



First report of *Melampsora ferrinii* causing willow leaf rust in Chile

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Willow (*Salix* spp.), as an agroforestry resource, has been subject to ongoing phytosanitary survey by the Servicio Agrícola y Ganadero (SAG) in Chile. Today, willows are found throughout the country as part of the rural landscape, becoming increasingly important in the protection of riverbanks, recovery of floodable lands, soil bioremediation, biomass production and wicker furniture manufacture. During surveillance activities carried out in February 2016, a *Melampsora* rust was detected on isolated trees of *Salix* sp. (phenotypically similar to *Salix viminalis*) in a farm located in the county of Chillán, region of Bío Bío (36°33'43" S, 72°03'10" W) (Figs. 1-2). Morphological observations determined that urediniospores collected from fresh pustules were sub globose to ellipsoid, hyaline to yellow in colour, uniformly echinulated, measuring 18–29 × 12–17 µm, with a wall 1.7–2.8 µm (Fig. 3). The paraphyses were up to 61 µm long and 17–22 µm wide (Fig. 4). Dried leaf material of this collection was deposited in the herbarium of the Regional Laboratory of Chillán under voucher reference number SAG-21943/2016.

Due to the limited morphological variation in the uredinial stage among *Melampsora* species, identification of willow rust fungi is difficult and incorporating DNA analysis in the diagnosis is often necessary (Pei & McCracken, 2005). To identify the specimen of *Melampsora* found in Chile, the internal transcribed spacer (ITS) and a portion of the 28S nuclear ribosomal large subunit gene (LSU) were amplified and sequenced using the primers ITS1 / ITS4 (White *et al.* 1990) and LR0R / LR5 (Moncalvo *et al.*, 1995; Vilgalys & Hester, 1990), respectively. The DNA sequences were deposited in the NCBI database under GenBank Accession Nos. KY053852 (ITS) and KY053853 (LSU). BLAST analysis showed that both sequences had 99% (1 bp difference) or 100% identity to all earlier sequences of *Melampsora ferrinii* (KJ136570 and KJ136563, respectively). Phylogenetic analysis of the combined sequence data using criteria of maximum parsimony with the software PAUP v4.0b10 confirmed that the specimen SAG-21943 clustered with the *M. ferrinii* clade (bootstrap = 94%) (Fig. 5).

Melampsora ferrinii was described in 2015 from specimens collected on *S. babylonica* in USA and Argentina (Toome & Aime, 2015). However, the distribution of *M. ferrinii* in North and South America may be wider as several herbarium specimens of *M. ferrinii* were previously misidentified as

a common willow rust, *M. epitea*. According to SAG records and Farr & Rossman (2016), *Melampsora* species associated with *Salix* spp. in Chile are limited to *M. bigelowii*, *M. epitea* and *M. humboldtiana*. Therefore, this is the first report of *M. ferrinii* from Chile and the first report of this species from a non-weeping willow host.

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Figure 1

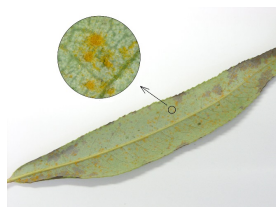


Figure 2

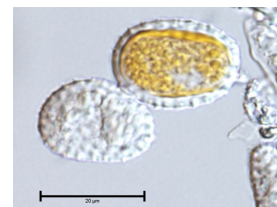


Figure 3

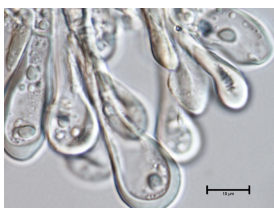


Figure 4

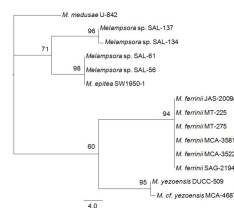


Figure 5

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