# Complete Genome Sequence of a Pepper Yellow Leaf Curl Indonesia Virus Isolated from Tomato in Bali, Indonesia

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**ABSTRACT**  We report a complete genome sequence of a pepper yellow leaf curl Indonesia virus (PepYLCIV) isolated in Bali, Indonesia. This virus shares around 90% identity with other PepYLCIV DNA-As and 86% identity with DNA-Bs, suggesting that it is a novel isolate of PepYLCIV.

Most begomoviruses (family *Geminiviridae*, genus *Begomovirus*) possess bipartite circular, single-stranded DNA genomes. Begomoviruses are transmitted by whitefly and cause typical mosaic, yellowing, curling symptoms on leaves and stunted growth of plants, resulting in serious damage to crop production in tropical and subtropical regions.

Plants infected with begomoviruses were reported on Bali Island, Indonesia (1), but no complete genome sequence of a begomovirus has been deposited in the DDBJ/ENA/GenBank database.

In August 2019, we collected tomato leaves showing yellowing and a mosaic pattern, typical of begomovirus infections in Bali (8°14′8″S, 115°24′19″E). Total DNA was extracted from collected tomato leaves using a DNeasy plant minikit (Qiagen, Germany), followed by PCR amplification (BIOTAQ, Bioline, UK) of a part of the DNA-A components of the begomovirus genome, using universal primers (UPV1 and PAV1c715; product size, 1,622 nucleotides [nt]) (2). Amplified fragments were cloned into the pGEM-T Easy vector (Promega, USA) or pCRZeroT (3), and at least three independent plasmids were sequenced using the BigDye Terminator version 3.1 cycle sequencing kit and the Applied Biosystems 3500 genetic analyzer (Thermo Fisher Scientific, USA) with vector-specific primers (5′-GTAAAACGACGGCCAG-3′ and 5′-CAGGAAACAGCTATGACC-3′ for pGEM-T Easy; 5′-CGCAATTAATGTGAGTTAGC-3′ and 5′-GGGCCTCTTCGCTATTAC-3′ for pCRZeroT). Sequences were assembled using ATGC version 4.3.5 (Genetyx, Japan). We designed a primer set (5′-GAAGTCTGTAT ATATTATTGGCAAAG-3′ and 5′-CCCAAGGTATACAACAATGAC-3′; 1,207 nt) for inverse PCR to clone the remainder of the genome to amplify the circular DNA fragment, covering the complete nucleotide of the genome, and sequenced it in the same manner. DNA-B was amplified using pepper yellow leaf curl Indonesia virus (PepYLCIV)-specific primers (PepYLCIV_BFs, 5′-GTCCGACGTGGAATATGCAAGTG-3′; PepYLCIV_BRs, 5′-GTGCGTTCTTTGACACGTTGCTG-3′, 1,831 nt), and inverse PCR was performed with PYLCIV-Bali-invBF (5′-AAAAGAAGTGCGTTGTAAATACC-3′) and PYLCIV-Bali-invBR (5′-AAAAAAGAGTGCATTCCAGC-3′; product size, 1,124 nt). These products were used for cloning and sequencing, and PYLCIV-Bali-B-2360F (5′-GTTCAAACATTTTAGCC AACA-3′) was used for internal sequencing. Nucleotide sequence identities were calcu-

**TABLE 1** Similarity analysis of PepYLCIV-[IN:Bali:Tom:19] with other PepYLCIV isolates

| PepYLCIV isolate | Accession no. of: | | Sequence identity (%) with: | |
|---|---|---|---|---|
| | DNA-A | DNA-B | DNA-A | DNA-B |
| Indonesia:Bogor:2000 | DQ083764 | NA[a] | 90.4 | NA |
| Indonesia:Bogor:Tomato:2000 | DQ083765 | NA | 90.2 | NA |
| Indonesia:2005 | AB267834 | AB267835 | 92.4 | 86.7 |
| Indonesia:Tomato:2005 | AB267836 | AB267837 | 90.1 | 86.9 |
| Indonesia:Ageratum:2005 | AB267838 | AB267839 | 91.3 | 85.4 |
| Indonesia:Sumatra:Pepper:2012, BA_A6-1 | LC051112 | LC314792 | 91.5 | 86.2 |
| Indonesia:Sumatra:Pepper:2012, BA_C1-1 | LC051113 | LC314793 | 89.9 | 85.9 |
| Indonesia:Sumatra:Pepper:2012, BA_D1-1 | LC051114 | LC314794 | 89.4 | 86.6 |
| Indonesia:Sumatra:Pepper:2012, BA_E2-1 | LC051115 | LC314795 | 89.5 | 87.3 |

[a] NA, not available; no sequence data were found in DDBJ/ENA/GenBank.

lated using GENETYX-MAC version 19 (Genetyx). No alphasatellite or betasatellite DNAs were detected using universal primers (4, 5).

DNA-A (2,743 nt; GC content, 41.6%) was predicted to have six open reading frames (ORFs) and DNA-B (2,721 nt; GC content, 39.5%) two ORFs, typical for bipartite Old World begomoviruses, using ORFfinder (https://www.ncbi.nlm.nih.gov/orffinder/). A BLASTn search (https://blast.ncbi.nlm.nih.gov/Blast.cgi) indicated that this virus shared high similarity with PepYLCIV isolates (Table 1). From a homology search analysis using the full-genome sequences of DNA-A and DNA-B, this isolate showed high sequence identity with PepYLCIV isolates (Table 1).

A total of 23 partial DNA-A sequences of PepYLCIV were reported (GenBank accession numbers LC381258 through LC381280). These sequences and this isolate shared 80.8 to 89.2% sequence identity, suggesting that our isolate is different from those previously reported.

According to the species demarcation criteria of the genus *Begomovirus* (6), this isolate was classified as a PepYLCIV. We propose that this isolate be named PepYLCIV-[Indonesia:Bali:Tomato:2019] (PepYLCIV-[IN:Bali:Tom:19]).

**Data availability.** The genome sequences of PepYLCIV-[IN:Bali:Tom:19] were deposited in the DDBJ/ENA/GenBank database under accession numbers LC542629 (DNA-A) and LC542630 (DNA-B).

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