) Qusus, 1983; (33) Rubio *et al.*, 1999; (34) Salem *et al.*, 2015; (35) Salem *et al.*, 2016; (36) Salem *et al.*, 2020a; (37) Salem *et al.*, 2020b; (38) Salem *et al.*, 2024; (39) Sweiss *et al.*, 2007.

الملخص

عودة، وفاء حسني، ميس عاهد صويص، فاطمة وليد حاج أحمد ولينا إرشيد. 2026. الفيروسات النباتية المؤثرة في أهم محاصيل الخضار التابعة للعائلة الباذنجانية والعائلة القرعية في الأردن: مراجعة علمية. مجلة وقاية النبات العربية، 44(1):1-12.
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يعدّ الأردن من البلاد ذات الموارد المحدودة من المياه والأراضي الزراعية. يشكل الأمن الغذائي حالياً واحدة من القضايا الرئيسية التي تحظى باهتمام كبير للتغلب على الجوع والفقر. تستحوذ زراعة الخضار حالياً على 40,000 هكتار من أصل مليون هكتار تُستخدم لإنتاج المحاصيل الزراعية في الأردن.. تعدّ خضار العائلة الباذنجانية (البطاطا/البطاطس، البندورة/الطماطم، الفلفل والباذنجان) والعائلة القرعية (الكوسا، الخيار، البطيخ والشمام) من أهم الخضروات المزروعة في الأردن. يواجه إنتاج الخضروات في الأردن تحديات كثيرة، مثل الإصابات المرضية المختلفة ومنها الفيروسات التي تشكل تحدياً وخطراً كبيراً على إنتاج هذه المحاصيل ذات القيمة الإقتصادية العالية مما يؤثر على إنتاجيتها كمّا ونوعاً. خلال العقود القليلة الماضية، أجريت في الأردن العديد من المسوحات لرصد الإصابات الفيروسية وانتشارها في مناطق زراعية مختلفة، وذلك باستخدام تقنيات حيوية، مصلية وجزيئية. وتمّ رصد إصابات فيروسية متعددة واعتبرت تهديداً وخطراً على إنتاجية هذه المحاصيل وعلى

الأمن الغذائي الأردني. كما تم تقييم أثر هذه الإصابات الفيروسية على إنتاجية محاصيل الخضروات المهمة. شكلت النتائج المتحصّل عليها خطوة رئيسية لإيجاد استراتيجيات فعالة للسيطرة على هذه الفيروسات، ذات الأثر الزراعي والاقتصادي، لضمان استدامة المحاصيل الزراعية المهمة بما يتناسب مع تلبية الطلب المتزايد على الغذاء الناجم عن زيادة الكثافة السكانية في الأردن.

كلمات مفتاحية: الأردن، الأمراض الفيروسية، محاصيل الخضار، الباذنجانيات، القرعيات.

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References

Abu-Shirbi, A., A. Mansour, N. Salem and N. Al-Tamimi. 2012. Viral diseases affecting open field tomato in Jordan. Jordan Journal of Agricultural Sciences, 8(1):15-21.

Alhudaib, K., A. Rezk and A.M. Soliman. 2018. Current status of watermelon chlorotic stunt virus (WmCSV) on some cucurbit plants (Cucurbitaceae) in Alahsa region of Saudi Arabia. Scientific Journal of King Faisal University, 19(2):37-45.

Alkowni, R. 2017. Phytoviruses in Palestine: Status and future perspectives. An-Najah University Journal for Research, 31(1):11-34.

Al-Mnayer, A. 1985. Occurrence of potato virus Y (PVY) and potato virus X (PVX) on potato in Jordan. MSc thesis, University of Jordan, Amman, Jordan. 56 pp.

Al-Musa, A. and A. Mansour. 1982. Some properties of a watermelon mosaic virus in Jordan. Plant Disease, 66(4):330-331. https://doi.org/10.1094/PD-66-330

Al-Musa, A. and A. Mansour. 1983. Plant viruses affecting tomatoes in Jordan: Identification and prevalence. Journal of Phytopathology, 106(2):186-190. https://doi.org/10.1111/j.1439-0434.1983.tb00042.x

Al-Musa, A., G. Anfoka, A. Al-Abdulat, S. Misbeh, F. Haj Ahmad and I. Otri. 2011. Watermelon chlorotic stunt virus (WmCSV): A serious disease threatening watermelon production in Jordan. Virus Genes, 43(1):79-89. https://doi.org/10.1007/s11262-011-0594-8

Al-Musa, A., S. Misbeh, M. Abhary and F. Haj Ahmad. 2008. Detection and molecular characterization of squash leaf curl virus (SLCV) in Jordan. Journal of Phytopathology, 156(5):311-316. https://doi.org/10.1111/j.1439-0434.2007.01389.x

Al-Musa, A., S. Qusus and A. Mansour. 1985. Cucumber vein yellowing virus on cucumber in Jordan. Plant Disease, 69:361. https://doi.org/10.1094/PD-69-361C

Al-Musa, A.M. 1982. Incidence, economic importance, and control of tomato yellow leaf curl in Jordan. Plant Disease, 66:561-563. https://doi.org/10.1094/PD-66-561

Al-Musa, A.M. 1988. Tomato yellow leaf curl virus in Jordan: Epidemiology and control. Dirasat (Jordan), 13(2):199-208.

Al-Musa, A.M. 1989. Severe mosaic caused by zucchini yellow mosaic virus in cucurbits from Jordan. Plant Pathology, 38(4):541-546. https://doi.org/10.1111/j.1365-3059.1989.tb01449.x

Al-Musa, A.M. and B. Lockhart. 1990. Occurrence of eggplant mottled dwarf virus in Jordan. Journal of Phytopathology, 128(4):283-287. https://doi.org/10.1111/j.1439-0434.1990.tb04275.x

Al-Nsour, A., A. Mansour, L. Al-Banna and N. Salem. 2010. Detection of tomato ringspot virus on stone fruit trees in Jordan. Jordan Journal of Agricultural Sciences, 6(2):240-247.

Al-Tamimi, N., H. Kawas and A. Mansour. 2009. Viral diseases affecting squash (*Cucurbita pepo*) in southern Syria and Jordan Valley. Jordan Journal of Agricultural Sciences, 5(2):226-236.

Al-Tamimi, N., H. Kawas, A. Mansour, A. Arabiat and N. Salem. 2010. Biological and molecular characterization of two zucchini yellow mosaic virus isolates from Syria. Jordan Journal of Agricultural Sciences, 6(3):479-493.

Al-Tamimi, N., H. Kawas, A. Mansour, A. Arabiat and N. Salem. 2011. Molecular characterization of two squash leaf curl virus (SLCV) isolates: One from the Jordan Valley and the other from southern Syria. Jordan Journal of Agricultural Sciences, 7(1):178-187.

Amer, M.A. and S.Y. Mahmoud. 2020. First report of tomato brown rugose fruit virus on tomato in Egypt. New Disease Reports, 41:24. https://doi.org/10.5197/j.2044-0588.2020.041.024

Anderson, P.K., A.A. Cunningham, N.G. Patel, F.J. Morales, P.R. Epstein and P. Daszak. 2004. Emerging infectious diseases of plants: Pathogen pollution, climate change and agrotechnology drivers. Trends in Ecology and Evolution, 19:535-544. https://doi.org/10.1016/j.tree.2004.07.021

Anfoka, G. and M. Abhary. 2007. Occurrence of tomato infectious chlorosis virus (TICV) in Jordan. EPPO Bulletin, 37(1):186-190. https://doi.org/10.1111/j.1365-2338.2007.01101.x

Anfoka, G., A.F. Hussain, M. Altaleb and M. Al Shhab. 2014a. Detection of satellite DNA beta in tomato plants with tomato yellow leaf curl disease in Jordan. Plant Disease, 98(7):1017. https://doi.org/10.1094/PDIS-02-14-0144-PDN

Anfoka, G., F. Haj Ahmad, M. Abhary and A. Hussein. 2009b. Detection and molecular characterization of viruses associated with tomato yellow leaf curl disease in cucurbit crops in Jordan. Plant Pathology, 58(4):754-762. https://doi.org/10.1111/j.1365-3059.2009.02060.x

Anfoka, G., F. Haj Ahmad, M. Altaleb, M. Al Shhab, S. Abubaker, D. Levy, A. Rosner and H. Czosnek. 2014b. First report of recombinant potato virus Y strains infecting potato in Jordan. Plant Disease, 98(7):1017. https://doi.org/10.1094/PDIS-03-14-0236-PDN

Anfoka, G., M. Abhary and M.K. Nakhla. 2005. Molecular identification of species of the tomato yellow leaf curl virus complex in Jordan. Journal of Plant Pathology, 87(1):65-70.

Anfoka, G., M. Abhary and R. Stevens. 2006. Occurrence of tomato spotted wilt virus (TSWV) in Jordan. EPPO Bulletin, 36(3):517-522. http://dx.doi.org/10.1111/j.1365-2338.2006.01052.x

Anfoka, G., **M. Abhary, F. Haj Ahmad, A.F. Hussein, A. Rezk, F. Akad, Y. Abou-Jawdah, M. Lapidot, F. Vidavski, M.K. Nakhla, H. Sobh, H. Atamian, L. Cohen, I. Sobol, H. Mazyad, D.P. Maxwell and H. Czosnek.** 2009a. Survey of tomato yellow leaf curl disease-associated viruses in the eastern Mediterranean basin. Journal of Plant Pathology, 90(2):313-322.

Anfoka, G., M. Al-Taleb and F. Haj Ahmad. 2016a. A new isolate of tomato yellow leaf curl Axarquia virus associated with tomato yellow leaf curl disease in Jordan. Journal of Plant Pathology, 98(1):145-149. https://doi.org/10.4454/JPP.V98I1.041

Anfoka, G., M. Altaleb and M. Abu-Obaida. 2016b. First report of potato virus Y strain N-Wilga affecting potato in Jordan. Plant Disease, 100(10):2176. https://doi.org/10.1094/PDIS-04-16-0506-PDN

Anfoka, G., M. Altaleb, F. Haj Ahmad and M. Abu Obaida. 2017. Charlock mustard (Sinapis arvensis): A weed reservoir for begomoviruses and associated betasatellite in Jordan. Canadian Journal of Plant Pathology, 39(3):325-333. https://doi.org/10.1080/07060661.2017.1354332

Annual Statistical Yearbook. 2023. Department of Statistics, Jordan. http://www.dos.gov.jo/owa-user/owa/FOCAL_AGR.agr_kk?LANG=E&dis=1

Caruso, A.G., S. Bertacca, G. Parrella, R. Rizzo, S. Davino and S. Panno. 2022. Tomato brown rugose fruit virus: A pathogen that is changing tomato production worldwide. Annals of Applied Biology, 181(3):258-274. https://doi.org/10.1111/aab.12788

Cohen, S. and I. Harpaz. 1964. Periodic, rather than continual acquisition of a new tomato virus by its vector, the tobacco whitefly (Bemisia tabaci Gennadius). Entomologia Experimentalis et Applicata, 7(2):155-166. https://doi.org/10.1111/j.1570-7458.1964.tb02435.x

Cohen, S. and Y. Antignus. 1994. Tomato yellow leaf curl virus, a whitefly-borne geminivirus of tomatoes. Pp. 259-288. In: Advances in Disease Vector Research, Volume 10. K.F. Harris (eds.). Springer New York, USA. https://doi.org/10.1007/978-1-4612-2590-4_10

Desbiez, C. 2020. The never-ending story of cucurbits and viruses. Acta Horticulturae, 1294:173-191. https://doi.org/10.17660/ActaHortic.2020.1294.23

Díaz-Martínez, L., I. Brichette-Mieg, A. Pineño-Ramos, G. Domínguez-Huerta and A. Grande-Pérez. 2018. Lethal mutagenesis of an RNA plant virus via lethal defection. Scientific Reports, 8:1444. https://doi.org/10.1038/s41598-018-19829-6

Duan, Q. and Y. Lin. 2024. Focus on vegetable crops. Plant Physiology, 195(2):901-905. https://doi.org/10.1093/plphys/kiae246

Duffus, J.E. 1995. Whitefly-transmitted yellowing viruses of the Cucurbitaceae. Pp. 12-16. In: Cucurbitaceae 94: Evaluation and Enhancement of Cucurbit Germplasm. G.E. Lester and J.R. Dunlap (eds.). Gateway Printing, South Padre Island, TX, USA.

FAO. 2024. FAOSTAT: Crops and livestock products (Production/Livestock). https://www.fao.org/faostat/en/#data/RL

Galipienso, L., L. Rubio, J. Aramburu, L. Velasco and D. Janssen. 2012. Complete nucleotide sequence of a severe isolate of cucumber vein yellowing virus from Jordan. Archives of Virology, 157(6):1189-1192. https://doi.org/10.1007/s00705-012-1264-4

Gill, U., J.W. Scott, R. Shekasteband, E. Ogundiwin, C. Schuit, D.M. Francis, S.C. Sim, H. Smith and S.F. Hutton. 2019. Ty-6, a major begomovirus resistance gene on chromosome 10, is effective against tomato yellow leaf curl virus and tomato mottle virus. Theoretical and Applied Genetics, 132:1543-1554. https://doi.org/10.1007/s00122-019-03298-0

Haj Ahmad, F., W. Odeh and G. Anfoka. 2013. First report on the association of squash leaf curl virus and watermelon chlorotic stunt virus with tomato yellow leaf curl disease. Plant Disease, 97(3):428. https://doi.org/10.1094/PDIS-08-12-0712-PDN

Hančinský, R., D. Mihálik, M. Mrkvová, T. Candresse and M. Glasa. 2020. Plant viruses infecting Solanaceae family members in cultivated and wild environments: A review. Plants, 9(5):667. https://doi.org/10.3390/plants9050667

Hussein, A., N.M. Salem, P. Margaria, W. Menzel and M. Abu Muslem. 2024. First report of squash vein yellowing virus naturally infecting cucumber, squash and melon in Jordan. Plant Disease, 108(10):3204. https://doi.org/10.1094/PDIS-06-24-1264-PDN

Hutton, S.F., J.W. Scott and D.J. Schuster. 2012. Recessive resistance to tomato yellow leaf curl virus from tomato cultivar Tyking is located in the same region as Ty-5 on chromosome 4. HortScience, 47(3):324-327. https://doi.org/10.21273/HORTSCI.47.3.324

Ismaeil, F., J. Mando, M. Alkhalaf and S.G. Kumari. 2023. Viruses and phytoplasma reported on the most important vegetable crops in Syria: A review. Arab Journal of Plant Protection, 41(4):444-458. https://doi.org/10.22268/AJPP-41.4.444458

Jones, R.A.C. 2021. Global plant virus disease pandemics and epidemics. Plants, 10(2):233. https://doi.org/10.3390/plants10020233

Khalifa, M.A.A., A.M. El-Shazly, M.A.S. El-Kady and A.M. Al-Naggar. 2024. Survey of viruses infecting solanaceous plants and characterization of tomato brown rugose fruit virus (ToBRFV) infecting pepper in Egypt. Fayoum Journal of Agricultural Research and Development, 38(1):56-76.

Kool, J. 2016. The Jordan Valley. Pp. xviii–xix. In: Sustainable Development in the Jordan Valley. Hexagon Series on Human and Environmental Security and Peace, Vol. 13. J. Kool (eds.). Springer International Publishing, Switzerland. https://doi.org/10.1007/978-3-319-30036-8_2

Kurowski, C., K. Conn, J. Lutton and S. Rosenberger. 2015. Cucurbit disease field guide: A disease reference guide for cucumber, melon, squash, and watermelon. Seminis and De Ruiter, USA.

Lapidot, M., U. Karniel, D. Gelbart, D. Fogel, D. Evenor, Y. Kutsher, Z. Makhbash, S. Nahon, H. Shlomo, L. Chen, M. Reuveni and I. Levin. 2015. A novel route controlling begomovirus resistance by the messenger RNA surveillance factor Pelota. PLOS Genetics, 11(10):e1005538. https://doi.org/10.1371/journal.pgen.1005538

Lecoq, H. and C. Desbiez. 2012. Viruses of cucurbit crops in the Mediterranean region: An ever-changing picture. Advances in Virus Research, 84:67-126. https://doi.org/10.1016/B978-0-12-394314-9.00003-8

Makkouk, K. 1978. A study on tomato viruses in the Jordan Valley with special emphasis on tomato yellow leaf curl. Plant Disease Reporter, 62(3):259-262.

Mansour, A., L. Al-Banna, N. Salem and N. Alsmairat. 2014. Disease management of organic tomato under greenhouse conditions in the Jordan Valley. Crop Protection, 60:48-55. https://doi.org/10.1016/j.cropro.2014.03.001

Mansour, A. 1999. Incidence of potato viruses in Jordan. Dirasat Agricultural Sciences, 26(3):313-319.

Mansour, A. and A. Al-Musa. 1993. Cucumber vein yellowing virus: Host range and virus-vector relationships. Journal of Phytopathology, 137(1):73-78.

Mansour, A., A. Al-Musa, H.J. Vetten and D.E. Lesemann. 1998. Properties of a cowpea mild mottle virus (CPMMV) isolate from eggplant in Jordan and evidence for biological and serological differences between CPMMV isolates from leguminous and solanaceous hosts. Journal of Phytopathology, 146:539-547.

Mansour, A. and A. Al-Musa. 1992. Tomato yellow leaf curl virus: Host range and virus-vector relationships. Plant Pathology, 41(2):122-125. https://doi.org/10.1111/j.1365-3059.1992.tb02328.x

Marchant, W.G., H. Mugerwa, S. Gautam, H. Al-Aqeel, J.E. Polston, G. Rennberger, H. Smith, B. Turechek, S. Adkins, J.K. Brown and R. Srinivasan. 2023. Phylogenomic and population genetics analyses of extant tomato yellow leaf curl virus strains on a global scale. Frontiers in Virology, 3:1221156. https://doi.org/10.3389/fviro.2023.1221156

Martelli, G.P. and M. Russo. 1976. Unusual cytoplasmic inclusions induced by watermelon mosaic virus. Virology, 72(2):352-362. https://doi.org/10.1016/0042-6822(76)90164-1

Mink, G.I. 1976. Plant virus disease in Jordan. Research report, Faculty of Agriculture, University of Jordan, Amman, Jordan. 55 pp.

Mohammed, M.S. and A.A. Lahuf. 2023. First report of cucumber vein yellowing virus in Iraq. New Disease Reports, 47(2): e12183. https://doi.org/10.1002/ndr2.12183

Naik, P.S. and T. Buckseth. 2018. Recent advances in virus elimination and tissue culture for quality potato seed production. Pp. 131–158. In: S.S. Gosal and S.H. Wani (eds.). Biotechnologies of Crop Improvement. Springer, Cham, Switzerland. https://doi.org/10.1007/978-3-319-78283-6_4

Navot, N., E. Pichersky, M. Zeidan, D. Zamir and H. Czosnek. 1991. Tomato yellow leaf curl virus: A whitefly-transmitted geminivirus with a single genomic component. Virology, 185(1):151-161. https://doi.org/10.1016/0042-6822(91)90763-2

Nienhaus, F. and A.T. Saad. 1967. First report on plant virus diseases in Lebanon, Jordan, and Syria. Zeitschrift für Pflanzenkrankheiten (Pflanzenpathologie) und Pflanzenschutz, 74(7):459-471.

Nimer, F.T. 1993. Study of potato virus Y and potato virus A in Jordan Valley: Inoculum sources and incidence. M.Sc. thesis, University of Jordan, Amman, Jordan. 71 pp.

Odeh, W. 2007. Characterization of plant viruses affecting potato crop in Jordan. M.Sc. thesis, Al-Balqa Applied University, Jordan. 76 pp.

Oraon, S., R. Padamini, Y. Shahni, N. Das, D. Sinha, G. Sujatha, O. Singh and R. Karanwal. 2024. Impact of emerging pathogens in crop production. Microbiology Research Journal International, 34(7):80-92. https://doi.org/10.9734/mrji/2024/v34i71460

Prasad, A., N. Sharma, G. Hari-Gowthem, M. Muthamilarasan and M. Prasad. 2020. Tomato yellow leaf curl virus: Impact, challenges, and management. Trends in Plant Science, 25(9):897-911. https://doi.org/10.1016/j.tplants.2020.03.015

Purcifull, D.E. and E. Hiebert. 1979. Serological distinction of watermelon mosaic virus isolates. Phytopathology, 69:112-116.

Qusus, S. 1983. Plant viruses affecting cucumbers grown under plastic houses in the Jordan Valley. M.Sc. thesis, Department of Plant Protection, University of Jordan, Amman, Jordan. 96 pp.

Radouane, N., S. Ezrari, Z. Belabess, A. Tahiri, R. Tahzima, S. Mssart, H. Jijakli, M. Benjelloun and R. Lahlali. 2021. Viruses of cucurbit crops: Current status in the Mediterranean region. Phytopathologia Mediterranea, 60(3):493-519. https://doi.org/10.36253/phyto-12340

Rubio, L., J. Soong, J. Kao and B.W. Falk. 1999. Geographic distribution and molecular variation of isolates of three whitefly-borne closteroviruses of cucurbits: Lettuce infectious yellows virus, cucurbit yellow stunting disorder virus, and beet pseudo-yellows virus. Phytopathology, 89(8):707-711. https://doi.org/10.1094/PHYTO.1999.89.8.707

Rybicki, E.P. 2015. A top ten list for economically important plant viruses. Archives of Virology, 160(1):17-20. https://doi.org/10.1007/s00705-014-2295-9

Salem, N., A. Mansour, M. Ciuffo, B.W. Falk and M. Turina. 2016. A new tobamovirus infecting tomato crops in Jordan. Archives of Virology, 161(2):503-506. https://doi.org/10.1007/s00705-015-2677-7

Salem, N., A. Sulaiman, N. Samarah, M. Turina and M. Vallino. 2022. Localization and mechanical transmission of tomato brown rugose fruit virus in tomato seeds. Plant Disease, 106(1):275-281. https://doi.org/10.1094/PDIS-11-20-2413-RE

Salem, N.M., A.N. Mansour, A.O. Abdeen, S. Araj and W. Khrfan. 2015. First report of tomato chlorosis virus infecting tomato crops in Jordan. Plant Disease, 99(9):1286. https://doi.org/10.1094/PDIS-01-15-0130-PDN

Salem, N.M., M.J. Cao, S. Odeh, M. Turina and M. Vallino. 2020a. First report of tobacco mild green mosaic virus and tomato brown rugose fruit virus infecting Capsicum annuum in Jordan. Plant Disease, 104(2):601. https://doi.org/10.1094/PDIS-06-19-1189-PDN

Salem, N.M., S. Araj, T. Alshareef, M. Abu Muslem, H. Bess and N.I. Katis. 2020b. First report of cucurbit chlorotic yellows virus from cucumber plants affected by interveinal yellowing disease in Jordan. Plant Disease, 104(12):3277. https://doi.org/10.1094/PDIS-03-20-0674-PDN

Sastry, S.K. and T.A. Zitter. 2014. Management of virus and viroid diseases of crops in the tropics. Pp. 149-480. In: Plant Virus and Viroid Diseases in the Tropics: Epidemiology and Management. S.K. Sastry and T.A. Zitter (eds.). Springer, Dordrecht, The Netherlands.

Scholthof, K., S. Adkins, H. Czosnek, P. Palukaitis, E. Jacquot, T. Hohn, B. Hohn, K. Saunders, T. Candresse, P. Ahlquist, C. Hemenway and G.D. Foster. 2011. Top 10 plant viruses in molecular plant pathology. Molecular Plant Pathology, 12(9):938-954. https://doi.org/10.1111/j.1364-3703.2011.00752.x

Sharaf, N.S. and T.F. Allawi. 1981. Control of *Bemisia tabaci* Genn., a vector of tomato yellow leaf curl virus disease in Jordan. Journal of Plant Diseases and Protection, 88(2/3):123-131.

Shelake, R.M., S.G. Wagh, A.M. Patil, J. Cerven, R.R. Waghunde and J.Y. Kim. 2024. Heat stress and plant–biotic interactions: Advances and perspectives. Plants, 13:2022. https://doi.org/10.3390/plants13152022

Sweiss, M., G. Anfoka and Y. Abou-Jawdah. 2007. Molecular characterization of Jordanian isolates of cucurbit yellow stunting disorder virus. Journal of Phytopathology, 155(9):557-562. https://doi.org/10.1111/j.1439-0434.2007.01280.x

Tatineni, S. and G. Hein. 2023. Plant viruses of agricultural importance: Current and future perspectives of virus disease management strategies. Phytopathology, 113(2):117-141. https://doi.org/10.1094/PHYTO-05-22-0167-RVW

Velasco, L., L. Ruiz, L. Galipienso, L. Rubio and D. Janssen. 2020. A historical account of viruses in intensive horticultural crops in the Spanish Mediterranean Arc: New challenges for a sustainable agriculture. Agronomy, 10(6):860. https://doi.org/10.3390/agronomy10060860

Walker, P.J., S.G. Siddell, E.J. Lefkowitz, A.R. Mushegian, E.M. Adriaenssens, P. Alfenas-Zerbini, A.J. Davison, D.M. Dempsey, B.E. Dutilh, M.L. García, B. Harrach, R.L. Harrison, R.C. Hendrickson, S. Junglen, N.J. Knowles, M. Krupovic, J.H. Kuhn, A.J. Lambert, M. Łobocka, M.L. Nibert, H.M. Oksanen, R.J. Orton, D.L. Robertson, L. Rubino, S. Sabanadzovic, P. Simmonds, D.P. Smith, N. Suzuki, K. Van Dooerslaer, A.M. Vandamme, A. Varsani and F.M. Zerbini. 2021. Changes to virus taxonomy and to the International code of virus classification and nomenclature ratified by the International Committee on Taxonomy of Viruses. Archives of Virology, 166:2633-2648. https://doi.org/10.1007/s00705-021-05156-1

World Bank. 2021. Climate-Smart Agriculture Action Plan: Jordan. World Bank document. https://documents1.worldbank.org/curated/en/099105005092240188/pdf/P16068202548b20c10b2940571353a64afa.pdf

Yan, Z., A. Wolters, J. Navas-Castillo and Y. Bai. 2021. The global dimension of tomato yellow leaf curl disease: Current status and breeding perspectives. Microorganisms, 9(4):740. https://doi.org/10.3390/microorganisms9040740

Yan, Z., A. Pérez-de-Castro, M.J. Díez, S.F. Hutton, R.G. Visser, A. Wolters, Y. Bai and J. Li. 2018. Resistance to tomato yellow leaf curl virus in tomato germplasm. Frontiers in Plant Science, 9:1198. https://doi.org/10.3389/fpls.2018.01198

Zhang, S., J.S. Griffiths, G. Marchand, M.A. Bernards and A. Wang. 2022. Tomato brown rugose fruit virus: An emerging and rapidly spreading plant RNA virus that threatens tomato production worldwide. Molecular Plant Pathology, 23(9):1262-1277. https://doi.org/10.1111/mpp.13229

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