Disease Note

PLUM HOSTS APRICOT VEIN CLEARING-ASSOCIATED VIRUS

R. Abou Kubaa[1], M. Digiaro[1], G. Bottalico[2] and T. Elbeaino[1]

[1]Istituto Agronomico Mediterraneo, Via Ceglie 9, 70010 Valenzano (Bari), Italy
[2]Dipartimento di Scienze del Suolo, della Pianta e degli Alimenti, Università degli Studi Aldo Moro, Via Amendola 165/A, 70126 Bari, Italy

Apricot vein clearing-associated virus (AVCaV), the representative of a putative new genus in the family *Betaflexiviridae*, was recently discovered in southern Italy in an apricot tree showing vein clearing of the leaves (Elbeaino *et al*., 2014). To assess its natural host range and distribution, RT-PCR assay was carried out using two specific sets of primers designed on the polymerase (Rps/Rpa: 5'-TTGATGCCTCACAAGACCAAT-3', 5'-CGTTACTCTGTTCCGCAAAAAG-3') and coat protein (CPs/CPa: 5'-CTTTTCCGGGATATCTGCACA-3', 5'-ACAGTACCTCTCGCCTCGAAA-3') genes of the viral genome, which amplified fragments of 629 bp and 607 bp, respectively. Tested samples consisted of leaf tissues (petioles and midveins) collected from a large number of cultivars of stone fruit species grown in a collection of the Faculty of Agriculture of the University of Bari (Italy), i.e. almond (39 cultivars), peach (47), cherry (34), plum (30), apricot (40) and 20 different rootstocks. Products of the expected size were amplified from three plums of cvs Angeleno, Autumn Giant and Stanley and one apricot of cv. Jameloppis in which AVCaV was originally detected (Elbeaino et al., 2014). All the other tested plum, apricot, cherry, peach and almond trees were PCR-negative, as well as the rootstocks. Sequences of the products amplified from the RdRp and CP genes were 99-100% identical to those of the AVCaV isolate from apricot deposited in Genbank (HG008921.2). No symptoms were observed on naturally infected trees nor on graft-inoculated woody indicators (GF 305, *P. armeniaca* cvs. Priana and Tilton, *P. persica* cv. Elberta, *P. cerasifera*), indicating that AVCaV infections to stone fruit species are largely latent.

Elbeaino T., Giampetruzzi A., De Stradis A., Digiaro M., 2014. Deep-sequencing analysis of an apricot tree with vein clearing symptoms reveals the presence of a novel betaflexivirus. *Virus Research* **181**: 1-5.

Corresponding author: T. Elbeaino
Fax: +39.080.4606275
E-mail: elbeaino@iamb.it

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Disease Note

NEW HOSTS OF *XYLELLA FASTIDIOSA* STRAIN CoDiRO IN APULIA

M. Saponari[1], D. Boscia[1], G. Loconsole[1], F. Palmisano[2], V. Savino[3], O. Potere[3] and G.P. Martelli[3]

[1]Istituto per la Protezione Sostenibile delle Piante del CNR, UOS Bari, Via Amendola 165/A, 70126 Bari, Italy
[2]Centro di Ricerca, Sperimentazione e Formazione in Agricoltura, Via Cisternino 281, 70100 Locorotondo (BA), Italy
[3]Dipartimento di Scienze del Suolo, della Pianta e degli Alimenti, Università degli Studi Aldo Moro Bari, Via Amendola 165/A, 70126 - Bari, Italy

In the course of surveys carried out in June 2014 in the Salento (Apulia, southern Italy) area affected by an epidemic of a strain of *Xylella fastidiosa* subsp. *pauca* (Cariddi *et al*., 2014) denoted CoDiRO (abbreviation from the Italian name "Complesso del Disseccamento Rapido dell'Olivo"), the following symptomatic plants were observed: (i) cherry (*Prunus avium*), 13 trees showing scanty vegetation and bud failure, but no leaf scorching; (ii) myrtle-leaf milkwort (*Polygala myrtifolia*), three shrubs showing extensive desiccation of twigs and scorched leaves; (iii) coastal rosemary (*Westringia fruticosa*), one shrub with extensive chlorosis and desiccation of the leaves. Samples collected from all these hosts (except for two of the 13 cherry plants) were ELISA- and PCR-positive upon testing with the protocols described by Loconsole *et al*. (2014). Sequencing of the amplified products from five housekeeping genes (*gyrB*, 16S rRNA, *dnaK*, *tonB*, RNA polymerase sigma factor) and of the PCR products obtained using the *X. fastidiosa* strain-specific primers 272-1int/272-2int, showed that all these amplicons, regardless of the host of origin, had 100% sequence identity with the homologous products amplified from diseased olive trees (Cariddi *et al*., 2014). These results provide evidence that all the analyzed positive samples contain the same *X. fastidiosa* strain infecting olives in the same area. With the exception of cherry, for which there is a recorded infection by *X. fastidiosa* subsp. *fastidiosa* in California (Hernandez-Martinez *et al*., 2007), to the best of our knowledge *P. myrtifolia* and *W. fruticosa* are hitherto unreported hosts of this bacterium.

Cariddi C., Saponari M., Boscia D., De Stradis A., Loconsole G., Nigro F., Porcelli F., Potere O., Martelli G.P., 2014. Isolation of a *Xylella fastidiosa* strain infecting olive and oleander in Apulia, Italy. *Journal of Plant Pathology* **96**: 425-429.

Hernandez-Martinez R., de la Cerda K.A., Costa H.S., Cockney D.A., Wong F.P., 2007. Phylogenetic relationships of *Xylella fastidiosa* strains isolated from landscape ornamentals in Southern California. *Phytopathology* **97**: 857-864.

Loconsole G., Potere O., Boscia D., Altamura G., Djelouah K., Elbeaino T., Frasheri D., Lorusso D., Palmisano F., Pollastro P., Silletti M.R., Trisciuzzi N., Valentini F., Savino V., Saponari M., 2014. Detection of *Xylella fastidiosa* in olive trees by serological and molecular methods. *Journal of Plant Pathology* **96**: 7-14.

Corresponding author: M. Saponari
Fax: +39 0805442911
E-mail: m.saponari@ba.ivv.cnr.it

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