Disease Note

FIRST REPORT OF *AGERATUM YELLOW VEIN VIRUS* ASSOCIATED WITH A NEW BETASATELLITE INFECTING *CARICA PAPAYA* IN CHINA

W. Shen*, D. Tuo*, Y. Yang, P. Yan, X. Li and P. Zhou

Key Laboratory of Biology and Genetic Resources of Tropical Crops, Ministry of Agriculture, Institute of Tropical Bioscience and Biotechnology & Analysis and testing center, Chinese Academy of Tropical Agricultural Sciences, Haikou 571101, China
**These authors contributed equally to this work.*

A *Carica papaya* plant exhibiting downward curling of the leaves and yellow vein was observed near Sanya (Hainan Province, China). Total DNA was extracted from three symptomatic samples (P1, P2 and P3) for amplifying part of begomovirus DNA-A and DNA-B using the primer pair PA/PB and PBL1v2040/PCRc1 (Zhou *et al*., 2001; Rojas *et al*., 1993). No DNA-B was detected but a *ca.* 500 bp DNA-A fragment amplified from all samples was cloned, sequenced and shown to have 100% nucleotide (nt) identity. The primer pair BE1 (5'-GGTACGCCGACGGCTGAACTTC-3') and BE2 (5'-CGTACCTTGGATGCGGGAGTTGAAATG-3') was designed to amplify the full-length DNA-A from P3, which was determined to be 2,759 nt in length (GenBank accession No. KM051844) and showed a nt sequence identity (99%) with *Ageratum yellow vein virus* (AYVV) from *Lycopersicon esculentum* (KC810890). When alpha- and betasatellite molecules were looked for using the universal primer pairs DNA101/102, UN101/102 and Beta01/02 by PCR, respectively (Briddon *et al*., 2002; Bull *et al*., 2003), no alphasatellite was detected, but a betasatellite amplicon of *ca*. 1.3 kb was obtained from the three samples. The complete betasatellite sequence from P2 (1,350 nt, GenBank accession No. KJ642219), shares the highest nucleotide sequence identity (66.6%) with *Tomato leaf curl China betasatellite* (GenBank accession No. AJ704617), and appears to be a new satellite species, for which the name *Papaya leaf curl China betasatellite* [China: Hainan: 2014] is proposed. To our knowledge, this is the first report of AYVV associated with a new betasatellite infecting papaya and their first identification in China.

Work supported by the National Natural Science Foundation of China (grant Nos 31371918 and 31171822), the Major Technology Project of Hainan (ZDZX2013023-1), and the National Nonprofit Institute Research Grant (ITBB110211).

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Corresponding author: P. Zhou
Fax: +86.898.66988559
E-mail: dnaswt@hotmail.com

Received August 18, 2014
Accepted August 20, 2014

Disease Note

FIRST REPORT OF PERSIMMON VIRUS A IN ITALY

M. Morelli[1], M. Chiumenti[1], P. La Notte[1], A. Minafra[1] and G.P. Martelli[2]

[1] Istituto per la Protezione Sostenibile delle Piante (CNR-IPSP) UOS Bari, Italy
[2]Dipartimento di Scienze del Suolo, della Pianta e degli Alimenti, Università degli Studi Aldo Moro, Bari, Italy

Extensive necrosis of the veinlets were observed in early summer of 2011 on both sides of the leaf blades of a Japanese persimmon (*Diospyros kaki*) tree growing in a private garden in the vicinity of Bari (Apulia, southern Italy). This tree (accession SSPI) hosted a previously uncharacterized cryptovirus whose presence was apparently unrelated to the vein necrosis condition as it occurred also in a large number of symptomless trees (Morelli *et al*., 2012). High-throughput sequencing analysis of the SSPI virome, performed on dsRNA extracts with an Illumina platform, allowed the identification of four contigs which, upon BLAST analysis (Altschul *et al*., 1997) showed a 97% sequence identity at the nucleotide level with sequences of the putative cytorhabdovirus Persimmon virus A (PeVA, GenBank AB735628), recently described in Japan (Ito *et al*., 2013). The sequence of the largest contig (983 bp), spanning part of the polymerase gene and the 3'-UTR, was deposited in GenBank under the accession No. KM407515. To confirm deep-sequencing findings, the PCR primer set PeVAfor/PeVArev (5'-AGGATCATTACAAAATCCGTGAGG-3'/ 5'-TTCCCGAAAGACAATCTGTCCC-3'), intended to amplify a 250 bp product, was designed on the KM407515 sequence. An amplicon of the expected size was repeatedly obtained from the symptomatic (SSPI) but not from 10 symptomless trees. This product was cloned into pSC-A-amp/kan and custom-sequenced (Macrogen Europe, The Netherlands). BLAST analysis matched previous identification, as cloned sequences shared *ca.* 98% identity with those of the Japanese PeVA isolate. There was no amplification when RT-PCR assays were extended to the 10 symptomless persimmon trees. Whether or not PeVA is involved in the induction of vein necrosis remains to be ascertained. To our knowledge, this is the first report of PeVA in a country other than Japan.

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Corresponding author: M. Morelli
Fax: +39.080.5442911
E-mail: massimiliano.morelli@uniba.it

Received June 12, 2013
Accepted July 10, 2013