Identitas dan Keragaman Genetik Begomovirus yang berasosiasi dengan Penyakit Keriting pada Tomat Berdasarkan Teknik Polymerase Chain Reaction (PCR)-Restriction Fragment Length Polymorphism (RFLP)

Abstrak

Identities and Genetic Diversities of Begomoviruses Associated with Leaf Curl Disease of Tomato Based on the Polymerace Chain Reaction-Restriction Fragment Length Polymorphism (PCR-RFLP) Technique. Tri J. Santoso, Sri H. Hidayat, M. Herman, H. Aswidinnoor, and Sudarsono. Begomoviruses, members of the Geminivirus, are considered as emerging plant viruses. This was due to the increasing incidences and severities of the diseases in a number of economically important crops, including tomato. Genetic diversities of the Begomovirus isolates infecting tomato (Lycopersicon esculentum) of several areas in Indo- nesia were analyzed by using Polymerase Chain Reaction- Restriction Fragment Length Polymorphism (PCR-RFLP) technique. A 1500 base pairs of PCR fragments amplified by using degenerate primers for Begomovirus was digested using four restriction enzymes, i.e., DraI, EcoRI, RsaI, and PstI. The pattern of RE digested fragments of 8 Begomovirus isolates and the predicted RFLP fragments of the Begomo- virus isolates in the GeneBank database were used to deter- mine the genetic identities and diversities among the isol- ates. Positive results of the PCR amplifications proved that diseased tomato plant samples collected from 8 locations in Java and Sumatra were infected with at least one Begomo- virus isolate. The PCR amplification products, which were digested using the four restriction enzymes indicated the presence of polimorfisms among the DNA fragments of the Begomovirus isolates. Identifications of the Begomovirus indicated that the Brastagi, Bogor, Sragen, Ketep, and Boyo- lali isolates were Tomato Leaf Curl Virus (ToLCV); the isolates from Malang and Blitar isolates were Ageratum Yellow Vein Virus (AYVV), while one isolate from Kaliurang was Tomato Yellow Leaf Curl Virus (TYLCV). Results of the phylogenetic analysis of the 8 Begomovirus isolates based on Begomoviruses from the DNA database indicated that they belonged to three different groups.