



INTISARI

Penentuan jenis tanaman budidaya dengan sistem polikultur berperan penting dalam persebaran dan keanekaragaman Begomovirus. Begomovirus merupakan virus tanaman yang memiliki inang sangat luas. Tanaman dari famili *Solanaceae* sering dipilih petani sebagai tanaman yang dibudidayakan secara polikultur merupakan inang dari Begomovirus. Penelitian ini bertujuan untuk mengidentifikasi spesies virus anggota genus *Begomovirus* sebagai penyebab penyakit kriting kuning pada famili *Solanaceae* yang ditanam di lahan campuran. Penelitian meliputi pengamatan kejadian penyakit, intensitas penyakit, variasi gejala, pengambilan sampel, deteksi molekuler dengan *Polymerase Chain Reaction* (PCR) menggunakan primer universal Begomovirus, sekvensing DNA, dan analisis filogenetik. Metode pengambilan sampel tanaman terung, cabai dan tomat yang dilakukan di lahan campuran di Gunungkidul, Bantul, dan Sleman, Provinsi DI Yogyakarta. Sampel daun tanaman bergejala Begomovirus diamplifikasi DNA dengan teknik *Polymerase Chain Reaction* (PCR) menggunakan primer Krusty-Homer. Hasil PCR menunjukkan bahwa sampel tanaman positif terinfeksi oleh Begomovirus ditandai dengan munculnya pita berukuran $\pm 580\text{bp}$. Hasil analisis sekvens Begomovirus menunjukkan bahwa setiap lahan dengan tanaman famili *Solanaceae* dapat terinfeksi virus anggota genus *Begomovirus* dengan spesies yang berbeda. Sampel lahan campuran Watusigar, Gunungkidul pada isolat terung memiliki kekerabatan terdekat 99,14% dengan *Tomato yellow leaf curl Kanchanaburi virus* (TYLCKaV), isolat cabai kekerabatan sebesar 98,91% dengan *Pepper yellow leaf curl Indonesia virus* (PepYLCIV), dan pada isolat tomat sebesar 97,89% dengan PepYLCIV. Berbeda halnya dengan hasil sekvens Begomovirus pada lahan campuran Selopamioro, Bantul, isolat terung memiliki kemiripan tertinggi (98,95%) dengan TYLCKaV. Pada isolat cabai, kemiripan tertinggi (97,14%) dengan PepYLCIV, dan pada isolat tomat kemiripan 99,12% dengan TYLCKaV. Sedangkan analisis sekvens Begomovirus di Hargobinangun, Sleman menunjukkan isolat terung memiliki kemiripan tertinggi sebesar 98,54% dengan TYLCKaV, dan isolat tomat yaitu memiliki kemiripan tertinggi (98,64%) TYLCKaV. Kesimpulannya, analisis sekvens Begomovirus di tiga kabupaten menunjukkan adanya lebih dari satu spesies virus anggota genus *Begomovirus* dalam satu lahan yaitu TYLCKaV dan PepYLCIV.

Kata Kunci: Polikultur, Solanaceae, Begomovirus, TYLCKaV, PepYLCIV



ABSTRACT

Determination of the type of cultivated plants by the polyculture system played an important role in the distribution and diversity of Begomovirus. Begomovirus is plants virus that has a very wide host. Plants from the *Solanaceae* family are often chosen by farmers, cultivate plants in polyculture is the host of Begomovirus. This study aims to identify the virus species member of the genus *Begomovirus* as the cause of yellow curl disease in plants of the *Solanaceae* family grown on mixed crop fields. The study included observation of disease incidence, disease intensity, sampling, molecular detection molecular detection by Polymerase Chain Reaction (PCR) technique using Begomovirus universal primers, DNA sequencing, and phylogenetic analysis. The sampling method for eggplant, chili, and tomato plants was carried out in mixed fields in Gunungkidul, Bantul, and Sleman, DI Yogyakarta Province. Leaf samples of plants with Begomovirus symptoms were DNA amplified by Polymerase Chain Reaction (PCR) technique using Krusty-Homer primers. The PCR results showed that eggplant, chili, and tomato samples were infected by Begomovirus with a band size of \pm 580bp. The results of analysis Begomovirus sample sequence in mixed plantation Watusigar, Gunungkidul in eggplant isolates had the closest relationship of 99.14% with *Tomato yellow leaf curl Kancanaburi virus* (TYLCKaV), chili isolates were 98.91% closely related to *Pepper yellow leaf curl Indonesia virus* (PepYLCIV), and tomato isolates have the closest relationship of 97.89% with PepYLCIV. Analysis sample sequence Begomovirus of Selopamioro, Bantul mixed plantation, eggplant isolate had the highest similarity of 98.95% with TYLCKaV. In chili isolates, the highest similarity was 97.14% with PepYLCIV, and in tomato isolates which had the highest similarity of 99.12% with TYLCKaV. Sample sequence analysis for Begomovirus mixed land Hargobinangun, Sleman was in eggplant isolates with the highest similarity of 98.54% with TYLCKaV, and tomato isolates which had the highest similarity of 98.64% with TYLCKaV. Begomovirus sequence analysis in three districts showed the presence of more than one virus species belonging to the Begomovirus genus in one field, name TYLCKaV and PepYLCIV.

Key Word: Policultur, Solanaceae, Begomovirus, TYLCKaV, PepYLCIV