ISOLATION, IDENTIFICATION AND CHARACTERIZATION OF POTATO VIRUS F (PVF)

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Abstract: *This study investigates the isolation, identification, and characterization of Potato Virus F (PVF), an economically important but understudied plant virus affecting potato (Solanum tuberosum L.). Infected plant samples were collected from different agro-ecological zones of Uzbekistan and subjected to morphological and serological examination. Serological detection was carried out using the enzyme-linked immunosorbent assay (ELISA), confirming the presence of PVF in symptomatic plants. Molecular diagnosis was performed using reverse transcription polymerase chain reaction (RT-PCR), which enabled the amplification and partial sequencing of the viral genome. The phylogenetic analysis of PVF isolates revealed genetic divergence from other geographically distinct strains. The biological impact of PVF was also assessed, showing significant reductions in plant growth and tuber yield. Additionally, the study discusses potential pathways of virus transmission, including vegetative propagation and insect vectors, and suggests management strategies to prevent the spread of PVF in potato cultivation.*

Keywords: *Potato Virus F (PVF), ELISA, RT-PCR, molecular diagnosis, plant virology, virus isolation, phylogenetic analysis, potato disease, virus transmission, crop protection*

Potato (Solanum tuberosum L.) is one of the most essential staple crops worldwide, providing a significant source of carbohydrates and nutrients for human consumption. However, its productivity is frequently compromised by viral diseases, among which Potato Virus F (PVF) has emerged as an important but relatively understudied pathogen. PVF, a member of the genus *Carlavirus*, is known to cause latent infections as well as visible symptoms such as leaf mosaic, curling, and growth retardation, particularly under stress conditions. The effective detection, identification, and management of PVF are therefore critical for ensuring sustainable potato production, especially in regions where vegetative propagation and seed tuber exchange are common agricultural practices.

The increasing economic impact of plant viruses has prompted the need for integrated diagnostic approaches that combine morphological observation with advanced molecular techniques. In this context, the accurate identification of PVF using serological assays such as ELISA (Enzyme-Linked Immunosorbent Assay) and molecular methods like RT-PCR (Reverse Transcription Polymerase Chain Reaction) is

vital. These tools enable early detection and help prevent large-scale crop losses. Despite its significance, there is limited research on the molecular diversity, epidemiology, and pathogenicity of PVF in Central Asian potato-growing systems, particularly in Uzbekistan. This study aims to fill that gap by characterizing PVF isolates through field sampling, laboratory analysis, and phylogenetic comparison.

The investigation revealed that PVF exhibits diverse pathological and molecular characteristics, depending on the environmental and biological context in which it occurs. Symptomatic plants showed mild to moderate chlorosis, leaf crinkling, and growth suppression. These symptoms, while non-specific, were consistently associated with PVF-positive samples confirmed through ELISA. The serological response suggested a high rate of latent infection in asymptomatic tubers, highlighting the potential for unnoticed virus transmission during vegetative propagation cycles.

RT-PCR analysis enabled the amplification of a partial genomic segment (~850 bp) specific to PVF, allowing for sequence comparison and phylogenetic placement. The isolates obtained from Uzbek agro-regions exhibited nucleotide variations distinct from those of PVF strains reported in Eastern Europe, suggesting localized evolution and possible host adaptation[1] Such genetic divergence may influence virus virulence, transmission efficiency, and host interactions, making phylogenetic tracking an essential component of virological surveillance.

In terms of transmission pathways, both mechanical means (tuber propagation, contaminated tools) and biological vectors (e.g., aphids) were implicated. The detection of PVF in tubers without visible symptoms underscores the inadequacy of visual inspection alone and the necessity for routine molecular diagnostics in seed certification programs. Moreover, the virus was found to reduce tuber yield by up to 35%, confirming its agricultural and economic significance[2]

These findings emphasize the urgent need for an integrated disease management framework, including the use of certified virus-free planting material, strict phytosanitary measures, and breeding programs focused on PVF resistance. Continuous monitoring using molecular tools will be vital to mitigate the spread of PVF and maintain potato production stability in virus-prone regions.

The experimental data generated through field sampling, serological diagnostics, and molecular characterization yielded several significant findings:

Symptomatology and Visual Assessment: Field observations indicated a range of PVF-associated symptoms in infected potato plants, including mild to moderate leaf mosaic, curling, chlorotic streaking, and notable reduction in plant vigor. Approximately 65% of the plants showing these symptoms tested positive for PVF[3]

Serological Detection via ELISA: Out of 120 collected samples, 89 tested positive for PVF using Double Antibody Sandwich ELISA (DAS-ELISA), indicating a 74.2% infection rate. This confirmed the reliability of ELISA for preliminary screening of PVF in field conditions[4]

Molecular Confirmation through RT-PCR: RT-PCR successfully amplified an ~850 base pair fragment corresponding to the coat protein gene of PVF in 77 of the ELISA-positive samples. The presence of distinct PCR bands further validated the accuracy of serological detection and confirmed the molecular identity of the virus[5]

Sequence Analysis and Phylogenetics: Partial sequencing of representative PVF isolates revealed nucleotide polymorphisms, with sequence identity ranging from 91% to 96% compared to global reference strains. Phylogenetic analysis placed the Uzbek isolates in a separate subclade, suggesting possible regional divergence and evolution.

Agronomic Impact Assessment: Controlled field trials showed that PVF-infected plants experienced an average yield reduction of 31.6% compared to virus-free controls. Infected plants also displayed delayed tuber formation and lower tuber uniformity, emphasizing the virus's economic significance.

This study has demonstrated that Potato Virus F (PVF) is a prevalent and economically impactful pathogen in potato cultivation systems within Uzbekistan. The integration of visual inspection, ELISA, and RT-PCR methodologies provided robust and complementary diagnostic data, confirming the virus's widespread incidence and molecular identity. Phylogenetic analysis suggests that the PVF isolates in Uzbekistan exhibit unique genetic traits, likely shaped by regional agroecological pressures and propagation practices.

Given the significant yield losses associated with PVF infection, urgent attention is required to implement virus-free seed certification protocols, vector management, and surveillance systems. Furthermore, long-term mitigation should focus on breeding and deploying PVF-resistant cultivars adapted to local conditions. Continued molecular monitoring will be essential for understanding viral evolution and enhancing crop protection strategies in the region.

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