

Intisari

Bean common mosaic virus (BCMV, *Potyvirus phaseovulgaris*) merupakan salah satu virus penting pada tanaman famili Fabaceae yang dapat menyebabkan gejala mosaik, malformasi daun, dan gangguan pertumbuhan. Penelitian ini bertujuan untuk mengidentifikasi keberadaan gulma dan tanaman hias famili Fabaceae di Daerah Istimewa Yogyakarta dan Jawa Tengah sebagai inang alternatif BCMV, menganalisis hubungan kekerabatan isolat yang terdeteksi, serta menguji penularannya pada tanaman Fabaceae. Sampel tumbuhan bergejala dikoleksi secara *purposive* dari beberapa lokasi, kemudian dilakukan deteksi molekuler menggunakan RT-PCR dengan target gen *coat protein* BCMV yang menghasilkan amplikon berukuran 469 bp. Hasil penelitian menunjukkan bahwa 11 dari 16 sampel terkonfirmasi positif BCMV, yang berasal dari *Centrosema* sp., *Macroptilium* sp., *Clitoria ternatea*, dan *Arachis pintoi*. Analisis filogenetik menggunakan metode Maximum Likelihood dengan model parameter Tamura 3 menunjukkan bahwa isolat-isolat hasil penelitian berada dalam satu kelompok dengan BCMV dan berkerabat dekat dengan isolat referensi dari Asia Timur, sedangkan yam bean mosaic virus (YBMV, *Potyvirus*) terpisah sebagai outgroup. Analisis kemiripan sekuens menunjukkan identitas nukleotida tinggi antar isolat Indonesia (90–97%) dan lebih rendah terhadap YBMV sebesar 82%. Penularan secara mekanis dan melalui vektor *Aphis craccivora* berhasil menimbulkan gejala mosaik pada tanaman uji: Kacang Panjang, Kacang hijau, Kacang Tunggak Kedelai dan Buncis, pada minggu keempat setelah inokulasi. Hasil ini mengindikasikan bahwa gulma dan tanaman hias Fabaceae berpotensi menjadi sumber inokulum BCMV di ekosistem pertanian.

Kata kunci: Analisis filogenetik, BCMV, Fabaceae, Penularan mekanis dan vektor, RT-PCR

Abstract

Bean common mosaic virus (BCMV, *Potyvirus phaseovulgaris*) is one of the major viruses infecting plants of the Fabaceae family, causing mosaic symptoms, leaf malformation, and growth disorders. This study aimed to identify the presence of weeds and ornamental plants of the Fabaceae family in the Special Region of Yogyakarta and Central Java as alternative hosts of BCMV, to analyze the phylogenetic relationships among the detected isolates, and to evaluate their transmission to Fabaceae plants. Symptomatic plant samples were purposively collected from several locations and subjected to molecular detection using RT-PCR targeting the BCMV *coat protein* gene, which produced a 469 bp amplicon. The results showed that 11 out of 16 samples were confirmed positive for BCMV, originating from *Centrosema* sp., *Macroptilium* sp., *Clitoria ternatea*, and *Arachis pintoi*. Phylogenetic analysis using the Maximum Likelihood method with the Tamura 3-parameter model indicated that the isolates obtained in this study clustered within the same group as BCMV and were closely related to reference isolates from East Asia, while yam bean mosaic virus (YBMV, *Potyvirus*) was separated as an outgroup. Sequence similarity analysis revealed high nucleotide identity among Indonesian isolates (90–97%) and lower identity with YBMV (82%). Mechanical transmission and transmission through the vector *Aphis craccivora* successfully induced mosaic symptoms on test plants : yardlong bean, mung bean, cowpea, soybean, and common bean, at four weeks after inoculation. These findings indicate that Fabaceae weeds and ornamental plants have the potential to serve as sources of BCMV inoculum in agricultural ecosystems.

Keywords: BCMV, Fabaceae, Mechanical and vector transmission, Phylogenetic analysis, RT-PCR