

Detection and molecular characterization of Tomato yellow leaf curl virus in Ukraine

Anton Gerilovych

antger2011@gmail.com

Institute for Problems of Cryobiology and Cryomedicine National Academy of Sciences of Ukraine: Institut problem kriobiologii i kriomedicini Nacional'na akademija nauk Ukraini <https://orcid.org/0000-0002-3280-4172>

Nadiia Shevchenko

Natalia Bashtan

Tetiana Miroshnichenko

Olha Chaiuk

Tetiana Ivchenko

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Abstract

Tomato yellow leaf curl virus (*Begomovirus flavisolanum*, TYLCV) is one of the most economically important viral pathogens of tomato worldwide, yet information regarding its molecular diversity in Ukraine has been limited. This study aimed to investigate the occurrence, molecular characteristics, and phylogenetic relationships of TYLCV isolates circulating in Ukrainian vegetable production systems. A total of 34 symptomatic tomato plants representing different cultivars were collected from several regions of Ukraine and analyzed by conventional PCR targeting the coat protein gene. Eighteen samples (52.9%) tested positive for TYLCV, while all healthy control plants were negative. In addition, TYLCV was detected in chili pepper (*Capsicum frutescens*) and zucchini (*Cucurbita pepo* var. *giraumontia*) growing adjacent to infected tomato plants, indicating a broader cultivated host range under field conditions. Partial genome sequencing of eight representative isolates generated GenBank accessions PX234052–PX234057, PX234062, and PX234063. Phylogenetic analyses based on Neighbor-Joining, Minimal Evolution, and Maximum Likelihood methods consistently demonstrated that Ukrainian isolates constitute a genetically homogeneous population with nucleotide identities exceeding 99%. Most isolates clustered tightly together, whereas isolate PX234052 represented the most divergent variant and the zucchini isolate (PX234057) formed a slightly differentiated branch while remaining within the TYLCV clade. Comparison with representative international sequences showed that all Ukrainian isolates grouped within the TYLCV-Israel (TYLCV-IL) lineage, exhibiting the closest relationship to isolates from Israel and Mediterranean countries, suggesting a common evolutionary origin. The limited genetic diversity observed among Ukrainian isolates indicates either a relatively recent introduction of TYLCV or the continued spread of a restricted number of closely related viral genotypes. These findings provide the first comprehensive molecular characterization of TYLCV populations in Ukraine and establish a baseline for future epidemiological surveillance, vector monitoring, and phytosanitary management. The detection of TYLCV in tomato, pepper, and zucchini further emphasizes the importance of integrated disease management and continuous monitoring of alternative cultivated hosts to reduce virus dissemination.

Introduction

Tomato yellow leaf curl virus (*Begomovirus flavisolanum*, TYLCV) is one of the most destructive plant viruses affecting tomato production worldwide. It belongs to the genus *Begomovirus* within the family *Geminiviridae* and is transmitted exclusively by the whitefly *Bemisia tabaci* in a persistent circulative manner. TYLCV causes Tomato yellow leaf curl disease, one of the most economically significant viral diseases of tomato, capable of causing yield losses approaching 100% when plants become infected at an early developmental stage (Glick, 2009; Welegama, 2021).

TYLCV possesses a monopartite genome that encodes six open reading frames involved in replication, movement, encapsidation, and suppression of host defense mechanisms. Viral replication occurs within the nuclei of infected phloem-associated cells (Li, 2022).

Host range of TYLCV involves tomato (*Solanum lycopersicum*) as the principal host, and numerous cultivated and wild plant species, including: pepper (*Capsicum annuum*), eggplant (*Solanum melongena*), common bean (*Phaseolus vulgaris*), tobacco (*Nicotiana tabacum*) and several weed species that serve as virus reservoirs. Alternative hosts facilitate virus persistence between cropping seasons and contribute to disease epidemiology (Dhaliwal, 2020; Li, 2022).

Disease severity depends on plant age at infection, environmental conditions, cultivar susceptibility, and viral strain. Typical symptoms include upward curling of young leaves, yellowing (chlorosis) along leaf margins, reduced leaf size, thickened and leathery leaf texture, shortened internodes, severe plant stunting, flower abortion, reduced fruit set, significant reduction in fruit size and yield (Prasad, 2020).

Successful management requires an integrated disease management approach combining host resistance, vector suppression, and phytosanitary practices, including cultivation of TYLCV-resistant cultivars, use of certified virus-free seedlings, removal of infected plants, elimination of weed hosts, installation of insect-proof greenhouse screens, application of reflective mulches to deter whitefly colonization, crop rotation and sanitation (Li, 2022).

Because whiteflies can transmit TYLCV rapidly after feeding, insecticide applications alone are generally insufficient to prevent disease spread (Welegama, 2021).

TYLCV has been reported from more than 50 countries across Europe, Asia, Africa, the Middle East, and the Americas. Global economic losses exceed US\$1 billion annually due to reduced yields, increased production costs, and limitations on international trade. The continuing expansion of *Bemisia tabaci*, climate change, and emergence of recombinant TYLCV strains continue to increase the global threat posed by this virus (Dhaliwal, 2020).

TYLCV has been formally identified alongside other critical tomato pathogens affecting production systems in Ukraine (Havryliuk, 2024; Shevchenko, 2022). Due to climate shifts and vector adaptability, it poses a direct biotic stress threat to both protected greenhouse facilities and open-field cultivation (Havryliuk, 2024). National reviews indicate that TYLCV is managed as a high-priority risk within the *Geminiviridae* family. Researchers observe that international trade and climate variations accelerate the potential distribution of these whitefly-transmitted begomoviruses into non-traditional geographic niches across the country (Kyrychenko, 2016).

Investigations into local epidemiology reveal that common agricultural weeds from families like *Asteraceae* and *Malvaceae* act as critical wild reservoirs for TYLCV in Ukrainian agroecosystems, allowing the virus to persist between commercial cropping seasons (Bohdan, 2023).

Ukrainian institutions have actively researched specialized mitigation techniques, including cryopreservation protocols for tomato meristems, to successfully eliminate vertically transmissible viral paths from domestic germplasm collections (Shevchenko, 2022).

The aim of our work was performing PCR-based surveillance of TYLCV in Ukrainian farms and study of genetic variability of detected viruses in comparison with world-wide detected strains of TYLCV.

Material and methods

Collection of TYLCV-symptomatic tomato and other crops. Sampling was performed in Kyiv oblast (2 farms), Sumy oblast (1 farm) and Kahrkiv oblast (3 farms and 1 backyard). In general 44 tomato leaf samples (34 tomato leaf specimens from plants with virus related symptoms and 12 samples from healthy plants) from plants representing different tomato cultivars were collected in 3 selected oblasts in Ukraine. Also the crops of chili pepper (*Capsicum frutescens*) and zucchini (*Cucurbita pepo* var. *giraumontia*) growing near tomatos were examined (n = 5 from each of species, from plants with and without clinical signs (leaf colour and form changes)).

Total DNA extraction. Extraction of total DNA from symptomatic and healthy tomato plants, and other crops was done by magnetic particles sorption method using Magnet Pure kits (Ukraine) using 200 mg of plant tissue per sample. Total DNA in TE-buffer was stored at -20°C until use for PCR analysis.

Detection of TYLCV. The presence of TYLCV has been proved in DNA extracts from crops by using primers TYLCV-TY1F, TYLCV-TY2R (Accotto et al., 2000), that amplify a region of 579 bp from the coat protein (CP) gene. PCR reaction was done in a total volume of 22 µl using HOT FIREPol MasterMix (Solis BioDyne OÜ, Estonia). PCR cycles included initial denaturation (94 °C, 2 min), 40 cycles (denaturation – 94 °C, 30 s; annealing – 57 °C, 30 s; and elongation – 72 °C, 60 s), and final elongation – 72 °C, 5 min. Products were visualized in 1% agarose gel by electrophoresis.

Sequencing and phylogenetic analysis. PCR for sequencing was performed by the technique described by Rabie (2017), using TYLCV FL F and TYLCV FL R primer pair (ATGCCTCTAATCCAG and GCGTACATGCCATATAC), proposed by this author to amplify V1, V2, C1, C2, C3, C4 region of TYLCV genome. Estimated length of amolicon was around 2700 bp. Obtained amplicons were used for Sanger sequencing under using Applied Biosystems Sanger Sequencing Kit (ThermoFisher Scientific, U.S.). The raw sequence data were assembled and edited using the SnapGene software package (v.8.2.1, snapgene.com). These sequenced fragments after correction and cutting of non-readable ends were represented 1,606 bp region of TYLCV genome. Sequences are available in GenBank with accession numbers: PX234063.1, PX234062.1, PX234052.1-57. They represent 8 viral isolates, including 6 tomato-derived isolates (3 from Kharkiv, 2 from Kyiv and 1 from Sumy region), and 1 isolate of TYLCV from zucchini and 1 from pepper.

The resulting nucleotide sequences from the Ukrainian TYLCV isolates were compared against the GenBank database using the BLASTn algorithm to confirm their identity as TYLCV. For phylogenetic reconstruction, reference sequences of TYLCV representing different strains and geographic origins were retrieved from GenBank.

Multiple sequence alignment of the Ukrainian isolates and reference sequences was performed using the MAFFT algorithm (Katoh & Standley, 2013). The best-fit nucleotide substitution model was determined using ModelFinder based on the Bayesian Information Criterion (BIC). Neighbour-Joining Algorithm was applied with 1000 bootstrap replications to compare Ukrainian isolates with other viruses, detected previously in different countries.

A maximum likelihood (ML) phylogenetic tree was constructed to compare sequences of Ukrainian TYLCV isolates using IQ-TREE with 1,000 ultrafast bootstrap replicates to assess nodal support (Nguyen et al., 2015). The final trees were visualized and annotated using MEGA 12 software (for ML tree) and treebuilding module from BLASTn (https://www.ncbi.nlm.nih.gov/blast/treeview/treeView.cgi?request=page&blastRID=DMT6CNAC014&queryID=lcl|Query_7188200&entrezLim=&ex=&exl=&exh=&ns=100&screenWidth=1470&screenHeight=956) (for NJ tree).

Results

Detection of TYLCV in crop samples. A total of 34 leaf samples were collected from tomato plants exhibiting symptoms characteristic of TYLCV infection, including leaf curling, chlorosis, reduced leaf size, and plant stunting (Fig. 1). The samples represented different tomato cultivars grown in several oblasts of Ukraine.

High-quality total DNA was successfully extracted from all symptomatic and healthy control plants using the magnetic particle-based extraction method (Table 1). The extracted DNA was suitable for downstream molecular analysis, and no evidence of DNA degradation or PCR inhibition was observed.

Table 1
Detection of Tomato yellow leaf curl virus in symptomatic tomato plants from Ukraine

Parameter	Result
Total tomato samples collected	46
Symptomatic plants	34
Healthy control plants	12
DNA extraction success (spectrophotometric assay)	46/46 (100%)
TYLCV-positive samples	18 (52,9%)
TYLCV-negative samples	16 (47,1%)

PCR amplification using the TYLCV-specific primer pair TYLCV-TY1F/TYLCV-TY2R generated the expected 579-bp amplicon in 18 of the 34 (52,9%) symptomatic tomato samples. These results confirmed the presence of TYLCV. No amplification products were detected in healthy control plants or in the no-template control, demonstrating the specificity of the assay (Table 1).

Positive samples were detected in several tomato cultivars collected from different regions of Ukraine (farms located Kyiv, Kharkiv and Sumy oblasts, and backyard from Kharkiv oblast, where tomatoes, zucchini and pepper growing together), indicating that TYLCV is distributed across multiple production areas, and makes a risk of infection for other plants (zucchini and chili pepper growing nearby infected tomatoes), where positive PCR-testing results were also obtained.. Representative PCR products from positive samples were subsequently selected for sequencing and phylogenetic analysis.

Figure 1 – Symptoms of TYLCV infection in tomato (A1-3), pepper (B), and zucchini (C1-2)

Table 1. Detection of Tomato yellow leaf curl virus in symptomatic tomato plants from Ukraine

Sequencing and phylogenetic analysis. 6 specimens of DNA from tomato derived TYLCV isolates, as well as 1 from zucchini and 1 from pepper were sequenced (Table 2).

Table 2
Molecular characteristics of Tomato yellow leaf curl virus (TYLCV) isolates identified in tomato, pepper and zucchini plants in Ukraine

Isolate	Host	Tomato cultivar/ other crops	Region (Oblast)	Genome region analyzed	Genetic fragment length, bp	GenBank accession	Divergence level, %
WT01	<i>Solanum lycopersicum</i>	Slyvka Debarau	Kyiv	V2, V1, C3, C2, C1 (partial) genes	1606	PX234052	Query
SP_Bseq	<i>Solanum lycopersicum</i>	Cherry Irishka	Sumy	V2, V1, C3, C2, C1 (partial) genes	1606	PX234053	0,31
Pink Heart V2	<i>Solanum lycopersicum</i>	Pink Heart	Kharkiv	V2, V1, C3, C2, C1 (partial) genes	1606	PX234054	0,44
Udavchyk	<i>Solanum lycopersicum</i>	Udavchyk	Kharkiv	V2, V1, C3, C2, C1 (partial) genes	1606	PX234055	0,31
Geyser 10B	<i>Solanum lycopersicum</i>	Geyser 10B	Kharkiv	V2, V1, C3, C2, C1 (partial) genes	1606	PX234056	0,44
Osnova	<i>Solanum lycopersicum</i>	Cherry rozhevyi	Kyiv	V2, V1, C3, C2, C1 (partial) genes	1606	PX234062	0,44
PCh	<i>Capsicum frutescens</i>	Chili pepper	Kharkiv	V2, V1, C3, C2, C1 (partial) genes	1606	PX234063	0,44
Chaklun	<i>Cucurbita pepo</i> var. <i>giraumontia</i>	Chaklun zucchini	Kharkiv	V2, V1, C3, C2, C1 (partial) genes	1606	PX234057	0,62

Table 2. Molecular characteristics of Tomato yellow leaf curl virus (TYLCV) isolates identified in tomato, pepper and zucchini plants in Ukraine

Phylogenetic analysis of the eight TYLCV isolates by Neighbor Joining algorithm revealed a high degree of genetic similarity, with all sequences clustering within a single lineage and exhibiting relatively short branch lengths, indicative of limited nucleotide divergence (Fig. 2). This interpretation is consistent with the very short branch lengths in the tree, indicating > 99% nucleotide identity among most Ukrainian TYLCV isolates, with PX234052.1 being the most genetically distinct sequence.

The dendrogram resolved two principal clusters. The first cluster comprised isolates PX234054.1, PX234063.1 (pepper), PX234062.1, PX234056.1, and PX234057.1 (zucchini). Within this group, isolates PX234054.1, PX234063.1 (pepper), PX234062.1, and PX234056.1 were nearly identical, displaying minimal evolutionary distances. Isolate PX234057.1 (zucchini), remained closely related to this subgroup but formed a separate terminal branch, suggesting the accumulation of a small number of additional nucleotide substitutions.

Figure 2. Phylogenetic relationships among eight Ukrainian TYLCV isolates based on nucleotide sequence analysis. Branch lengths are proportional to the number of nucleotide substitutions per site. The scale bar represents 0.0005 substitutions per site, illustrating the low overall genetic diversity among the analyzed isolates (Neighbour Joining, BS 1000)

The second cluster included isolates PX234053.1 and PX234055.1, which were closely related to one another and formed a distinct sister clade. In contrast, isolate PX234052.1 occupied the most divergent position in the phylogeny, forming a separate branch with a genetic distance of approximately 0.0031 substitutions per nucleotide site from the remaining isolates. Although genetically distinct, PX234052.1 remained within the same TYLCV lineage, indicating that it represents a divergent variant rather than a separate viral species.

Phylogenetic analysis was also performed using nucleotide sequences of Tomato yellow leaf curl virus (TYLCV) isolates obtained in this study together with representative TYLCV sequences retrieved from GenBank, encompassing isolates from Europe, the Middle East, Asia, Africa, Australia, and the Americas. The evolutionary relationships were inferred using the Neighbor-Joining method, and branch lengths were estimated based on nucleotide substitutions per site. The final tree included both complete genome sequences and partial genomic regions, with a scale bar corresponding to 0.001 nucleotide substitutions per site.

The Ukrainian isolates (Udavchyk, SP_Bseq, Pink Heart, Chaklun, and WT01) clustered within the Tomato yellow leaf curl virus species and formed a well-supported clade with previously reported TYLCV isolates from Israel and the Mediterranean region. The four partial genome sequences (Udavchyk, SP_Bseq, Pink Heart, and Chaklun) exhibited very short branch lengths, indicating a high degree of nucleotide conservation and suggesting that these isolates are closely related genetically. The WT01 isolate also grouped within the same lineage, confirming its classification as TYLCV despite being represented by a shorter genomic fragment.

The Ukrainian isolates showed the greatest phylogenetic affinity to Israeli reference isolates (e.g., IS60 and TYLCV-IL23) and several Mediterranean isolates from Italy and Portugal, supporting the hypothesis that the circulating virus population belongs to the classical TYLCV-Israel lineage. In contrast, isolates originating from East Asia, Australia, and the Americas formed distinct subclusters within the TYLCV species, reflecting their independent evolutionary histories and regional diversification.

Overall, the phylogenetic reconstruction demonstrated limited genetic divergence among the Ukrainian TYLCV isolates and their closest international relatives. The short genetic distances observed across the tree indicate that the virus population circulating in Ukraine is highly conserved and belongs to a globally distributed lineage that has undergone relatively limited evolutionary change.

Discussion

The present study provides the pilot molecular characterization of TYLCV isolates detected in different regions of Ukraine using PCR, partial genome sequencing, and phylogenetic analysis. TYLCV was detected in 52.9% of symptomatic tomato plants, demonstrating that the virus is distributed in Ukrainian tomato plants and produce risks for tomato production in those regions. This detection rate is comparable with reports from other countries where TYLCV has become endemic following the establishment of its insect vector, *Bemisia tabaci*, and reflects the continuing expansion of begomovirus-associated diseases worldwide (Dhaliwal et al., 2020; Li et al., 2022).

The observed symptoms, including severe leaf curling, chlorosis, reduced leaf size, shortened internodes, and plant stunting, were consistent with the classical symptomatology described for TYLCV infections. However, only approximately half of the symptomatic plants tested positive for TYLCV, indicating that similar symptoms may also be induced by other tomato viruses such as *Tomato chlorosis virus* (ToCV), *Tomato spotted wilt virus* (TSWV), *Cucumber mosaic virus* (CMV), *Tomato mosaic virus* (ToMV), or mixed viral infections, as well as by abiotic stress factors. Similar observations have been reported previously, emphasizing that symptom-based diagnosis alone is insufficient and should always be confirmed using molecular diagnostic techniques (Prasad et al., 2020; Li et al., 2022).

Figure 3. Phylogenetic analysis of Tomato yellow leaf curl virus (TYLCV) isolates detected worldwide and in Ukraine (Neighbour Joining algorithm, BS 1000). Ukrainian isolates are marked by red box.

The successful amplification of TYLCV-specific DNA fragments from more than half of the symptomatic samples demonstrates that conventional PCR remains a highly reliable diagnostic approach for routine surveillance. The primer pair described by Accotto et al. (2000) produced highly specific amplification without false-positive reactions in healthy controls, confirming its suitability for diagnostic laboratories. Such PCR-based detection protocols remain the cornerstone of phytosanitary surveillance because of their sensitivity, specificity, and relatively low cost (Accotto et al., 2000; Rabie et al., 2017).

An important finding of this study is the detection of TYLCV not only in tomato but also in chili pepper (*Capsicum frutescens*) and zucchini (*Cucurbita pepo* var. *giraumontia*) growing adjacent to infected tomato plants in the confitions of backyard farms, common for Ukraine (Kyrychenko, 2016).

Although TYLCV is primarily regarded as a tomato pathogen, infections have previously been reported in several solanaceous crops, including pepper, as well as in numerous cultivated and wild plant species that serve as alternative hosts (Dhaliwal et al., 2020; Li et al., 2022). The identification of TYLCV in zucchini is particularly noteworthy because cucurbit infections are reported much less frequently than infections in solanaceous hosts. Whether zucchini functions as a true epidemiologically significant host or represents an incidental spillover host requires further investigation involving complete genome sequencing, infectivity assays, and transmission experiments with *Bemisia tabaci*. Nevertheless, these findings suggest that mixed vegetable production systems may facilitate virus maintenance and local spread by providing additional host plants for vector-mediated transmission.

Phylogenetic analyses consistently demonstrated remarkably low genetic diversity among Ukrainian TYLCV isolates regardless of the reconstruction method employed. Nucleotide identities exceeding 99% for all analyzed viral isolates. Similar low intraspecific diversity has been observed in TYLCV populations shortly after successful invasion of new geographical regions, where founder effects and intensive vector-mediated dissemination contribute to genetic uniformity (Glick et al., 2009; Li et al., 2022).

Although the Ukrainian population appeared highly conserved overall, two isolates exhibited measurable divergence (WT01, PX234052, and Chaklun, PX234057). Geminiviruses are characterized by relatively high mutation rates despite replicating with host DNA polymerases, and continuous accumulation of point mutations contributes to adaptation to different hosts and environments (Prasad et al., 2020). Future whole-genome sequencing will be necessary to determine whether these divergent isolates harbor recombination events or adaptive mutations affecting pathogenicity, host range, or vector interactions.

Comparison with international reference sequences demonstrated that Ukrainian isolates cluster within the classical TYLCV-Israel (TYLCV-IL) lineage, showing the highest nucleotide similarity to isolates originating from Israel and Mediterranean countries such as Italy (100% similarity of WT01 with Sardinian recombinant strain, PQ873011), and Portugal. This observation agrees with previous studies demonstrating that TYLCV-IL represents the globally dominant lineage responsible for the majority of recent epidemics throughout Europe, the Mediterranean Basin, Asia, and subsequently other continents (Glick et al., 2009; Dhaliwal et al., 2020).

Nevertheless, continuous monitoring remains essential because recombination represents one of the principal evolutionary mechanisms in begomoviruses and has repeatedly resulted in the emergence of more aggressive TYLCV variants with expanded host ranges or increased epidemic potential (Prasad et al., 2020; Li et al., 2022).

Climate warming, prolonged vegetation seasons, increasing greenhouse production, and the gradual establishment of *Bemisia tabaci* populations create increasingly favorable conditions for TYLCV persistence and spread. Recent Ukrainian reviews have already identified TYLCV among the most important emerging viral threats affecting vegetable production, emphasizing that climate change and international trade substantially increase the probability of further virus dissemination (Havryliuk et al., 2024; Kyrychenko, 2016). The widespread detection of TYLCV in geographically separated regions observed in this study supports these concerns and indicates that the virus has already become established in multiple tomato-growing areas.

Several limitations of the present study should also be acknowledged. First, only partial genome sequences were obtained for most isolates, preventing comprehensive analysis of recombination events and genome-wide variability. Second, the number of sequenced isolates remained relatively small compared with the overall number of PCR-positive samples. Third, vector populations were not simultaneously investigated, precluding direct assessment of relationships between viral genotypes and *Bemisia tabaci* biotypes circulating in Ukraine. Future investigations should therefore incorporate complete genome sequencing using next-generation sequencing technologies, broader geographic sampling, characterization of whitefly populations, and long-term molecular surveillance to better understand the epidemiology and evolution of TYLCV under changing climatic conditions.

Overall, the present study demonstrates that TYLCV circulating in Ukraine belongs to a genetically homogeneous population closely related to the globally distributed TYLCV-Israel lineage. The detection of the virus in tomato, pepper, and zucchini highlights the potential involvement of multiple cultivated hosts in local virus ecology. These findings provide the first molecular baseline for future epidemiological surveillance and contribute valuable information for the development of evidence-based phytosanitary strategies aimed at limiting the further spread of TYLCV in Ukraine.

Conclusions

This study provides the first comprehensive molecular characterization of Tomato yellow leaf curl virus (TYLCV) circulating in tomato production systems in Ukraine. Conventional PCR confirmed TYLCV infection in 52.9% of symptomatic tomato plants, demonstrating that the virus is established in geographically distinct production regions. In addition to tomato, TYLCV was detected in chili pepper (*Capsicum frutescens*) and zucchini (*Cucurbita pepo* var. *giraumontia*), suggesting that cultivated non-tomato hosts may contribute to virus persistence and local epidemiology in mixed vegetable production systems.

The close relationship of Ukrainian isolates to Mediterranean and Israeli reference isolates suggests a common evolutionary origin and indicates that the virus population currently circulating in Ukraine is highly conserved. Although one tomato isolate (PX234052) and the zucchini isolate

(PX234057) displayed slightly greater genetic divergence, both remained within the TYLCV clade, indicating natural intraspecific variation rather than the emergence of novel viral lineages.

The findings demonstrate that TYLCV represents an important emerging threat to Ukrainian vegetable production under conditions favorable for the establishment and spread of its whitefly vector, *Bemisia tabaci*. The molecular data generated in this study provide an essential baseline for phytosanitary surveillance, breeding programs aimed at TYLCV resistance, and the development of evidence-based integrated disease management strategies for sustainable tomato production in Ukraine.

Declarations

Acknowledgements

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Ethics declarations

Human and animal rights

The present research did not involve human participants and/or animals.

Conflict of interest

The authors have no relevant financial or non-financial interests to disclose.

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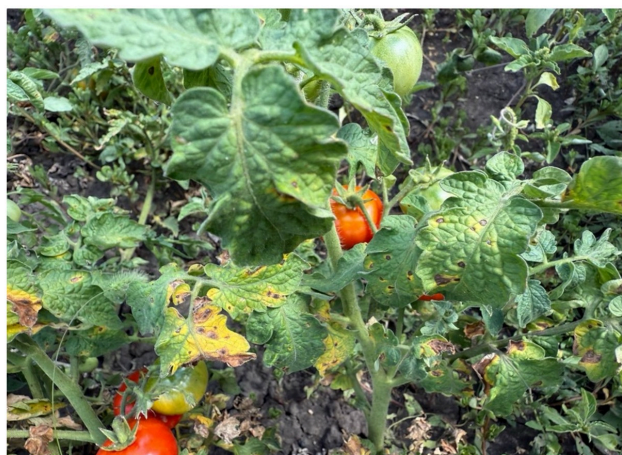
Figures



A-1



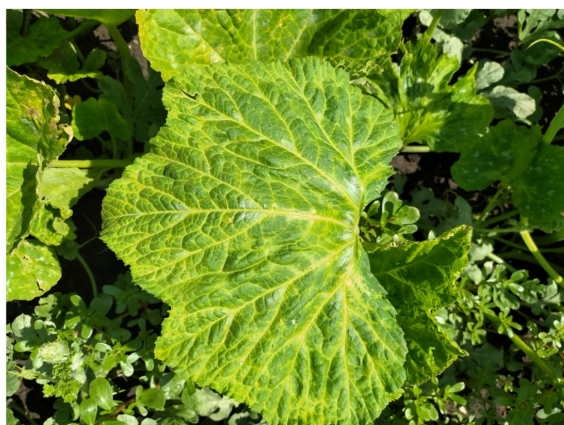
A-2



A-3



B



C1



C2

Figure 1

Symptoms of TYLCV infection in tomato (A1-3), pepper (B), and zucchini (C1-2)

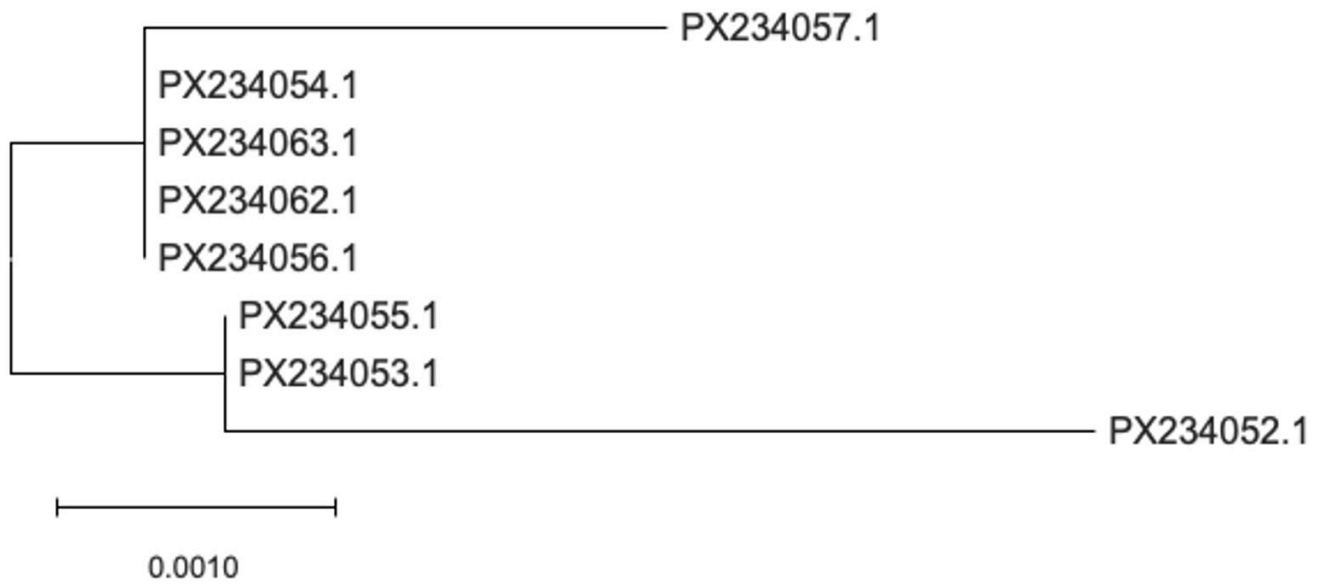


Figure 2

Phylogenetic relationships among eight Ukrainian TYLCV isolates based on nucleotide sequence analysis. Branch lengths are proportional to the number of nucleotide substitutions per site. The scale bar represents 0.0005 substitutions per site, illustrating the low overall genetic diversity among the analyzed isolates (Neighbour Joining, BS 1000)

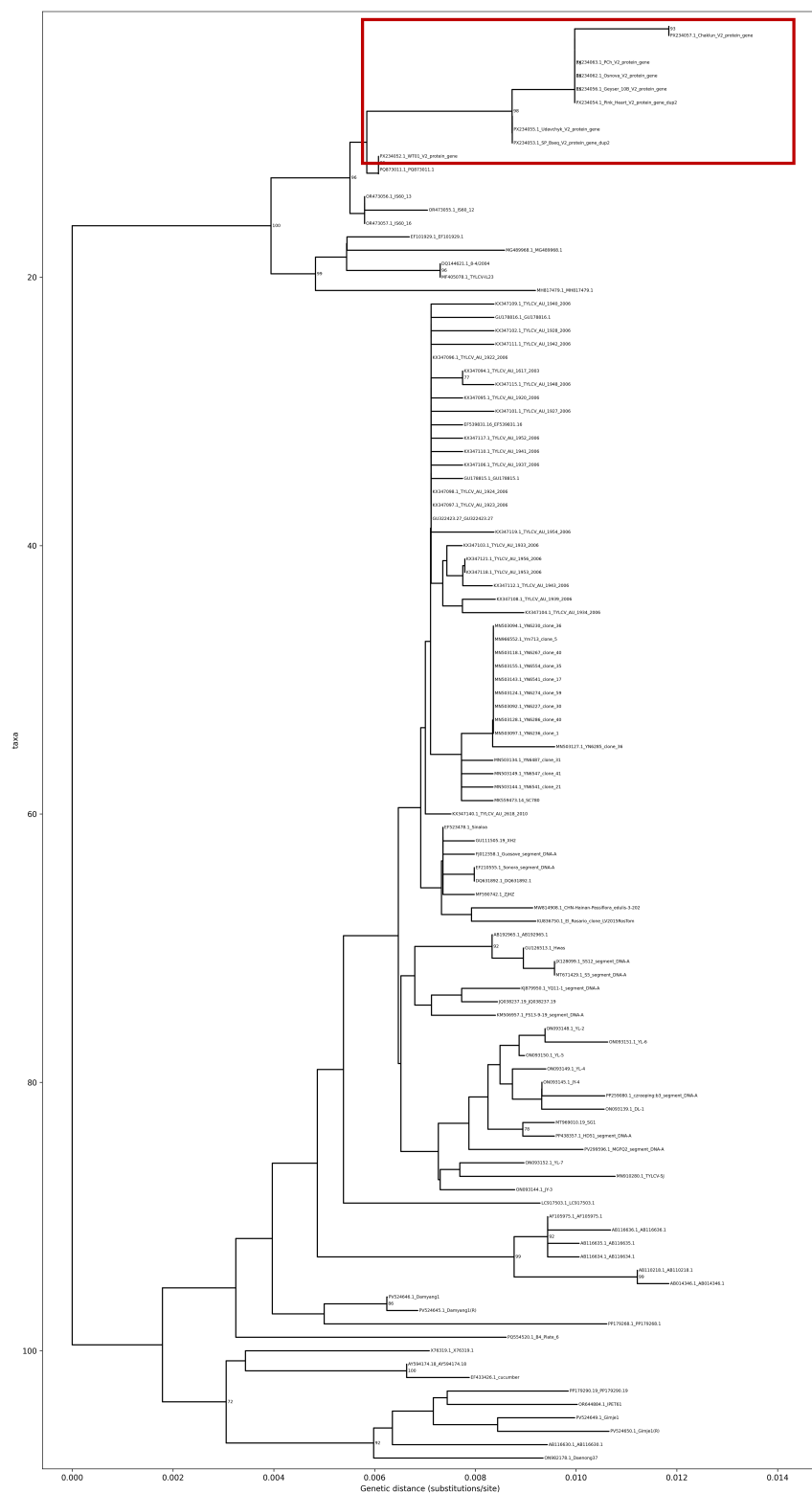


Figure 3

Phylogenetic analysis of Tomato yellow leaf curl virus (TYLCV) isolates detected worldwide and in Ukraine (Neighbour Joining algorithm, BS 1000). Ukrainian isolates are marked by red box.