**Disease Note**

# FIRST REPORT OF A MOSAIC DISEASE CAUSED BY *TOMATO RINGSPOT VIRUS* ON ROSE AND ALMOND PLANTS IN IRAN

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During the 2012 growing season, samples were collected from five rose plantations and five almond orchards in the Fars province (Iran) showing virus-like symptoms such as line-pattern, wrinkling, malformation and chlorotic spots on the leaves. A total of 50 rose and 50 almond leaf samples were tested for the presence of *Tomato ringspot virus* (ToRSV), *Arabis mosaic virus* (ArMV) and *Tobacco ringspot virus* (TRSV) by DAS-ELISA and DBIA using a polyclonal antiserum (Agdia, USA). ToRSV was detected in 22% of the roses and in 10% of almond trees, whereas ArMV and TRSV were not detected in any of the tested samples. ELISA-positive rose and almond samples used for mechanical inoculation of herbaceous hosts yielded necrotic local lesions on *Chenopodium amaranticolor*, systemic mosaic and mottling on *Cucumis sativus*, and systemic rugosity on *Phaseolus vulgaris*. ToRSV was also detected by RT-PCR using the primers ToRS2Vf/ ToRS2Vr (Stewart *et al*., 2007) and a DNA fragment with expected size *ca.* 330 bp was amplified from all serologically-positive rose, almond and infected herbaceous plants but not from the apparently healthy ones. Tospoviruses (Ghotbi and Shahraeen, 2012) and *Prunus necrotic ringspot virus* (PNRSV) (Rakhshandehroo *et al*., 2006) have previously been found in roses in Iran, which might explain some of the symptoms observed in plants that were ToRSV-negative in ELISA. ArMV, previously found in roses in Iran (Rakhshandehroo *et al*., 2006), was not detected during this study. ToRSV, which occurs in apple, eggplant, grapevines and pepper in Iran (Moini, 2010; Sokhansanj *et al*., 2012) has now been found in almond and rose.

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**Disease Note**

# FIRST PRESUMPTIVE DIAGNOSIS OF *XYLELLA FASTIDIOSA* CAUSING OLIVE SCORCH IN ARGENTINA

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In December 2013, in Aimogasta (La Rioja province) and Cruz del Eje (Córdoba province) olive trees older than 50 years of age were observed in six orchards of cv. Arauco, which showed symptoms recalling those induced by *Xylella fastidiosa.* Some branches displayed desiccated leaves at the top and basal leaves with apical scorching. Additional symptoms were slow decay, dull green coloration, curling and necrosis of the leaves, partial defoliation and rapid death of shoots and branches. Petiole and midrib samples from symptomatic trees reacted positively when ELISA-tested (Agdia, USA) for *X. fastidiosa.* Furthermore, PCR assays using primers targeting the conserved hypothetical HL protein (Francis *et al*., 2006) and the RNA polymerase sigma-factor 70 (rpoD) (Minsavage *et al*., 1994) amplified the expected products of 220 and 733 bp. Amplicons from the *rpoD* gene of three isolates were sequenced (nucleotide similarity 100%) and the sequences submitted to GenBank (KM206739, KM206740 and KM206741). BLASTN analysis indicated 100% identity with the *rpoD* gene from strain 9a5C (AE003849) from citrus and 97% with isolate OL-G (HG532022) from olive (Loconsole *et al.,* 2014). In a phylogenetic tree constructed with *rpoD* gene sequences, the Argentinean olive isolates grouped with subspecies *pauca*. Our data match those from Italy, indicating that *X. fastidiosa* subsp. *pauca* is also involved in olive infections in Argentina. Isolation (Cariddi *et al*., 2014), pure culture and pathogenicity tests have to confirm our presumptive diagnosis and additional research is needed to elucidate the epidemiology of the disease and its potential vectors in our country.

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