First Report of Pepper yellow leaf curl Indonesia virus in *Ageratum conyzoides* in Indonesia. Y. Shibuya and J. Sakata, Department of Life Science, Graduate School of Agricultural Science, Tohoku University, 1-1 Tsutsunitori-Amemiyamachi, Aoba-ku, Sendai, Miyagi 981-8555, Japan; N. Sukanto, Laboratory of Plant Pathology, Indonesia Spice and Medical Crops Research Institute, Bogor 16111, Indonesia; and T. Kon, P. Sharma, and M. Ikegami, Department of Life Science, Graduate School of Agricultural Science, Tohoku University, 1-1 Tsutsunitori-Amemiyamachi, Aoba-ku, Sendai, Miyagi 981-8555, Japan. Plant Dis. 91:1198, 2007; published online as doi:10.1094/PDIS-91-9-1198B. Accepted for publication 6 June 2007.

Ageratum conyzoides L. plants affected with yellow vein disease were collected from Magelang, Bandung, and Purwokerto locations in Indonesia during 2001. *A. conyzoides* is a naturally occurring weed that is found in and around fields of cultivated pepper (*Capsicum annuum* L.) and tomato (*Lycopersicon esculentum* L.). It is frequently found with symptoms of yellow vein disease and the abundance of whiteflies on the affected plants suggested the possible involvement of a geminivirus. Total nucleic acids were extracted from nine samples collected from these locations of *A. conyzoides*-affected plants exhibiting yellow vein disease and amplified using PCR with geminivirus DNA-A-specific designed primers (virion-sense primer 5'-GAGCTCTTAGCCGCCTGAATGTC-3'; complementary-sense primer 5'-GAGCTCGTCAGATGTTAAGACCTAC-3') (1). A PCR-amplified product of approximately 2.7 kbp was obtained from each sample. Five independent sequences were cloned and sequenced from each sample. Sequence analysis showed that five of nine samples were *Ageratum yellow vein virus* (one each from Bandung and Purwokerto and three from Magelang) and the remaining four samples (two samples each from Bandung and Purwokerto) were a strain of *Pepper yellow leaf curl Indonesia virus* (PepYLCIDV). Full-length DNA-A of PepYLCIDV from systemic *A. conyzoides* was amplified using PCR with additional primers designed at only one restriction site (*Bam*HI) (5'-GGATCCGCTTGTTTCATCCTTTTCCAG-3'/5'-GGATCCCACATCTTTGGTTAGTGGAGGGTG-3') and cloned. Three independent clones obtained were sequenced and analyzed. The sequence of a full-length DNA-A component was determined (2,760 bases, GenBank Accession No. AB267838). PCR using degenerate primers (DNABLC1: 5'-GTVAATGGRGTDCACTTCTG-3'; DNABLC2: 5'-RGTDCACTTCTGYARGATGC-3'; DNABLV2: 5'-GAGTAGTAGTGBAKGTTGCA-3') of begomovirus DNA-B component (2), five independent clones were obtained and sequenced. Primers designed to amplify a full-length B component were constructed around a unique restriction site (*Bam*HI) (5'-GGATCCCCTCATTCCTTTTGCGGAG-3'/5'-GGATCCACAGAGGAAAACGCAAGGC-3'). A PCR product was obtained from *A. conyzoides* samples and three independent clones were sequenced and analyzed. A full-length sequence of a begomovirus B component was determined (2,746 bases, GenBank Accession No. AB267839). Five open reading frames (ORF) were found in DNA-A and two in DNA-B. The DNA-A and DNA-B had a common region (CR) (74% nucleotide sequence identity) that comprised approximately 160 nucleotides. The DNA-A and DNA-B had an identical 31-base stem loop region in the CR. In addition, DNA-A and DNA-B had the highest nucleotide sequence identity (93%) with those of PepYLCIDV (GenBank Accession Nos. AB267834 and AB267835), suggesting it is a strain of PepYLCIDV, which is widely prevalent in Indonesia. To our knowledge, this is the first report of PepYLCIDV isolated from *A. conyzoides* plants affected with yellow vein disease.

References: (1) R. W. Briddon and P. G. Markham. Mol. Biotechnol. 1:202, 1994. (2) S. K. Green et al. Plant Dis. 85:1286, 2001.