Begomoviruses Associated with Leaf Curl Disease of Tomato in Java, Indonesia

Sukamto 1, T. Kon 1, S. H. Hidayat 2, K. Ito 1, S. Hase 1, H. Takahashi 1 and M. Ikegami 1

Authors' addresses: 1Department of Life Science, Graduate School of Agricultural Science, Tohoku University, 1-1 Tsutsumidori-Amamiyamachi, Aoba-ku, Sendai 981–8555 Japan; 2Department of Pests and Disease, Faculty of Agriculture, Bogor Agricultural University, Indonesia (correspondence to M. Ikegami. E-mail: ikegami@bios.tohoku.ac.jp)
Correspondence to Department of Applied Plant Science, Graduate School of Agricultural Science, Tohoku University, Sendai, Japan

*The sequences reported in this paper will appear in the DDBJ, EMBL and GenBank Nucleotide Sequences under accession numbers AB189845 to AB189849 for ToBadI-5, ToBadII-20, ToPur-6, ToMag-2, ToBadII-23, respectively; AB189851 to AB189854 for AgPur-2, AgBadI-1, AgMal-4, AgMag-5, respectively; AB205117 for ToBadIII-1, AB189913 for AgBadII-5 and AB213599 for ToBadI-5B.

Received October 29, 2004; accepted July 5, 2005

Keywords
tomato leaf curl disease • begomovirus • Tomato leaf curl Indonesia virus • Ageratum yellow vein virus • pepper yellow leaf curl Indonesia virus

Abstract

We report that several begomoviruses are associated with tomato leaf curl disease in Java, Indonesia. Tomato plants with leaf curl symptoms were collected from Bandung (west Java), Purwokerto (central Java), Magelang (central Java) and Malang (east Java) of Indonesia, the major tomato-growing areas of the country. Viruses were detected using the polymerase chain reaction (PCR), with universal primers for the genus Begomovirus. PCR-amplified fragments were cloned and sequenced. Based on sequence comparisons and phylogenetic analyses, the viruses were divided into three groups. With respect to amino acid (aa) identities of the N-terminal halves of the coat proteins compared in this study, group I was most closely related to Ageratum yellow vein virus (AYVV) (97%), Ageratum yellow vein China virus-[Hn2] (AYVCNV-[Hn2]) (96%) and Ageratum yellow vein virus-[Taiwan] (AYVV-[Tai]) (95%), and ageratum-infecting begomovirus from Java (99%). Group II had high sequence identity with a tentative species of tomato leaf curl Java virus (ToLCJAV) (96% aa) for the CP. Group III was most closely related to a proposed species of Pepper yellow leaf curl Indonesia virus (PepYLCIDV) (90% aa identity) by its partial CP sequence.