



INTISARI

Penelitian ini bertujuan untuk mengetahui insidensi dan distribusi penyebab penyakit keriting pada jaringan tanaman melon dengan melakukan deteksi secara molekuler. Pengamatan dan pengambilan sampel dilakukan pada *greenhouse* melon di Blulukan, Colomadu, Kabupaten Karanganyar, Jawa Tengah dengan mengamati insidensi penyakit dan gejala. Identifikasi dan deteksi distribusi penyebab penyakit keriting dilakukan dengan metode *Polymerase Chain Reaction* (PCR) menggunakan primer universal Begomovirus yaitu Krusty-Homer. Hasil identifikasi menunjukkan bahwa sampel tanaman positif terinfeksi Begomovirus ditandai dengan munculnya band berukuran ± 580 bp. Hasil analisis sekuens DNA isolat virus dari memiliki kemiripan tertinggi dengan SLCCNV Kulonprogo dengan nomor aksesori MZ458530 sebesar 99,7%. Distribusi SLCCNV secara PCR ditemukan berada pada bagian pucuk daun, batang, daun tua, kulit buah melon, daging buah melon, dan kulit biji buah melon. Laporan ini dapat menjadi informasi mengenai penyebaran SLCCNV di dalam jaringan tanaman melon. Insidensi penyakit keriting tertinggi selama 4 minggu pengamatan ditunjukkan di GH 3 sebesar 24.4%, sedangkan insidensi penyakit terendah ditunjukkan di GH 1 sebesar 15.6 %.

Kata Kunci: SLCCNV, *Bemisia tabaci*, PCR

ABSTRACT

This study aims to determine the incidence and distribution of the cause of curly disease in melon plant tissue by conducting molecular detection. Observations and sampling were carried out in melon greenhouses in Bluluk, Colomadu, Karanganyar Regency, Central Java by observing disease incidence and symptoms. Identification and detection of the distribution of the cause of curly disease was carried out by Polymerase Chain Reaction (PCR) method using Begomovirus universal primer, Krusty-Homer. The identification results showed that the plant samples were positively infected with Begomovirus characterized by the appearance of a band measuring ± 580 bp. The results of DNA sequence analysis of virus isolates had the highest similarity with SLCCNV Kulonprogo with accession number MZ458530 of 99.7%. The distribution of SLCCNV by PCR was found in the tops of leaves, stems, old leaves, melon rind, melon flesh, and melon seed coat. This report can provide information on the distribution of SLCCNV in melon plant tissues. The highest incidence of curl disease during the 4 weeks of observation was shown in GH 3 at 24.4%, while the lowest disease incidence was shown in GH 1 at 15.6%.

Keywords: SLCCNV, *Bemisia tabaci*, PCR