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ToMV IN WATER: MOLECULAR DETECTION, PHYLOGENY AND INDICATOR POTENTIAL

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Aquatic environments are important reservoirs of phytopathogens capable of prolonged survival outside their hosts. Due to high environmental stability, certain plant viruses, and tobamoviruses in particular, can persist in natural and anthropogenically impacted water systems. While plant viruses are well documented in agriculture, their occurrence in Ukrainian aquatic ecosystems remains understudied. Growing anthropogenic pressure and the need for reliable viral markers highlight the importance of identifying suitable indicators and assessing their genetic diversity. This study aimed to detect plant viruses in aquatic ecosystems and reusable organic bioresources in Ukraine, and to evaluate the genetic relatedness of identified isolates through phylogenetic analysis to assess their potential as indicators of anthropogenic contamination. A total of 22 water samples (river, lake, tap, and wastewater) from Kyiv and four other regions, along with horse manure, tobacco dust, and chicken compost, were analyzed. Viral concentration was performed by adsorption–elution. RT-PCR with specific primers was used to screen samples for a number of relevant pathogens identified in literature, including PMMoV, ToMV, ToBRFV, TMV, TSWV, CGMMV, TAV, ZYMV, CMV, WMV-2, and PSTVd. ToMV-positive amplicons were Sanger-sequenced, and phylogenetic analysis was conducted using Maximum Likelihood (Tamura 3-parameter model, MEGA7) with 1000 bootstrap replicates. Among all targets, only tomato mosaic virus (ToMV) was detected, in 5 of 22 water samples (Lake Verkhovyna, Lake Nyvky, Kytaiv ponds, Rusanivka canal, and Bortnychi wastewater). No viral or viroid signatures were found in manure, tobacco dust, or compost. Phylogenetic analysis of partial coat protein gene sequences placed the Ukrainian isolates within clade I, clustering with the Turkish isolate CAN53 (91.8%

identity). However, pairwise comparisons showed higher similarity (93.2–97.3%) to isolates from Brazil, South Korea, the Netherlands, Serbia, and China, reflecting a complex phylogeography. Two Ukrainian isolates shared 97% identity, suggesting a common contamination source. Selective detection of ToMV across diverse water bodies, despite the absence of other widespread plant viruses, confirms its environmental stability and supports its consideration as a promising viral contamination indicator. Phylogenetic clustering with a Turkish isolate, along with Ukraine's substantial tomato imports from Turkey, points to potential introduction pathways via contaminated plant material. These findings emphasize the need for region-specific validation of viral markers and highlight the value of phylogenetic surveillance in tracking phytopathogen circulation through aquatic ecosystems and recycled bioresources.

Keywords: virus; ToMV; aquatic ecosystems; recycled bioresources; phylogenetic analysis.

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