Diseases Caused by Fungi and Fungus-Like Organisms

First Report of Fruit Rot of Sweet Cultivars of Japanese Plum Caused by *Alternaria alternata*, *A. arborescens*, and *A. tenuissima* in Chile

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Plant Dis. 105:4167, 2021; published online as <https://doi.org/10.1094/PDIS-03-21-0465-PDN>. Accepted for publication 4 June 2021.

During the last two seasons, an unusual fruit rot was observed in four orchards of sweet Japanese plum (*Prunus salicina*) cultivars located in the Chilean Central Valley (30°00'S, 70°42'W). The incidence was 5% in Black Majesty, 4% in Red Lyon, and 6% in Sweet Mary cultivars in 2020. Fruits in the field showed a firm, dehydrated, and slightly sunken rot on the blossom end, along with rough and irregular epidermis in the affected area. Internally, the fruit flesh appeared light to dark-brown or olive-green. Symptomatic fruits ($n = 119$) were superficially disinfected (75% ethanol), and pieces of the pericarp (3×3 mm) were removed and placed on potato dextrose agar (PDA). Isolates of *Alternaria* spp. were obtained, and nine of these were selected for identification. Colonies were dark olive to gray-brown with white margins, small, catenulate and muriform conidia, produced in single or branched conidiophores. Isolates produced brown to golden-brown, ovoid, ellipsoidal to obclavate conidia with dimensions of 19.7 to 26.7×10.0 to 11.9 μm with two to four transverse and zero to three longitudinal septa on 0.05% PDA (Pryor and Michailides 2002) after 7 days at 20°C under 10-h/14-h light/dark cycles. A molecular analysis was performed by sequencing the nuclear RNA polymerase II subunit (RPB2), plasma membrane ATPase (ATP), and calmodulin (Cal) genes using primers RPB2-5F2/fRPB2-7cR, ATPDF1/ATPDR1, and CALDF1/CALDR1, respectively (Lawrence et al. 2013; Woudenberg et al. 2013). A BLAST search revealed the presence of *Alternaria* spp. with a 99 to 100% identity with the reference sequences of *Alternaria alternata* (JQ905182, JQ671874, JQ646208), *A. arborescens* (JQ646487, JQ671880, JQ646214), and *A. tenuissima* (JQ811961, JQ811989, JQ646209). Maximum parsimony phylogenetic analysis confirmed the

identifications. Sequences were deposited in GenBank as numbers MW514249 to MW514257, MT872324 to MT872332, and MT872314 to MT872322 for RPB2, ATP, and Cal sequences, respectively. All these *Alternaria* isolates were deposited in the Colección Chilena de Recursos Genéticos Microbianos – INIA, Chillán, Chile (RGM3069 to RGM3077). Pathogenicity of *A. alternata* ($n = 4$), *A. arborescens* ($n = 3$), and *A. tenuissima* ($n = 2$) was tested in Red Lyon plum fruits. Plums were disinfected in 1% sodium hypochlorite for 2 min, rinsed in sterile distilled water for 1 min, and dried on absorbent towels in a laminar flow hood. Then, the plums were wounded on the blossom end with a sterile needle (1×0.5 mm), inoculated with 10 μl of a conidial suspension (10^6 conidia/ml), wrapped with Parafilm, and maintained in a humid chamber (>95% relative humidity). An equal number of fruits wounded and inoculated with sterile water were used as a control. After 7 days at 20°C, all inoculated fruits developed a dark-brown firm rot with lesion lengths of 24.4 ± 3.0 mm, 19.6 ± 0.7 mm, and 16.8 ± 2.4 mm for *A. alternata*, *A. arborescens*, and *A. tenuissima*, respectively. *A. alternata* was the most aggressive species ($P < 0.001$). Control fruits remained asymptomatic. Koch's postulates were fulfilled after reisolating the causal agent from the border of the lesions. Leaf spots and fruit rots caused by *Alternaria* isolates have been reported in stone fruits, including plums (Kim et al. 2005; Long et al. 2021; Moosa et al. 2019; Yang et al. 2015). To our knowledge, this is the first report of *A. alternata*, *A. arborescens*, and *A. tenuissima* associated with fruit rot in sweet Japanese plum cultivars in the field, in Chile.

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The author(s) declare no conflict of interest.

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Keywords: Japanese plum, *Alternaria* complex, blossom end rot

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