

## DISEASE NOTE

## ASSOCIATION OF BERMUDA WHITE LEAF PHYTOPLASMA WITH *JUSTICIA GENDARUSSA* WITH WITCHES' BROOM SYMPTOMS IN INDIA

A.K. Tiwari<sup>1</sup>, M. Priya<sup>2</sup>, K. Kumari<sup>1</sup>,  
N. Mishra<sup>1</sup> and G.P. Rao<sup>1</sup>

<sup>1</sup>Central Lab, UP Council of Sugarcane Research,  
Shahjahanpur-242001, U.P., India

<sup>2</sup>Division of Plant Pathology, Indian agricultural Research Institute,  
Pusa campus-110012, New Delhi, India

*Justicia gendarussa* Burm. f. (family Acanthaceae) is a shade-loving, quick-growing evergreen ornamental hedge plant mostly found in moist areas. It is believed to be native to China and is distributed widely across India, Sri Lanka and Malaysia. Witches' broom and little leaf symptoms were observed on *J. gendarussa* plants in Shahjahanpur district, Uttar Pradesh, India in 2013-14 with 2% incidence. Three symptomatic and one symptomless plants were analyzed by nested PCR using primer pairs P1/P6 (Deng and Hiruki, 1991) and R16F2n/R2 (Gundersen and Lee, 1996), which yielded products *ca.* 1.2 kbp in size only in nested PCR assays from symptomatic samples. All three amplicons were directly sequenced from both directions and one sequence was submitted to the GenBank (accession No. KT365865). In pairwise sequence comparison, 100% sequence identity was observed with members of the 'Candidatus Phytoplasma cynodontis' taxon (16SrXIV group) reported from various parts of the world, which was confirmed upon analysis of a phylogenetic tree constructed by neighbor-joining method. The *iPhyClassifier* virtual RFLP analysis (Zhao *et al.*, 2009) using 17 restriction enzymes revealed that the *J. gendarussa* phytoplasma produced RFLP profiles identical to those of the reference strain of 'Ca. P. cynodontis' (KM220612) classified in the 16Sr XIV-A subgroup. To the best of our knowledge, *J. gendarussa* is a new host of a phytoplasma belonging to the 16Sr XIV-A subgroup in India.

The Senior author is thankful to the Department of Science and Technology, New Delhi for providing financial assistance.

- Deng S., Hiruki C., 1991. Amplification of 16S rRNA genes from culturable and nonculturable mollicutes. *Journal of Microbiological Methods* **14**: 53–61.
- Gundersen D.E., Lee I.-M., 1996. Ultrasensitive detection of phytoplasmas by nested-PCR assays using two universal primer pairs. *Phytopathologia Mediterranea* **35**: 144-151.
- Zhao Y., Wei W., Lee I.-M., Shao J., Suo X., Davis R.E., 2009. Construction of an interactive online phytoplasma classification tool, *iPhyClassifier*, and its application in analysis of the peach X-disease phytoplasma group (16SrIII). *International Journal of Systematic and Evolutionary Microbiology* **59**: 2582-2593.

Corresponding author: G.P. Rao  
Email: gprao\_gor@rediffmail.com

Received December 23, 2015  
Accepted January 14, 2016

## DISEASE NOTE

## FIRST REPORT OF PERSIMMON CRYPTIC VIRUS IN TURKEY

M. Morelli<sup>1</sup> and M. Arli-Sokmen<sup>2</sup>

<sup>1</sup>Istituto per la Protezione Sostenibile delle Piante (CNR-IPSP)  
UOS Bari, Italy

<sup>2</sup>Department of Plant Protection, Faculty of Agriculture,  
Ondokuz Mayıs University, Samsun, Turkey

Persimmon cryptic virus (PeCV), a putative member of the genus *Deltapartitivirus*, family *Partitiviridae*, was first identified in a Japanese persimmon (*Diospyros kaki*) tree growing in Apulia (southern Italy), and showing an extensive necrosis of the veinlets on both sides of the leaf blades (Morelli *et al.*, 2012). In the early summer of 2015, similar symptoms were observed on several trees of some autochthonous cultivars growing in two distinct orchards in Samsun province (northern Turkey).

The presence of PeCV was ascertained in Turkish persimmon accessions by RT-PCR using the specific primer pair CryKaF/CryNeR, designed in the coat protein (CP) gene encoded by RNA2 (Morelli *et al.*, 2015). A 144-bp amplicon, obtained from symptomatic accession S3, was cloned into pSC-A-amp/kan and custom-sequenced (Macrogen Europe, The Netherlands). BLAST analyses showed that the cloned PeCV sequence, deposited in GenBank under accession no. KT962117, shared *ca.* 96% identity at the nucleotide level with that of the Italian isolate SSPI (HE805114). All tested samples were negative for Persimmon virus A (PeVA), another cytorhabdovirus species putatively associated with persimmon vein necrosis disease (Morelli *et al.*, 2014). Nevertheless, whether or not PeCV is involved in symptom appearance, remains to be ascertained. To our knowledge, this is the first report of PeCV in a country other than Italy.

- Morelli M., De Stradis A., La Notte P., Merkuri J., Boscia D., Minafra A., 2012. Detection and molecular characterization of a novel cryptovirus from persimmon (*Diospyros kaki*). In: *Proceedings of the 22nd International Conference on Virus and other Transmissible Disease of Fruit Crops*, Rome, Italy: 117.
- Morelli M., Chiumenti M., La Notte P., Minafra A., Martelli G.P., 2014. First report of Persimmon virus A in Italy. *Journal of Plant Pathology* **96**: 610.
- Morelli M., Chiumenti M., De Stradis A., La Notte P., Minafra A., 2015. Discovery and molecular characterization of a new cryptovirus dsRNA genome from Japanese persimmon through conventional cloning and high-throughput sequencing. *Virus Genes* **50**: 160-164.

Corresponding author: M. Morelli  
E-mail: massimiliano.morelli@ipsp.cnr.it

Received January 2, 2016  
Accepted January 4, 2016