



POLA TEMPORAL, SPASIAL, DAN GENETIK INFEKSI *BEGOMOVIRUS* PADA TANAMAN MELON (*Cucumis melo* L.)

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Intisari

Melon merupakan salah satu produk pertanian hortikultura dengan nilai jual tinggi. *Begomovirus*, di sisi lain, merupakan salah satu virus yang banyak dipelajari pada dasawarsa terakhir ini. Penelitian ini bertujuan melaporkan infeksi *Begomovirus* di tanaman melon yang terjadi pada ekosistem *greenhouse* dengan iklim alami pada dataran rendah dan dataran tinggi, yang dijabarkan sebagai mengetahui gejala dan pola temporal dari infeksi *Begomovirus* pada melon dan mengetahui efek perbedaan ekosistem artifisial, perbedaan genotip inang, dan perbedaan lokasi terhadap infeksi *Begomovirus* pada melon. Penanaman melon dan pengambilan data lapangan dilakukan pada *greenhouse* di dua lokasi : Pangalengan, Jawa Barat (Nudira Farm, PT. Nudira Sumber Daya Indonesia) dan Prambanan, Daerah Istimewa Yogyakarta. Benih melon yang digunakan dalam penelitian ini adalah kultivar Hikapel yang berasal dari Laboratorium Genetika dan Pemuliaan, Fakultas Biologi UGM dan benih melon komersial. *Begomovirus* didapatkan dari infeksi yang ditularkan secara alami oleh vektor kutu kebul. *Simple Random Sampling* dilakukan untuk pemeriksaan gejala infeksi virus, dilanjutkan dengan skala keparahan infeksi. Pengukuran karakter fisiologis tanaman melon dan jumlah kutu kebul serta pendokumentasian kondisi *greenhouse*, variabel iklim dan geografi juga dilakukan. Analisis molekular dilakukan dengan PCR. Data keparahan infeksi virus digunakan untuk analisis intensitas gejala penyakit dan digunakan untuk membandingkan tingkat ketahanan terhadap *Begomovirus* pada tanaman yang ditumbuhkan pada *greenhouse*. Karakter fisiologis tanaman dianalisis menggunakan ANOVA. Seluruh data dianalisis menggunakan korelasi Pearson. Hasil penelitian menunjukkan bahwa gejala infeksi *Begomovirus* pada tanaman melon terutama berupa *mosaic* kuning pada pertulangan daun dan daging daun di sekitar pertulangan daun. Hasil penelitian juga menunjukkan bahwa infeksi *Begomovirus* pada tanaman melon mengalami peningkatan dari sejak pertama kali paparan hingga setelah fase reproduktif. Berdasarkan penelitian ini diketahui bahwa infeksi *Begomovirus* pada tanaman melon memiliki perbedaan pola : pada ekosistem artifisial dengan ukuran mesh dan vegetasi sekitar berbeda; pada genotip inang, dengan kondisi infeksi yang rendah secara berurutan yaitu kultivar Kinanti, Kinanti super, Hikapel, dan Kirani; serta pada dataran rendah dan dataran tinggi. Hasil PCR dengan primer universal Krusty-Homer memastikan bahwa sampel terinfeksi *Begomovirus*.

Kata kunci : Melon, *Begomovirus*, *greenhouse*, gejala, karakter kuantitatif, genotip inang, perbedaan lokasi



TEMPORAL, SPATIAL AND GENETIC PATTERNS OF BEGOMOVIRUS INFECTIONS ON MELON (*Cucumis melo* L.) PLANT

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Abstract

Melon is one of the horticultural agriculture products with high selling value. Begomovirus, on the other hand, is one of the most widely studied viruses in the last decade. Objective of this study was to report Begomovirus infections in melon plants that occurred in greenhouse ecosystems with natural climate in the lowlands and highlands, which were described as to know the symptoms and temporal patterns of Begomovirus infections in melons and to know the effects of differences in artificial ecosystems, host genotype, and location of Begomovirus infection in melons. Melon cultivation and field data collection were carried out in greenhouses in two locations: Pangalengan, West Java (Nudira Farm, PT. Nudira Sumber Indonesia) and Prambanan, Special Region of Yogyakarta. Melon seeds used in this study were Hikapel cultivar originated from the Laboratory of Genetics and Breeding, Faculty of Biology, UGM and commercial melon seeds. Begomoviruses were obtained from infections that were transmitted naturally by whitefly vector. Simple Random Sampling was conducted to check for symptoms of viral infection, followed by scaling of the infection severity. Measurement of the physiological characteristics of melon plants and whitefly number as well as documentation of greenhouse conditions, climate and geographic variables were also carried out. Molecular analysis was performed by PCR. Data on the severity of viral infections were used to analyze the intensity of disease symptoms and were used to compare the level of resistance to Begomovirus in plants cultivated in greenhouses. The physiological characteristics of plants were analyzed using ANOVA. All data were analyzed using Pearson correlation. The study results showed that the symptoms of Begomovirus infection in melon plants were mainly in the form of yellow mosaic on leaf venation and leaf flesh around leaf venation. The results also showed that Begomovirus infections in melon plants had increased from the first exposure to after the reproductive phase. Based on this study it was revealed that Begomovirus infections in melon plants have different patterns : in artificial ecosystems with different mesh sizes and surrounding vegetation; on the hosts genotypes, with low infection condition i.e. Kinanti, Kinanti super, Hikapel, and Kirani, consecutively; as well as in the lowland and highland. PCR results with the Krusty-Homer universal primer confirmed that the sample was infected with Begomovirus. PCR with Krusty-Homer universal primers confirmed that the samples were infected with Begomovirus.

Keywords : Melon, Begomovirus, greenhouse, symptoms, quantitative characters, host genotype, different location