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BIOLOGY OF THE UZBEK ISOLATE M-1 OF THE POTATO LEAFROLL VIRUS AND ITS PHYLOGENETIC ANALYSIS

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SUMMARY

This study investigated the distribution, molecular identification, and genetic analysis of Potato leafroll virus (PLRV) in the Yukari-Chirchik District of Tashkent Region, Uzbekistan, during 2022–2024. Field surveys revealed characteristic PLRV symptoms, including leaf chlorosis, upward rolling, and interveinal yellowing in potato cultivars Arizona, Zarzara, Gala, and Santa. Reverse transcription polymerase chain reaction (RT-PCR) successfully amplified a 726 bp fragment of the coat protein (CP) gene. A novel isolate designated 'Potato leafroll M-1' attained successful identification and depositing in the NCBI GenBank (accession number PP981686). Phylogenetic analysis demonstrated 99.58% genetic similarity with the African isolate JEO11-34 and close relationships with German and Canadian strains. Several detected single nucleotide polymorphisms in the CP gene promoter region indicated evolutionary divergence. Reservoir host analysis using real-time PCR identified PLRV in *Datura stramonium*, *Solanum nigrum*, *Solanum lycopersicum*, *Physalis floridana*, and *Dolichos lablab*, confirming these species as potential virus reservoirs. This research provides the first molecular evidence of PLRV occurrence in Uzbekistan and validates RT-PCR as an efficient diagnostic tool for early virus detection. The findings establish a scientific foundation for developing virus-resistant potato cultivars and managing reservoir hosts to reduce viral spread.

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Keywords: Potato (*S. tuberosum* L.), potato leafroll virus (PLRV), isolate, RT-PCR, coat protein (CP) gene, Potato leafroll M-1, primer design, phylogenetic analysis

Key findings: The spread of potato (*S. tuberosum* L.) leafroll virus (PLRV) required monitoring. Through molecular genetic analysis, a new isolate designated as 'Potato leafroll M-1' succeeded in being deposited in the NCBI GenBank with the accession number PP981686.

INTRODUCTION

Potato leafroll virus (PLRV) is the most dangerous and widespread viral disease affecting potato crops (Kumar *et al*., 2011). The said virus causes characteristic symptoms, such as chlorosis and roughening of leaves, upward rolling of leaf blades, yellow mottling, necrotic curling, and interveinal chlorosis, which eventually lead to a significant reduction in potato tuber yield (Jones, 2005). In PLRV-infected potato plants, the leaves' upward rolling often precedes their desiccation. The said viral infection reduces the photosynthetic activity, disrupts metabolic processes, and consequently slows down the overall growth and development of the plant (Gray and Gildow, 2003).

The main viral diseases affecting potato crops are PVX, PVY, PVS, PVL, PVM, and PVA, having a negative impact on tuber yield and quality in Uzbekistan (Fayziev *et al*., 2020). In particular, mixed infections of these viruses cause significant economic losses in potato-growing areas annually (Awasthi and Verma, 2017). The wide distribution and yield impact of the potato leafroll virus (PLRV) represent a serious concern for potato crops in the country (Yusubakhmedov and Fayziev, 2022; Xolmatova *et al*., 2024). Detection and monitoring of viral diseases are crucial for effective management in crop production. Therefore, molecular identification of the virus, along with the study of its genetic variations and evolutionary relationships, became a research priority (Niblett and Van-Ryk, 2004).

In the present era, molecular biological techniques, particularly quantitative reverse transcription polymerase chain reaction (qRT-PCR), gene sequencing, and phylogenetic analysis, have provided the highest precision in identifying and classifying viral isolates (Janse and Koppel, 2011). However, molecular analyses of the potato leafroll virus (PLRV) have not yet occurred, and the molecular-genetic data on local isolates remain limited in Uzbekistan (Yusubakhmedov and Fayziev, 2022). In Uzbekistan, the systematic studies conducted continue to elucidate the viruses affecting economically important crops (Fayziev *et al.,* 2020; Sobirova *et al.,* 2024, 2025). These past studies include determining the infection rate of various plant genotypes (Sobirova *et al.,* 2024) and the molecular detection of viruses (Sattorov *et al.,* 2020; Makhmudov *et al.,* 2023; Sobirova *et al.,* 2025a,2025b). Others focused on producing and applying specific antisera for immunodiagnostics (Jovlieva *et al.,* 2024), as well as examining the physiological effects of viral infections on crop plants (Sobirova *et al.,* 2024).

Influencing the epidemiology of potato leafroll virus comes from the presence of alternative host plants that serve as virus reservoirs and aphid breeding sites. Weed species within and surrounding potato fields play a critical role in maintaining viral inoculum between growing seasons and facilitating vector population buildup. Among solanaceous weeds, the identification of *Solanum sarrachoides* has become a particularly important reservoir host for PLRV in the Pacific Northwest region of the United States, supporting higher populations of the green peach aphid (*Myzus persicae*) than potato itself (Eigenbrode *et al*., 2002).

This weed not only harbors the virus but also enhances aphid fecundity and survival, thereby increasing the risk of viral transmission to neighboring potato crops (Venkata, 2025). Similarly, *Datura stramonium* and *Physalis floridana* have several documentations as natural hosts of PLRV, capable of maintaining viral titers sufficient for aphid acquisition and subsequent transmission. The presence of

these reservoir hosts complicates disease management by providing external sources of inoculum that bypass seed certification programs (Awasthi and Verma 2017).

The transmission dynamics of PLRV from reservoir weeds to potato crops receives primary mediation from aphid vector behavior and host plant quality. Studies have demonstrated that aphids reared on certain reservoir hosts exhibit enhanced vector competence compared with those maintained on non-host plants. For instance, *Myzus persicae* reared on *Physalis* species showed significantly higher PLRV transmission efficiency than aphids reared on turnip, a non-host plant, due to physiological changes in the aphid gut environment (Kenzhebekova *et al*., 2025). Furthermore, aphid transmission of PLRV from infected *Solanum sarrachoides* to potato appeared to be four times greater than transmission from potato to potato, highlighting the disproportionate epidemiological risk posed by weed reservoirs. These findings underscore the necessity of integrated weed management strategies in seed potato production systems. Effective control of reservoir hosts, such as hairy nightshade, black nightshade (*Solanum nigrum*), and other solanaceous weeds, is essential for reducing primary inoculum sources and disrupting the transmission cycle of PLRV in agroecosystems (Srinivasan and Alvarez, 2008).

Developing effective control measures against plant viruses, it is essential to thoroughly study and identify their biological characteristics, distribution levels, the influence of environmental and soil factors, and various genetic properties (Clark and Bar-Joseph, 1984). Moreover, the rapid and sensitive detection of viruses in plant buds is crucial, as it helps to reduce viral spread and prevent crops from economic losses (Jeevalatha *et al.,* 2013; Malko *et al.,* 2019). In this study, collected samples of potato cultivars Arizona, Zarzara, Gala, and Santa showing typical PLRV symptoms came from potato fields in District Yuqori Chirchiq, Tashkent Region, Uzbekistan. The molecular identification of the potato leafroll virus (PLRV) ensued using the RT-PCR method (Figure 1).

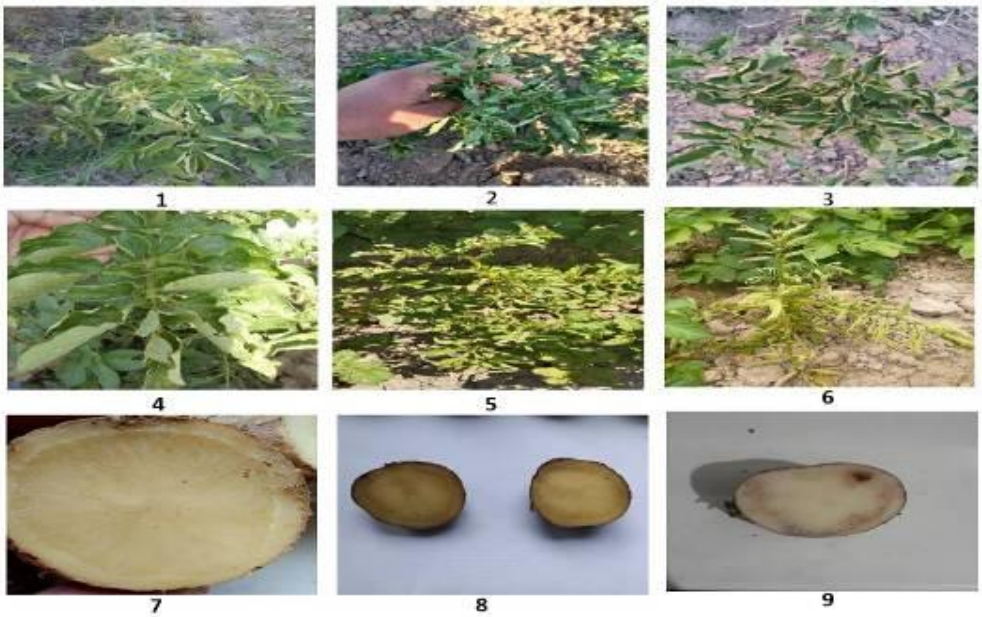

Figure 1. Typical symptoms of viral diseases in potato plants. Note: 1 - lightening and roughening of the leaf; 2-3 - upward boat-shaped twisting of the leaf plate; 4 - yellow spotting and curling of the leaf; 5 - necrosis and curling of the leaf; 6 - interveinal roughening of the leaf; 7 -circular spotting of the node; 8 - spotting of the potato node; and 9 - spotting and rotting of the node.

Table 1. Names and nucleotide sequences of forward and reverse PCR primers designed for PLRV detection.

Gene	Primer name	Nucleotide sequence (5′–3′)	PCR product size (bp)	Reference
CP	PRLV-F	AGCCGGTTTATAYTTHGTTTA	726	Okonya *et al*. (2021)

MATERIALS AND METHODS

This study investigated the circulation of PLRV in nature. For this purpose, the object of research was natural reservoir plants distributed in the Tashkent Region. Identifying potential reservoir hosts enabled the conduct of field surveys in potato-growing areas during the 2022–2024 cropping seasons. Leaf sample collection from weed and crop species commonly found in and around potato fields comprised 16 samples. These were *Datura stramonium* L., *Dolichos lablab, Solanum nigrum*, *Solanum lycopersicon, Physalis floridana* L., *Cynodon dactylon* L*., Capsella bursa-pastoris, Amaranthus retroflexus, Chenopodium album, Convolvulus sepium, Brassica campestris* L., *Malva* L*., S. melongena* L*., Persica, Trifolium, Cirsium arvense.* Each specimen succeeded in testing for PLRV presence by real-time PCR (Table 1). Susceptibility of confirmed reservoir hosts underwent further evaluation under controlled greenhouse conditions by mechanical inoculation and aphid transmission. Isolation of PLRV RNA from a sample consisted of using the "Fito Sorb" RN-520 reagent kit from the "SINTOL" scientific production company (Russia) on the plant sample (leaf, stem, nodule) to isolate a 150–300 mg RNA sample.

Sample collection

The conduct of a comprehensive survey ran from 2022 to 2024 in potato fields (*S. tuberosum* L.) in the Yukori-Chirchik District of Tashkent Region, Uzbekistan. Collecting leaf samples from diseased plants included those exhibiting both leaf curl and asymptomatic symptoms from the apical, mid-root, and basal parts of potato plants. The collected leaf samples proceeded to the laboratory for storage in a freezer at –18 °C.

Extraction and purification of total RNA

The leaf samples (0.1 g) underwent homogenization in liquid nitrogen before extracting total RNA using the Invitrogen™ PureLink™ RNA Mini Kit (Thermo Fisher Scientific, USA), according to the manufacturer's protocol. In determining the quantity and quality of the total RNA, the study used a NanoDrop eight spectrophotometer (Thermo Fisher Scientific, USA)**.** The RNA samples subsequently reached storage at –80 °C until use for reverse transcription polymerase chain reaction (RT-PCR) analysis.

Synthesis of the cDNA

The cDNA synthesis proceeded in a total reaction volume of 20 µL using SuperScript™ IV Reverse Transcriptase (Thermo Fisher Scientific, USA) and the corresponding buffers. A mixture comprised a 5 µL aliquot of total RNA with 1 µL of 10 µM reverse primer Lu4 (Table 2), 4 µL of 2.5 mM dNTPs**,** and 3 µL of nuclease-free water**.** The mixture's incubation continued at 65 °C for 5 min before chilling on ice for 3 min. Subsequently, adding 4 µL of 5× PCR buffer**,** 1 µL of 0.1 M dithiothreitol (DTT)**,** 0.5 µL (20 U) of SuperScript IV reverse transcriptase**,** and nuclease-free water ensured reaching the final volume of 20 µL. The research carried out the reaction in a T960 PCR thermal cycler at 37 °C for 1 h, followed by 70 °C for 10 min to inactivate the enzyme.

Amplification by PCR

Using the PLRV-R (reverse) and RPV-F (forward) primers enabled the amplification of a 726 bp fragment of the coat protein (CP) gene of the potato leafroll virus (PLRV). The PCR reaction, as carried out in a 25 µL total volume, used the Platinum™ Hot Start PCR 2×

Table 2. Identification of natural reservoirs of PLRV using real-time PCR.

No.	Plant name	PCR summary (Ct)
1	*Datura stramonium* L.	36.51
2	*Dolichos lablab*	33.48
3	*Chenopodium album*	-
4	*Brassica campestris L.*	-
5	*Trifolium*	-
6	*Convolvulus sepium*	-
7	*Solanum nigrum*	15.24
8	*Cynodon dactylon L.*	-
9	*Solanum lycopersicum*	27.48
10	*Malva L.*	-
11	*Amaránthus retrofléxus*	-
12	*Phisalis floridana* L.	30.51
13	*Persica*	17.15
14	*Capsella bursa-pastoris L.*	-
15	*Solanum melongena* L.	27.51
16	*Cirsium arvense*	-

Master Mix (Thermo Fisher Scientific, USA). The reaction mixture contained 4 µL of 2× Master Mix, 0.5 µL of each primer (10 µM), 0.9 µL of 25 mM $MgCl_2$, and 4 µL of cDNA. The thermal cycling conditions were as follows: an initial denaturation at 94 °C for 2 min, followed by 45 cycles of denaturation at 94 °C for 30 s, annealing at 56 °C for 30 s, and extension at 72 °C for 45 s. A final extension step ensued at 72 °C for 2 min. The names and nucleotide sequences of the primers used for PLRV detection are available in Table 2.

Electrophoresis in agarose gel

The PCR products' analysis proceeded on a 2% agarose gel prepared in 1× Tris-borate-EDTA (TBE) buffer (Thermo Scientific) before staining with ethidium bromide. For electrophoresis, 2 µL of 6× DNA gel loading dye and 1.3 µL of 100 bp DNA ladder entailed loading into the first well. Then, loading 10 µL of PCR product mixed with 3 µL of 6× DNA gel loading dye followed into the remaining wells. Electrophoresis occurred using an SE-1 horizontal electrophoresis system (Helicon, Russia) at a voltage of 100 V for 100 min. The amplified DNA bands received visualization under UV light and documentation using a BK-AG100 gel imaging system (Biobase, China).

Sequencing of PCR products

Excising the PCR products from the gel preceded purification using the PureLink™ Quick Gel Extraction Kit (Thermo Fisher Scientific, USA). Sequencing reactions followed using the BigDye® Terminator v3.1 Cycle Sequencing Kit (Thermo Fisher Scientific, USA). The reaction mixture (total volume 9 µL) contained 3.5 µL ddH_2O**,** 1 µL BigDye**,** 2 µL 5× sequencing buffer**,** 0.5 µL sequencing primer, and 2 µL purified PCR product**.** The primers RPV-L1 and RPV-R served for sequencing. Thermal cycling conditions were as follows: initial denaturation at 94 °C for 2 min**,** followed by 45 cycles of 94 °C for 30 s (denaturation)**,** 50 °C for 45 s (annealing), and 72 °C for 1 min (extension)**.** The sequencing reaction products remained in storage at 4 °C until purification.

Performing purification of sequencing products employed the Dynabeads Sequencing Clean-Up Kit (Thermo Fisher Scientific, USA). DNA sequencing proceeded on an Applied Biosystems 3500 Genetic Analyzer (Thermo Fisher Scientific) using capillary gel electrophoresis with laser-induced fluorescence detection**.** Raw sequence data editing engaged the Snap Gene 5.3.1 software. Comparing nucleotide sequences with existing sequences in the GenBank database used BLASTN (Basic

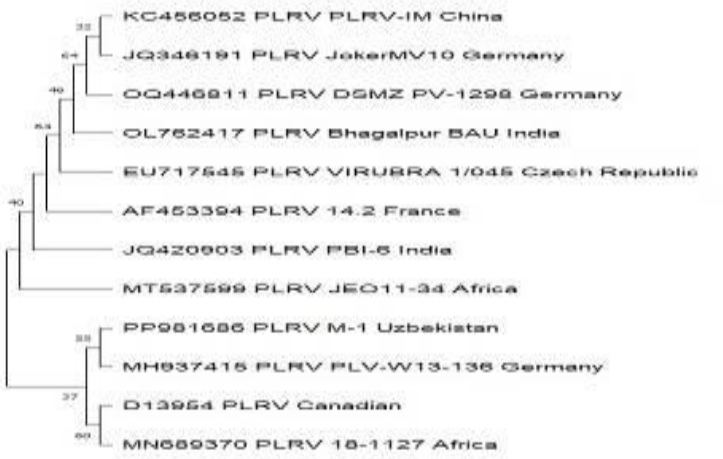

Figure 2. Phylogenetic tree based on the coat protein (CP) gene sequence of the potato leafroll virus (PLRV). The numbers shown above the branches represent bootstrap confidence values obtained after 1000 replicates, indicating the reliability of each branch grouping.

Local Alignment Search Tool; http://www.ncbi.nlm.nih.gov/BLAST/) (Camacho *et al*., 2009). Performing multiple sequence alignments utilized ClustalW, with the phylogenetic analysis conducted using the neighbor-joining (NJ) method based on the Kimura 2-parameter model (Kimura, 1980). Bootstrap analysis assessed the reliability of the tree branches, with the final phylogenetic tree visualized using MEGA11 software (Tamura *et al*., 2021) (Figure 2).

RESULTS

From 2022 to 2024, field studies were progressive in the potato-growing areas of the Yukor Chirchik District of the Tashkent Region of Uzbekistan, during which observations on characteristic symptoms of infection with potato leaf curl virus (PLCV) occurred. These included chlorosis and roughness of leaves, upward curling of the leaf blade, curling of leaves with yellow spots and necrotic areas, as well as interveinal chlorosis with thickening of leaves, recognized as characteristic signs of infection with PLRV (Figure 1).

The results of a study determined the reservoir properties of the KLV virus in wild grasses growing in potato fields. This mentioned the following plants in the literature: *Datura stramonium* L.*, Solanum nigrum, Solanum lycopersicon, Physalis floridana* L.*, Chenopodium album*, *S. melongena* L., *Dolichos lablab,* and *Persica.* The analysis of said plants by PCR detected high virus titers in their leaves. These plants clearly serve as indicator plants for this study. According to PCR data, PLRV virus was undetected in the following plants: *Cynodon dactylon* L., *Capsella bursa-pastoris, Amaranthus retroflexus, Cirsium arvense, Trifolium,* and *Convolvulus sepium* (Table 1).

PLRV overwinters in the roots and rhizomes of these wild plants and is transmitted to healthy crop plants, such as potatoes and tomatoes by aphid vectors. Further studies included molecular genetic identification to study the phylogeny of PLRV.

The samples collected from potato plants showing typical symptoms, a ~726 bp fragment corresponding to the viral RNA, attained successful amplification by PCR (Figure 3). Based on sequencing and BLAST analyses, the obtained sequence was 'Potato leafroll M-1,' which has been deposited in the NCBI GenBank database with the accession number PP981686 (ID). The phylogenetic analysis revealed that bioinformatic evaluation and tree construction of the PLRV isolates showed two distinct clusters. The Uzbek isolate 'Potato leafroll M-1' entailed grouping within

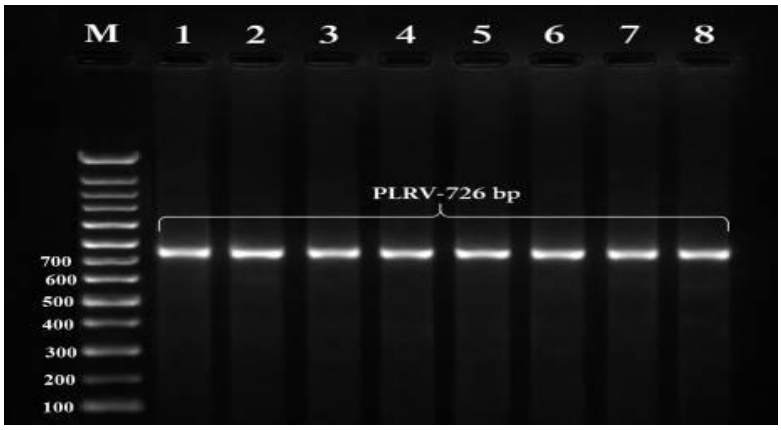

Figure 3. Electropherogram of RT-PCR amplification products of the PLRV CP gene from potato leaf samples collected in Yuqori Chirchiq District, Tashkent Region, Uzbekistan. Lanes 1–4 represent amplified samples; M – 100 bp DNA ladder; 1,2 – Arizona, 3,4– Zarzara, 5,6– Galla, and 7,8 – Santa.

the same cluster as W13-136 (Germany), PLRV-Canada, and 18-1127 (Africa) (Figure 2).

According to BLAST analysis of the potato leafroll M-1 isolate's coat protein (CP) gene nucleotide sequence in the NCBI GenBank database, the said isolate shared 96.22%–99.58% sequence homology with other PLRV isolates. The potato leafroll M-1 isolate expressed the highest genetic similarity (99.58%) with the African isolate JEO11-34 (GenBank ID: MT537599). Moreover, the sequence comparison revealed nucleotide substitutions in isolates W13-136 (Germany) (GenBank ID: MH937415) and D13954 (Canada). Multiple alignment of the potato isolates, leafroll M-1 and JEO11-34, using Clustal W identified three-point mutations: −120 G > T, −126 A > G, and −146 A > T (Figure 4). It is noteworthy to mention that these mutations showed a location in the promoter region of the CP gene. No other mutations were notable within the coding sequence of the gene between the two isolates. However, comparing the potato leafroll M-1 isolate with sequences from other countries further identified the additional nucleotide variations.

The bioinformatic analysis revealed that the amino acid sequence of the coat protein of the isolate potato leafroll M-1 obtained from Uzbekistan appeared to be closely associated but not identical with other comparable isolates. The nucleotide sequences with observed differences between the isolates potato leafroll M-1 and the African JEO11-34 share 99.58% similarity and also clustered together in the phylogenetic tree. The results suggested that various abiotic and biotic factors may have contributed to the genetic variability in PLRV.

Under Uzbekistan's environmental conditions, the PLRV isolate succeeded in molecular identification based on its CP gene, with the isolate potato leafroll M-1 (ID: PP981686) identified and deposited in the NCBI GenBank database for the first time. Based on this newly identified gene, the phylogenetic tree construction of the virus was successful, and the bioinformatic analysis revealed these isolates likely originated from closely related ancestral viruses within the same phylogenetic branch.

DISCUSSION

Potato infection with multiple viruses can affect and alter plant morphology and considerably increase the crop's economic losses (Adolf *et al.,* 2020; Fayziev *et al*., 2020). Therefore, studying the biological, molecular, and genetic characteristics of the virus is crucial for accurate identification of specific symptoms and management of these viruses (Jovlieva *et al.,* 2024).

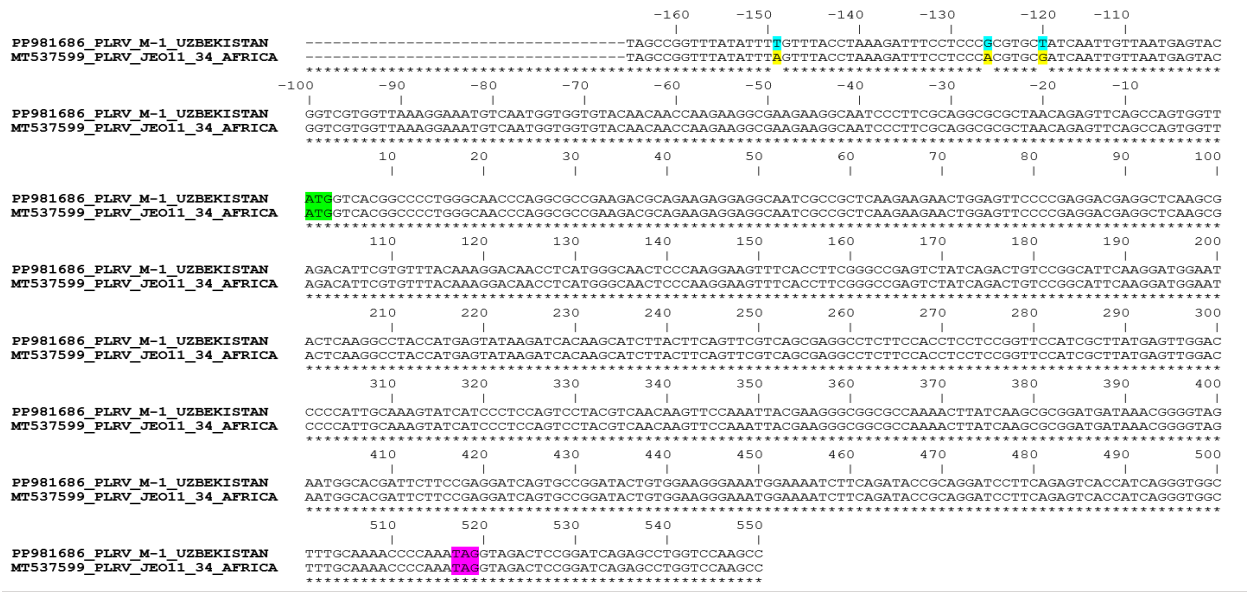

Figure 4. Comparative analysis of the Potato leafroll M-1 isolate's CP gene nucleotide sequence with other isolates.

The conduct of RT-PCR analysis determined the molecular and genetic properties of the virus, which revealed the infection in potato cultivars Arizona, Zarzara, Gala, and Santa with PLRV. Based on the RNA extracted from the potato's infected plants, the isolate potato leafroll M-1 succeeded in its identification for the first time under Uzbekistan's climatic conditions, with its submission to the NCBI GenBank database receiving accession number PP981686. Earlier virus studies had only provided preliminary information about the occurrence of PLRV in Uzbekistan (Fayziev *et al*., 2020), while more recent research has also reported the economic impact of the virus on potato crops (Yusubakhmedov and Fayziev, 2023; Xolmatova *et al*., 2024).

The nucleotide sequence of the coat protein (CP) gene of the potato leafroll virus (PLRV) isolate recognized in Uzbekistan showed the highest degree of similarity with several other isolates from different countries. According to bioinformatic analysis using the NCBI GenBank database, the maximum sequence similarity (99.58%) was notable with the African isolate JEO11-34 (ID: MT537599). Furthermore, the Uzbek isolate exhibited 99.44% similarity with isolates from Germany (W13-136 and MH937415) and the Czech Republic (VIRUBRA 1/045 and EU717545). Single-stranded RNA (ssRNA) of positive polarity represents the PLV genome, approximately 6000 nucleotides in length (Tacke *et al*., 1991; Brault *et al*., 2000).

Despite the low overall level of genetic variability, major events appeared to have occurred in the evolutionary history of PLRV. Firstly, the 27 nt deletion found in ORF1 of isolate Noir sat in a region with a concentration of active sites: the cis-acting signals involved in the ®1 ribosomal frameshifting (Kim *et al*., 2000).

With the Canadian (D13954) and African (18-1127, MN689370) isolates, the 99.30% level of homology was evident, with 99.16% nucleotide identity shared by the isolates from China (PLRV-IM and KC456052), Germany (DSMZ PV-1298 and OQ446811), and India (PBI-6, JQ420903; PLRV Bhagalpur BAU; and OL762417). Additionally, the French isolate PLRV 14.2 (AF453394) and the German isolate Joker MV10 (JQ346191) demonstrated 99.02% similarity with the isolate potato leafroll virus (PLRV ID = PP981686). The potato leafroll M-1 isolate identified in Uzbekistan showed the highest genetic similarity (99.58%) with the African isolate

JEO11-34 (GenBank ID: MT537599) based on the CP gene sequence. In contrast, detecting the minor nucleotide substitutions (mutations) resulted in isolates W13-136 (Germany, MH937415) and D13954 (Canada) (Figure 4).

The highest sequence similarities revealed the global distribution and close phylogenetic relationships among different PLRV isolates. The particularly high homology observed with African and European isolates suggested possible sources and routes of viral introduction into the potato-growing regions of Uzbekistan. Phylogenetic analysis revealed that the Uzbek isolate clustered closely with African and European isolates, supporting its genetic relatedness to these groups. Recently, information has emerged on the ability to confer multiple transgenic resistances to three major viruses (PVY, PVX, and PLRV) on potato plants using their specific sequences (Arif *et al*., 2012).

The RT-PCR assay proved a reliable and sensitive method for the early detection of PLRV infection in potato plants cultivated under Uzbek agroclimatic conditions. The obtained results confirmed the presence of PLRV in potato cultivars Arizona, Zarzara, Gala, and Santa, characterized by distinct symptoms, such as leaf curling, chlorosis, interveinal yellowing, and leaf rolling with necrotic patches. These findings reinforce the importance of regular virological monitoring and early-stage molecular diagnostics to prevent large-scale dissemination. Therefore, integrating RT-PCR into routine seed-potato certification programs in Uzbekistan would significantly reduce the risk of distributing infected planting materials (Yusubakhmedov and Fayziev, 2023).

Early detection of PLRV infection and molecular characterization of its genome are crucial for understanding the virus's epidemiology and for developing effective management strategies. Investigations on the genetic diversity of PLRV isolates contribute significantly to designing virus-resistant potato genotypes, which play a viable role in minimizing disease spread and tuber yield losses. The molecular and genetic characterization of PVM has been investigated in numerous studies, and its genome consists of 8534 nucleotide sequences and contains six open reading fragments (ORFs), each of which encodes separate proteins (Gramstat *et al*., 1990; Zavriev *et al*., 1991; Fujita *et al*., 2018).

Field surveys conducted in the Tashkent Region of Uzbekistan revealed the presence and wide distribution of potato leafroll virus (PLRV) in local potato fields, accompanied by characteristic disease symptoms. The molecular identity of PLRV gained validation by RT-PCR analysis, with a novel isolate designated as 'Potato leafroll M-1' identified and deposited in the NCBI GenBank database with accession number PP981686. Phylogenetic analysis demonstrated that this isolate shared the highest degree of genetic similarity with PLRV isolates from Africa, Europe, and several other countries, providing valuable insights into the virus's global dissemination patterns and possible evolutionary origins. The phylogenetic placement of isolate M-1 provides essential insight into the probable origin of PLRV in Uzbekistan and underscores the need for strengthened phytosanitary monitoring of imported seed potatoes. Such genetic information is crucial for tracing viral introduction routes, understanding virus evolution, and developing more effective disease management and breeding strategies (Yusubakhmedov and Fayziev, 2022).

CONCLUSIONS

This study confirmed the widespread distribution of potato leafroll virus in the Tashkent Region, Uzbekistan, affecting major potato cultivars. The novel isolate 'Potato leafroll M-1' (GenBank: PP981686) showed 99.58% similarity with African and European strains. Reservoir host screening identified infected weed species, including *Datura stramonium* and *Solanum nigrum*, highlighting their role in viral overwintering and transmission. Detected mutations in the CP gene indicate ongoing viral evolution. RT-PCR proved effective for early PLRV detection. These findings provide crucial data for breeding

resistant varieties, managing reservoir plants, and strengthening seed certification programs to prevent economic losses.

REFERENCES

Adolf B, Andrade-Piedra J, Molina FR, Przetakiewicz J, Hausladen H, Kromann P (2020). Fungal, oomycete, plasmodiophorid diseases of potato. In: The Potato Crop, H. Campos and O. Ortiz (Eds.). Cham: Springer, 307–350. doi: 10.1007/978-3-030-28683-5_9.

Arif M, Azhar U, Arshad M, Zafar Y, Mansoor S, Asad S (2012). Engineering broad-spectrum resistance against RNA viruses in potato. *Transgenic Res.* 21: 303–311. doi: 10.1007/s11248-011-9533-7.

Awasthi LP, Verma HN (2017). Current status of viral diseases of potato and their eco-friendly management – A critical review. *Virol. Res. Rev*. 1: 1–16. doi: 10.15761/VRR.1000122.

Brault V, Mutterer J, Scheidecker D, Simonis MT, Herrbach E, Richards K, Ziegler-Graff V (2000). Effects of point mutations in the readthrough domain of the beet western yellows virus minor capsid protein on virus accumulation in planta and on transmission by aphids. *J. Virol.* 74(3): 1140–1148. doi: 10.1128/ JVI.74.3.1140-1148.

Camacho C, Coulouris G, Avagyan V, Ma N, Papadopoulos J, Bealer K, Madden TL (2009). BLAST+: Architecture and applications. *BMC Bioinfor.* 10: 421.

Clark M, Bar-Joseph M (1984). Enzyme immunosorbent assays in plant virology. *Meth. Virol*. 7: 51–85. doi: 10.1016/B978-0-12-470207-3.50009-7.

Eigenbrode SD, Ding H, Shiel P, Berger PH (2002). Volatiles from potato plants infected with potato leafroll virus attract and arrest the virus vector, *Myzus persicae* (Homoptera: Aphididae). *Proc Biol Sci*. 269(1490): 455-60. doi: 10.1098/rspb.2001.1909.

Fayziev VB, Jovlieva DT, Juraeva UM, Shavkiev JM, Eshboev FM (2020). Effects of PVXN-UZ 915 necrotic isolate of Potato virus X on amount of pigments of *Datura stramonium* leaves. *J. Crit. Rev*. 7(9): 400–403.

Fujita N, Komatsu K, Ayukawa Y, Matsuo Y, Hashimoto M, Osamu N (2018). The N terminal region of cysteine-rich protein (CRP) in carlaviruses is involved in the determination of symptom types. *Mol. Plant Pathol*. 19: 180–190.

Gramstat A, Courtpozanis A, Rohde W (1990). The 12 kDa protein of potato virus M displays the properties of a nucleic acid-binding regulatory protein. *FEBS Lett.* 276: 34–38.

Gray SM, Gildow FE (2003). Luteovirus-aphid interactions. *Annu. Rev. Phytopathol.* 41: 539–566. https://doi.org/10.1146/annurev.phyto.41.052002.095536.

Janse J, Koppel P (2011). Advances in molecular diagnosis of plant viruses: qRT-PCR and sequencing approaches. *Plant Pathol*. 60(3): 509–518. https://doi.org/10.1111/j.1365-3059.2010.02430.x.

Jeevalatha A, Kaundal P, Shandil RK, Sharma NN, Chakrabarti SK, Singh BP (2013). Complete genome sequence of Potato leafroll virus isolates infecting potato in the different geographical areas of India shows low- level genetic diversity. *Indian J. Virol*. 24: 199–204. doi: 10.1007/s13337-013-0138-z.

Jones RAC (2005). Plant virus epidemiology: Recent progress and future prospects. *Eur. J. Plant Pathol*. 113(2): 103–121.

Jovlieva D, Fayziev V, Vakhobov A, Mirzaeva Z, Nugmonova K (2024). Preparation of polyclonal antiserum for potato X virus. *J. Wild. Biodivers*. 8(1): 268–278.

Kenzhebekova R, Pozharskiy A, Adilbayeva K, Gritsenko D (2025). Molecular mechanisms of potato plant–virus–vector interactions. *Plants* 14, 2282. https://doi.org/10.3390/plants14152282.

Kim YG, Maas S, Wang SC, Rich A (2000). Mutational study reveals that tertiary interactions are conserved in ribosomal frameshifting pseudoknots of two luteoviruses. *RNA* 6(8): 1157–1165. doi: 10.1017/ s1355838200000510.

Kimura M (1980). A simple method for estimating evolutionary rates of base substitutions through comparative studies of nucleotide sequences. *J. Mol. Evol.* 16(2): 111–120.

Kumar S, Choudhury N, Sharma A (2011). Impact of Potato leafroll virus on potato crops in India. *Int. J. Plant Pathol.* 3(2): 58–64.

Makhmudov T, Kadirova ZN, Adilov BS, Abdikarimov BQ, Abduvaliev BA, Ziyaev ZM, Sherimbetov AG, Kurganov S (2023). Molecular characterization of barley yellow dwarf virus (BYDV) isolate t-uzb2 in Uzbekistan. *Pak. J. Phytopathol*. 35(1): 127–135.

Malko A, Frantsuzov P, Nikitin M, Statsyuk N, Dzhavakhiya V, Golikov A (2019). Potato pathogens in Russia's Regions: An instrumental survey with the use of realtime PCR/RT-PCR in matrix format. *Pathogens* 8(1): 18. doi: 10.3390/pathogens8010018.

Niblett CL, Van-Ryk D (2004). Molecular analysis of Potato leafroll virus diversity. *Plant Dis*. 88(4): 335–342. https://doi.org/10.1094/ PDIS.2004.88.4.335.

Okonya JS, Gamarra H, Nduwayezu A, Bararyenya A, Kroschel J, Kreuze J (2021). Serological survey and metagenomic discovery of potato viruses in Rwanda and Burundi reveals absence of PVY in Burundi and first report of TRV in potatoes in Sub-Saharan Africa*. Virus Res.* 302, 198487. https://doi.org/10.1016/j.virusres.2021.198 487.

Sattorov M, Sheveleva A, Fayziev V, Chirkov S (2020). First report of plum pox virus on plum in Uzbekistan. *Plant Dis*. 104(9): 2533.

Sobirova ZS, Fayziev VB, Akhmadaliev BJ, Omonov NS, Sobirova KG, Akhmedova ZY, Egamberdiyeva L. (2024). MDMV influence on the productivity of maize (*Zea mays* L.). *SABRAO J. Breed. Genet*. 56(6): 2196–2204. http://doi.org/10.54910/sabrao2024. 56.6.2.

Sobirova ZSh, Dalimova SN, Umarova GB, Kucharova ISH, Boltayeva NO, Sobirova KG, Abdurashitova YE, Akhmadaliev BJ, Fayziev V (2025a). Characterization of MDMV under ecological conditions of Uzbekistan. *SABRAO J. Breed. Genet*. 57(4): 1518–1527. http://doi.org/10.54910/sabrao2025.57.4.

Sobirova ZSh, Makhmudov TH, Temirov AA, Sattorov MS, Yusubakhmedov AA, Valieva ZO, Akhmedova M, Akhmedova ZY, Egamberdiyeva L, Tukhtaeva F, Rakhmatullaeva A, Fayziev V (2025b). MDMV spread and its control under the climatic conditions of Tashkent Region, Uzbekistan. *SABRAO J. Breed. Genet*. 57(6). 57 (6) 2299–2310.

Srinivasan R, Alvarez JM (2008). Effect of an alternate weed host, hairy nightshade, *Solanum sarrachoides*, on the biology of the two most important potato leafroll virus vectors, Myzus persicae and Macrosiphum euphorbiae. *Environ. Entomol.* 37(2): 579–587.

Tacke E, Priifer D, Schmitz J, Rohde W (1991).The potato leafroll luteovirus 17K protein is a single-stranded nucleic acid-binding protein. *J. Gen. Virol*. 72: 2035–2038. doi: 10.1099/0022-1317-728-2035.

Tamura K, Stecher G, Kumar S (2021). MEGA11: Molecular evolutionary genetics analysis version 11. *Mol. Biol. Evol.* 38(7): 3022–3027.

Venkata SS. (2025). Virus Transmission by Insect Vectors Affecting Tuber Crops: A Comprehensive Analysis of Crop Health and Global Food Security. 10.13140/RG.2.2.10574.52804.

Yusubakhmedov AA, Fayziev VB (2022). Determination of some biological properties and identification of potato virus M using PCR method. *J. Mod. Biol. Genet*. 1-2(1): 14–20.

Yusubakhmedov AA, Fayziev VB (2023). Effect of viruses on the amount of starch in the potato nodule, international scientific-practical conference" Actual problems of modern biology: Solutions, prospects and integration of science and education in teaching. Chirchik State Pedagogical University October, pp. 26–27.

Zavriev SK, Kanyuka KV, Levay KE (1991). The genome organization of potato virus M RNA. *J. Gen. Virol*. 72: 9–14. https://doi.org/10.1099/0022-1317-72-1-9.