## Disease Notes (continued)

Veronica sibirica Leaf Spots Caused by Phacellium veronicae, a New Disease in China. Q. R. Bai, S. Han, Y. Y. Xie, and J. Gao, Laboratory of Plant Pathology, College of Agronomy, Jilin Agricultural University, Changchun 130118, Jilin Province, P. R. China; and Y. Li, Engineering Research Center of Chinese Ministry of Education for Edible and Medicinal Fungi, Jilin Agricultural University, Changchun 130118, Jilin Province, P. R. China and Laboratory of Plant Pathology, College of Agronomy, Jilin Agricultural University, Changchun 130118, Jilin Province, P. R. China. Plant Dis. 97:1662, 2013; published online as http://dx.doi.org/10.1094/PDIS-11-12-1052-PDN. Accepted for publication 8 April 2013.

Veronica sibirica (Veronicastrum sibiricum) is an erect perennial herb, an ornamental, and a traditional Chinese medicine plant distributed mostly in northeastern, northern, and northwestern China. It has dehumidifying and detoxifying properties, and is mainly used for the treatment of cold, sore throat, mumps, rheumatism, and insect bites (4). In June 2008 through 2012, leaf spots of V. sibirica were observed in the Medicinal Herb Garden of Jilin Agricultural University (43°48'N, 125°23'E) and the medicinal plantations of Antu County (43°6'N, 128°53'E), Jilin Province. Leaf spots were amphigenous, subcircular, angular-irregular, brown, and 1 to 10 mm in diameter; they occasionally merged into a larger spot with an indefinite margin or with a pale center and dark border. Pale conidiomata were hypophyllous and scattered on the spots. The conidiophores were 100 to 400 µm high and clustered together to form synnemata 20 to 50 µm in diameter, which splayed out apically and formed loose to dense capitula. Conidiophores occasionally emerged through the stomata individually and produced conidia on the surface of the infected leaves. The conidiogenous cell terminal was geniculate-sinuous with somewhat thickened and darkened conidial scars. Conidia were solitary or catenulate, ellipsoid-ovoid or subcylindric-fusiform, hyaline and spinulose, 4.01 to  $7.18 \times 11.16$  to 20.62 µm with obtuse to somewhat attenuated ends, and slightly thickened, darkened hila. Six isolates were obtained from necrotic tissue of leaf spots and cultured on potato dextrose agar at 25°C. After incubation for 14 days, colony surfaces were white to pinkish. The colony diameter increased by 12 mm after 21 days' incubation. Hyphae were hyaline, septate, and branched. Conidiophores grew individually or fascicularly. The symptoms and morphological characteristics were consistent with previous descriptions (1,2), and the fungus was identified as Phacellium veronicae (Pass.) (U. Braun 1990). The internal transcribed spacer (ITS) region of the nuclear rDNA was amplified using primers ITS4/ITS5 (3). The ITS was identical among all six isolates (HE995799) and 98% identical to that of P. veronicae (JQ920427, HQ690097). Pathogenicity was confirmed by spraying five 1-year-old V. sibirica seedlings with a conidial suspension (106 conidia/ml) of each isolate and five seedlings with sterile water as a control treatment. Plants were grown in the greenhouse at 20 to 25°C and were covered with plastic bags to maintain humidity on the foliage for 72 h. After 15 days, the same symptoms appeared on the leaves as described earlier for the field-grown plants; the control plants remained healthy. The same fungus was reisolated from the leaf spots of inoculated plants. Currently, the economic importance of this disease is limited, but it may become a more significant problem, as the cultivated area of V. sibirica is increasing. To our knowledge, although P. veronicae was recorded on the other species of Veronica (V. austriaca, V. chamaedrys, V. grandis, V. longifolia, V. paniculata, and V. spicata ssp. incana) in Europe (Germany, Denmark, Ireland, Romania) and V. wormskjoldii in North America (Canada) (1), this is the first report of V. sibirica leaf spots caused by P. veronicae in the world, and it is a new disease in China.

References: (1) U. Braun. A monograph of Cercosporella, Ramularia and allied genera (phytopathogenic Hyphomycetes) 2, IHW-Verlag, Germany, 1998. (2) U. Braun. Nova Hedwigia 50:499, 1990. (3) D. E. L. Cooke et al. Mycol. Res. 101:667, 1997. (4) Jiangsu New Medical College. Dictionary of Chinese Materia Medica. Shanghai: Shanghai Scientific and Technical Publishers, China, 1977.

## **Diseases Caused by Viruses**

## e-Xtra\*

First Report of *Tomato rugose yellow leaf curl virus* Infecting Tomato in Argentina. E. Ben Guerrero; Centro de Investigaciones de Fitopatología (CIDEFI) Facultad de Ciencias Agrarias y Forestales, Universidad Nacional de La Plata, Calle 60 y 119, La Plata (1900) Pcia de Buenos

Aires, Argentina; A. De Francesco and M. L. García, Instituto de Bioquímica y Biología Molecular, Facultad de Ciencias Exactas Universidad Nacional de la Plata-CONICET; and P. A. Balatti and E. Dal Bó, Centro de Investigaciones de Fitopatología (CIDEFI) Facultad de Ciencias Agrarias y Forestales, Universidad Nacional de La Plata, Calle 60 y 119, La Plata (1900) Pcia de Buenos Aires, Argentina. Plant Dis. 97:1662, 2013; published online as http://dx.doi.org/10.1094/PDIS-01-13-0003-PDN. Accepted for publication 27 June 2013.

Tomato plants exhibiting typical symptoms of begomovirus infection, including leaf deformation, curling, and yellowing, were collected from cultivated fields in Lavalle Department, Corrientes, Argentina, in 2010. Although the number of affected plants was only 2% within a farm, the finding is of considerable importance since the white fly Bemisia tabaci is widely spread within the country, even in other southernmost areas such as the cinturón hortícola de Buenos Aires (horticultural belt around Buenos Aires). DNA isolated from infected tomato leaves collected from three symptomatic tomato plants was amplified by PCR with specific primers designed to amplify a region of component A and B of the Begomovirus genome (3). The amplified DNA fragment was sequenced and a new set of primers were designed based on the obtained sequences. A DNA fragment of about 1,300 bp was amplified and later the complete genome, which was 2,683 bp long. No fragments were obtained when template DNA was from non-infected leaf samples. The 2,683-bp fragment was annotated at the NCBI under Accession No. KC132844. Analysis by NCBI BLAST showed that it was highly homologous to DNA-A component of Begomovirus. Furthermore, the genome organization was typical of DNA-A component of bipartite New World begomovirus. The sequence had one open reading frame (ORF) on the viral-sense strand (AV1/CP) and four ORFs on the complementary-sense strand (AC1/Rep, AC2/TrAp, AC3/REn, and AC4). In order to confirm this finding, the viral genome was amplified by rolling circle amplification (RCA, TempliPhi 100 Amplification Kit, Amersham Biosciences) as described by the manufacturer instructions. The RCA full-length product was digested with XhoI generating a 2,700-bp DNA fragment, suggesting the presence of only one restriction site, in agreement with the bioinformatics analysis of the KC132844 sequence. This PCR product was used as template in PCR reactions with specific primers to DNA-A or DNA-B components. While the DNA-A primers generated the expected 1,300-bp fragment, those homologous to the DNA-B component did not generate amplifications. These results confirmed the identity of the DNA-A component of the isolate MT8. The full sequence of the DNA-A component was 94% homologous to the DNA-A sequence of the Uruguayan begomovirus Tomato rugose yellow leaf curl virus-[U4.1] (JN381823.1). Therefore, considering our results and the criteria proposed by Fauquet (1), isolate MT8 is a new species of begomovirus described recently (2). This is the first report of TRYLCV in one of the main areas of tomato production in Argentina. This virus might be accompanying another begomovirus TYVSV that provoked yellow veins symptoms in tomato plants cultivated in the same area of Corrientes. These viruses appeared recently and concomitantly with the introduction of the white fly Bemisia spp. in the area, which is one of the main production areas of tomato and provides fresh tomatoes to the whole country, and in wintertime to the city of Buenos Aires, when the horticultural belt around Buenos Aires is not under production.

References: (1) C. M. Fauquet et al. Arch Virol 153:783, 2008. (2) B. Márquez-Martín et al. Arch Virol 157:1137, 2012. (3) M. R. Rojas et al. Plant Dis. 77:340, 1003

\*The e-Xtra logo stands for "electronic extra" and indicates this Disease Note online contains supplemental material not included in the print edition.

First Report of *Hop stunt viroid* Infecting Japanese Plum, Cherry Plum, and Peach in Greece. M. S. Kaponi, Plant Pathology Laboratory, Department of Agricultural Development, Democritus University of Thrace, 193 Pantazidou Str. 68200 N. Orestiada, Greece; and P. E. Kyriakopoulou, Department of Crop Science, Laboratory of Plant Pathology, Agricultural University of Athens, Iera Odos 75, Athens 11855, Greece. Plant Dis. 97:1662, 2013; published online as http://dx.doi.org/10.1094/PDIS-03-13-0235-PDN. Accepted for publication 12 June 2013.

Dapple plum and peach fruit is a widely distributed disorder of plum and peach resulting in significant economic losses (4). During a survey for the presence of *Hop stunt viroid* (HSVd) on stone fruit trees in Greece, samples from 30 European plums (*Prunus domestica* L., cvs. President,

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