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DISEASE NOTES



First Report of Little Cherry Virus 1 Infecting Apricot (*Prunus armeniaca*) in Morocco

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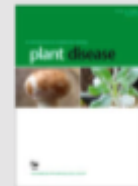
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Little cherry disease (LChD) is an important viral disease of many stone fruit species (*Prunus* spp.), sweet cherry (*Prunus avium* L.) being the most common host. It is associated with two different virus species belonging to the family *Closteroviridae*, namely, *Little cherry virus 1* (LChV-1, *Velarivirus*) and *Little cherry virus 2* (LChV-2, *Ampelovirus*). The impact of LChD on sweet cherry production consists in the decrease of yield and fruit quality, which is mainly associated with LChV-2, whereas most of LChV-1 reported infections remain associated with an unclear etiology. Other stone fruit species, such as peach and plum, hosting LChV-1 have been reported (Matic et al. 2007; Šafářová et al. 2017). LChV-1 is mainly transmitted through propagation of infected plant material, and no vector transmission is known (Jelkmann and Eastwell 2011). In 2018, during the early vegetative season, a limited survey was carried out for virus detection in apricot and sweet cherry orchards in the main southern Moroccan stone fruit-producing regions of Agadir, Agdez, and Dayat Aoua. Two sweet cherry trees (*P. avium* 'Coeur de Pigeon' and 'Bigarreau') and three apricot trees (*Prunus armeniaca* L.), all asymptomatic, were sampled (five branches with leaves) from three different orchards. RNA was extracted (both leaves and cambial scrapings) using the Spectrum Plant Total RNA kit (Sigma-Aldrich, Belgium), prior to cDNA synthesis using the iScript Reverse Transcription Kit (Bio-Rad, Belgium). LChV-1 detection was done by reverse transcription PCR (RT-PCR) using the specific primers LCUW7090 (5'-GGTTGTCCTCGGTTGATTAC-3')/LCUWc7389 (5'-GGCTTGGTCCATACATCTC-3') (Bajet et al. 2008), amplifying a 300-bp fragment spanning the ORF1b encoding the RdRp gene, and 1LC_12776F (5'-TCAAGAAAAGTTCTGGTGTGC-3')/1LC_13223R (5'-CGAGCTAGACGTATCAGTATC-3') (Glasa et al. 2015), targeting a 456-bp fragment of the CP gene. LChV-2 specific primers were used according to Eastwell and Bernardy (2001). RT-PCR results revealed the presence of LChV-1 in two apricot samples from Agdez. No LChV-1 was detected in the sweet cherry samples. The presence of LChV-1 was confirmed by means of the LChV-1 specific reverse transcription loop-mediated isothermal amplification approach as described by Tahzima et al. (2019). No LChV-2 was detected in any of the samples. The RdRp and CP specific amplification products were bidirectionally sequenced (Genewiz, Leipzig, Germany) and assembled. RdRp and CP partial nucleotide sequences of the Moroccan LChV-1 isolates MOT2 and MOA1 were deposited in GenBank (accession nos. MK905349, MK905350; and MK905351, MK905352, respectively). Based on BLAST analysis of RdRp and CP, the Moroccan LChV-1 sequences shared 99% nucleotide identity (99.55% amino acids) with the No2ISTO isolate (HG792418) from Greece and 97.96% (98.64% amino acids) with the Spanish Ponferrada isolate (KX192367), respectively. Although the presence of LChV-1 has previously been reported in many countries in different continents, to our knowledge, this represents the first detection of LChV-1 in Africa.

The author(s) declare no conflict of interest.

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Caption

Advanced symptoms of bacterial blotch disease on mushroom caps (Osdaghi et al.). Photo credit: C. Bull. Powdery mildew caused by *Golovinomyces neosalviae* on *Salvia fruticosa* (Soylu et al.). Photo credit: S. Soylu.

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