Disease Notes

Molecular Characterization of Pepper yellow leaf curl Indonesia virus in Leaf Curl and Yellowing Diseased Tomato and Pepper in Indonesia

W. S. Tsai,

Department of Plant Pathology, National Chung Hsing University, 250 Kuo-Kuang Rd., Taichung 402, Taiwan,

R.O.C.; S. L. Shih and S. K. Green, AVRDC-The World Vegetable Center, Shanhua, Tainan 741, Taiwan,

R.O.C.; A. Rauf and S. H. Hidayat,
Department of Plant Pests and Diseases, Faculty of Agriculture, Bogor Agriculture University, Indonesia;

F.-J. Jan, Department of Plant Pathology, National Chung Hsing University, 250 Kuo-Kuang Rd., Taichung 402, Taiwan, R.O.C.

Open Access.

Yellowing and leaf curl symptoms were observed in tomato and pepper fields near Bogor, Java, Indonesia in 2000. Samples were collected from one diseased tomato (Lycopersicum esculentum) and three diseased chili pepper (Capsicum annuum) plants. Viral DNA was extracted (2) and tested for the presence of geminiviral DNA-A, DNA-B, and associated satellite DNA using polymerase chain reaction (PCR) with previously described primers (1,3,4). The begomovirus DNA-A general primer pair PAL1v1978/PAR1c715 amplified the predicted 1.4-kb DNA fragment from the tomato and two of the chili samples. DNA-B and satellite DNA were not detected using PCR with DNA-B general primer pairs (DNABLC1/DNABLV2 and DNABLC2/DNABLV2) and satellite detection primer pair (Beta01/Beta02). The amplicons from the tomato and from one of the chili samples were cloned and sequenced. On the basis of the 1.4-kb DNA sequences, specific primers were designed to complete the DNA-A sequences. Following sequence assembly, the full-length DNA-A nucleotide sequences were determined as 2,744 nt (GenBank Accession No. DQ083765) for the tomato- and 2,743 nt (GenBank Accession No. DQ083764) for the chili-infecting begomoviruses. Sequence comparisons and analyses were conducted using the DNAMAN sequence analysis software (Lynnon Corporation, Quebec, Canada). The DNA-A of both begomoviruses contained six open reading frames, including two in the virus sense and four in the complementary sense, and the geminivirus conserved nanosequence-TAATATTAC in the loop of the hairpin structure of the intergenic region. Because of their high nucleotide sequence identities of 99%, the tomato- and chili-infecting begomovirus are considered the same virus. When compared by using BLAST with available gem-iniviral sequences in the GenBank database, the DNA-A sequences of the tomato and the chili isolates showed highest nucleotide

sequence identity (95%) with the partially sequenced Pepper yellow leaf curl Indonesia virus (GenBank Accession No. AB189849) in the 1,842 nt to 660 nt region and in the 1,841 nt to 659 nt region, respectively. Comparisons with full-length DNA-A sequences of begomoviruses available in the GenBank database indicated high sequence identities of 76 and 77% for the tomato and chili isolates, respectively, with an eggplant isolate of Tomato yellow leaf curl Kanchanaburi virus (GenBank Accession No. AF511530) from Thailand. According to our knowledge, this is the first report of full-length DNA-A sequence of the Pepper yellow leaf curl Indonesia virus and its natural occurrence in tomato and pepper in the Bogor area of Indonesia. References: (1) R. W. Briddon et al. Virology 312:106, 2003. (2) R. L. Gilbertson et al. J. Gen. Virol. 72:2843, 1991. (3) S. K. Green et al. Plant Dis. 85:1286, 2001. (4) M. R. Rojas et al. Plant Dis. 77:340, 1993.