Disease Note

XYLELLA FASTIDIOSA subsp. *PAUCA* ST69 IN OLIVE IN ARGENTINA

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In Argentina, the bacterium *Xylella fastidiosa* was detected in late 2013 in traditional olive orchards of more than 50 years of age, in the provinces of La Rioja, Córdoba and Catamarca; plants showed marked decline, desiccated branches and apical necrosis in leaves. Olive cultivar Arauco was the most severely affected, whereas the bacterium was detected only in isolated individuals of the cultivar Frantoio. There are few reports of the bacterium in olive, having been reported the subspecies *pauca* strain CoDiRO (ST53) in Italy, and strain ST16 in Brazil. Multilocus sequence typing (MLST) was used to determine the allelic profile corresponding to this host in Argentina, according to the protocol of Yuan *et al.* (2010). Amplification of the involved genes was performed from total DNA of infected plants, then PCR products were purified and sequenced. The comparative analysis of the sequences of the seven genes coincided with the sequences of the alleles *leuA7*, *petC6*, *malF7*, *cysG9*, *holC23*, *nuoL17*, and *gltT8*; the type sequence (ST) 69 was assigned to the obtained allelic profile. Coletta-Filho *et al.* (2017) obtained the same ST in an analysis of citrus from northeastern Argentina (Misiones and Corrientes). This ST has been found only in Argentina. In Brazil, the strain ST16 is present in olive and coffee, but not in citrus, whereas the hosts of ST69 from Argentina are olive and citrus. The strain CoDiRO from Italy was detected in several hosts (Saponari *et al.*, 2014) but not in citrus.

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Disease Note

FIRST REPORT OF GRAPEVINE VIRUS D (GVD) IN AUTOCHTHONOUS GRAPEVINE VARIETIES IN TURKEY

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Rugose wood is a complex of graft-transmissible disorders of the grapevine (*Viti*s spp.). At least six different viruses belonging to the genera *Vitivirus* and *Foveavirus* in the family *Betaflexiviridae* are associated with the disease which is distributed worldwide (Martelli, 2015). Among these viruses, grapevine virus A, grapevine virus B and grapevine rupestris stem pitting-associated virus were reported in Turkish vineyards (Martelli, 2014; Buzkan *et al.*, 2015), whereas no information is available on the occurrence of grapevine virus D (GVD). Therefore, the presence of GVD was investigated in autochthonous grapevine cultivars from two viticultural areas in Turkey, i.e. Eastern Mediterranean and Southeast Anatolia. Total RNA was extracted from 142 samples and tested for the presence of GVD by RT-PCR using primers CP7V/CP471C (Abou-Ghanem *et al.*, 1997). A 474 bp product corresponding to a fragment of the coat protein gene was amplified from 13 samples, accounting for a prevalence of 9%. The nucleotide sequence obtained from PCR amplicons was subjected to BLASTN analysis to confirm the identity of the target virus. The Turkish isolates showed 90% nucleotide sequence identity with a GVD isolate from Italy passaged onto a herbaceous host (*Nicotiana occidentalis*) (GenBank accession No. Y07764) and 98% with a GVD isolate from Brazil (JQ031716). GVD was only detected in grapevines from Southeast Anatolia, where it is a very common practice to establish vineyards with propagation material exchanged among growers without any pathogen testing. To our knowledge, this is the first report on the occurrence of GVD in Turkish grapevines.

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