

**KERAGAMAN VIRUS PADA TANAMAN CABAI KERITING  
(*Capsicum annuum* L.) DI DESA KARANGSEWU, KULON PROGO,  
DAERAH ISTIMEWA YOGYAKARTA**

Muhammad Naufal Dzakwan Luzen

21/477095/BI/10745

Dosen Pembimbing : Dr. Aprilia Sufi Subiastuti, S.Si.

**INTISARI**

Penyakit keriting kuning akibat infeksi virus pada tanaman cabai keriting ditemukan hampir di seluruh wilayah Indonesia dan memengaruhi produktifitas cabai keriting nasional. Perkembangan teknologi sekuensing nanopore yang dikembangkan oleh Oxford Nanopore Technologies (ONT) mampu untuk mengidentifikasi virus dan novel virus dengan cepat dan dalam skala besar. Oleh karena itu, perlu adanya perhatian lebih terkait deteksi potensi infeksi virus sebagai salah satu penyebab penyakit keriting kuning. Tujuan penelitian ini adalah untuk mengetahui tingkat infeksi virus, keberagaman virus, dan mengkonfirmasi keberadaan *Begomovirus* yang ditemukan pada sampel tanaman cabai keriting varietas Dji-Tu F1 usia 90 HST di Desa Karangsewu, Kulon Progo, Daerah Istimewa Yogyakarta. Keberagaman virus dideteksi menggunakan teknologi sekuensing nanopore. Hasil sekuensing nanopore dari sampel menunjukkan keberadaan empat genus virus yang diasosiasikan dengan penyakit keriting kuning, yaitu *Begomovirus*, *Solendovirus*, *Polerovirus*, dan *Orthospovirus*. Selain itu, ditemukan spesies *Begomovirus*, yaitu *Pepper yellow leaf curl Indonesia virus* (PepYLCIV) yang telah memiliki banyak riwayat penyebaran di Indonesia. Hasil analisis virome tersebut masih perlu divalidasi menggunakan metode molekular PCR karena potensi kesalahan preparasi sampel atau keterbatasan kemampuan analisis bioinformatika. Digunakan primer universal *Begomovirus* PAL1v1978 dan PAR1c715 dengan hasil pita DNA  $\pm$  1500 bp. Data sekuensing hasil PCR kemudian dianalisis filogenetik dengan model Kimura-2-parameter dan algoritma *neighbor-joining* untuk mengetahui hubungan kekerabatannya. Hasil penelitian menunjukkan bahwa sampel memiliki hubungan kekerabatan yang dekat dengan PepYLCIV isolat APWS dan TDWS-21 dari Sumatera Barat. Penelitian ini diharapkan dapat memberikan informasi terkait virus apa saja yang menyerang tanaman cabai keriting di Desa Karangsewu, Kulon Progo, Daerah Istimewa Yogyakarta.

Kata kunci : *Begomovirus*, HTS, PCR, tanaman cabai

## VIRUS DIVERSITY IN CURLY CHILI PLANTS (*Capsicum annuum* L.) IN KARANGSEWU VILLAGE, KULON PROGO, SPECIAL REGION OF YOGYAKARTA

Muhammad Naufal Dzakwan Luzen

21/477095/BI/10745

Supervisor : Dr. Aprilia Sufi Subiastuti, S.Si.

### ABSTRACT

Yellow leaf curl disease caused by viral infection in curly chili plants (*Capsicum annuum* L.) has been reported in nearly all regions of Indonesia and significantly affects national chili productivity. The advancement of nanopore sequencing technology developed by Oxford Nanopore Technologies (ONT) enables rapid and large-scale identification of viruses, including novel viruses. Therefore, greater attention is needed regarding the detection of potential viral infections as one of the causes of yellow leaf curl disease. This study aimed to determine the level of viral infection, viral diversity, and to confirm the presence of *Begomovirus* in samples of curly chili plants (Dji-Tu F1 variety) aged three months after planting in Karangsewu Village, Kulon Progo, Special Region of Yogyakarta. Viral diversity was detected using nanopore sequencing technology. The sequencing results revealed the presence of four viral genera associated with yellow leaf curl disease: *Begomovirus*, *Solendovirus*, *Polerovirus*, and *Orthotospovirus*. Additionally, a specific species of *Begomovirus*, namely *Pepper yellow leaf curl Indonesia virus* (PepYLCIV), was detected, which has previously been reported in various regions across Indonesia. The virome analysis results were further validated using molecular methods, specifically PCR, to account for possible sample preparation errors and limitations in bioinformatic analyses. Universal *Begomovirus* primers, PAL1v1978 and PAR1c715, were used and successfully amplified a DNA band of approximately 1500 bp. The PCR amplicons were then sequenced and analyzed phylogenetically using the Kimura-2-parameter model and the *neighbor-joining* algorithm. The analysis showed that the sample had a close genetic relationship with PepYLCIV isolates APWS and TDWS-21 from West Sumatera. This study is expected to provide preliminary information regarding viruses infecting curly chili plants in Karangsewu Village, Kulon Progo, Special Region of Yogyakarta.

Keywords: *Begomovirus*, HTS, PCR, curly chili pepper