

First Report of Tomato Leaf Curl Laos Virus Causing Leaf Curl Disease in Tomato in Vietnam

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Tomato (*Solanum lycopersicum*) cultivation has been hampered by the emergence of begomoviruses causing leaf curl diseases, resulting in significant yield reduction (Charoenvilaisiri et al. 2020; Lai et al. 2024). During field surveys between December 2024 and May 2025 in Hue City, Vietnam, we surveyed five tomato gardens ($n = 100$ plants, 100 to 200 m² per garden) but found the occurrence of leaf curl disease symptoms only in two plants. Disease symptoms included upward leaf curling and stunted and chlorotic leaves. Whiteflies (*Bemisia tabaci*) were observed on the abaxial leaf surface of symptomatic plants. Total DNA was isolated from two plants using a cetyltrimethylammonium bromide-based DNA extraction protocol (Doyle and Doyle 1987). The presence of begomovirus was confirmed by polymerase chain reaction (PCR), using the degenerate begomovirus-specific primers SPG1/SPG2 (Li et al. 2004). The SPG1/SPG2 amplified products (from two plants) were sequenced using the Sanger sequencing method (Apical Scientific, Selangor, Malaysia) and the subsequent BLASTn analysis of nucleotide sequencing results returned tomato leaf curl Laos virus (ToLCLV) as the closest match (percent identity of 97.46 and 97.57%; e-value of 0.0). Taxonomically, ToLCLV (*Begomovirus solanumlaosense*) belongs to the genus *Begomovirus* under the family *Geminiviridae*. Due to

the limited publicly available sequences of ToLCLV genomes, we sequenced the ToLCLV genome using the primer walking approach. Based on SPG1/SPG2 sequences, ToLCLV_A_F3 (5'-GCAGATCTTCCATCGATC TG-3') and ToLCLV_A_R3 (5'-GGAGCCACTGTACTCAGGT-3') were designed to amplify the rest of the ToLCLV circular DNA-A, and the 2,120-bp PCR product was sequenced by Sanger sequencing. In addition, the primer pairs ToLCLV_A_F4 (5'-AGCCTATTTAGTGTGTGGTC-3') and ToLCLV_A_R1 (5'-CATCACTGCAACTCAAGCAGA-3') were used for PCR diagnostics and sequencing. The complete DNA-A sequence was assembled based on read overlaps to obtain the full 2,758-nt sequence (GenBank accession PX020954). It shared 91.41% identity to the nucleotide sequence of ToLCLV in Laos (GenBank accession NC_004613). The phylogenetic tree was constructed in MEGA12 using the neighbor-joining method with a bootstrap of 1,000 replicates. The analysis displayed the ToLCLV Vietnam isolate "Hue01" with the Laos isolate of ToLCLV (NC_004613) in the same clade. Both the ToLCLV isolates are most closely related to the tomato leaf curl Malaysia virus (NC_004648). Based on the International Committee on Taxonomy of Viruses (ICTV) species and strain demarcation thresholds for begomoviruses (Brown et al. 2015), this begomovirus species was designated as the ToLCLV strain "Hue01." This is the first report of ToLCLV in Vietnam. Further investigations are needed to determine the distribution of ToLCLV in the broader Southeast Asia geographic region and its infectivity and effects on tomato cultivation.

References:

- Brown, J. K., et al. 2015. Arch. Virol. 160:1593.
- Charoenvilaisiri, S., et al. 2020. Crop Prot. 127:104948.
- Doyle, J. J., and Doyle, J. L. 1987. Phytochem. Bull. 19:11.
- Lai, H.-C., et al. 2024. Plant Dis. 108:2688.
- Li, R., et al. 2004. Plant Dis. 88:1347.

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