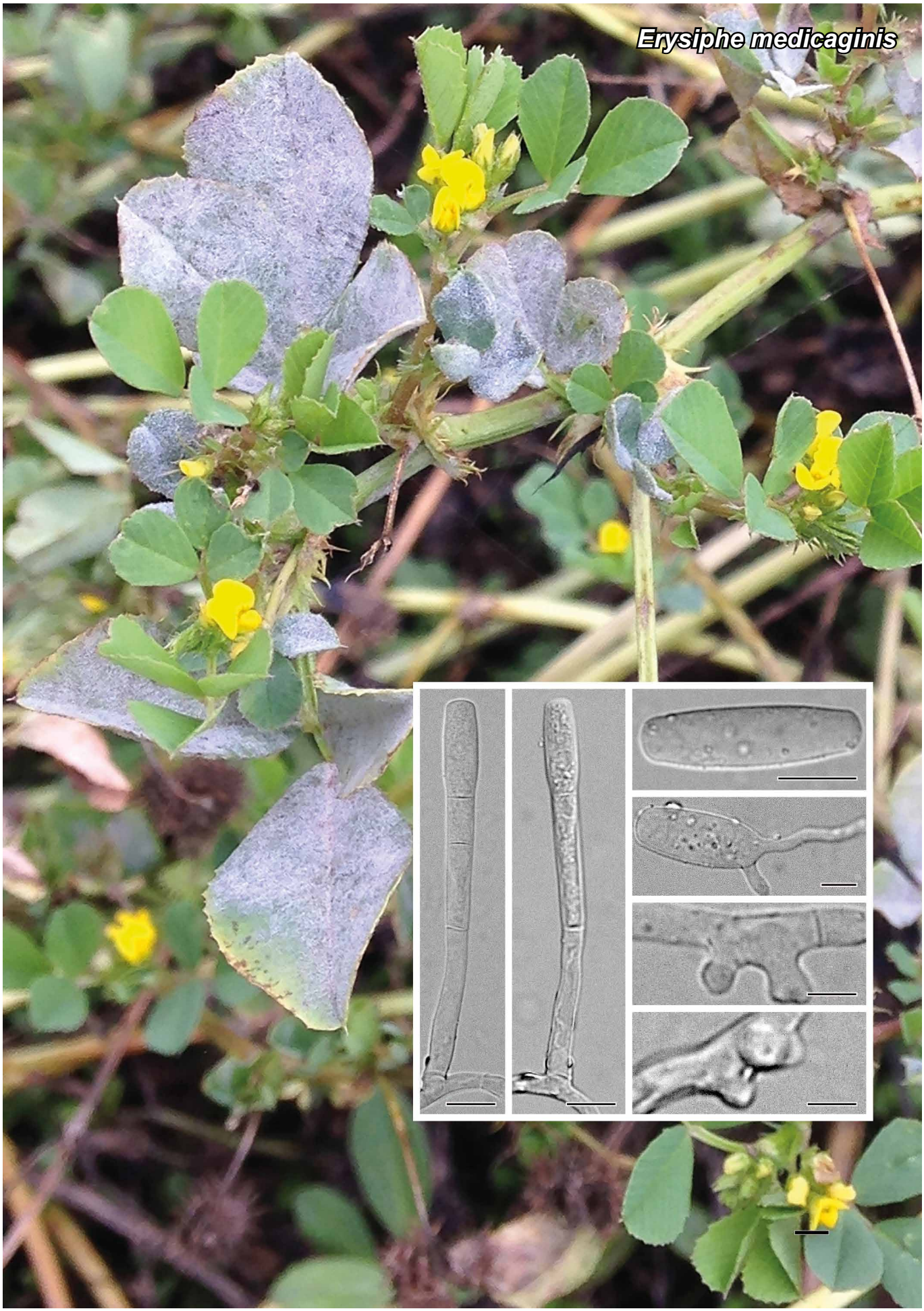

Erysiphe medicaginis

Fungal Planet 1078 – 29 June 2020

Erysiphe medicaginis L. Kiss, L. Kelly & Vaghefi, *sp. nov.*

Etymology. Name refers to the genus *Medicago*, from which this obligate biotrophic fungus was isolated.

Classification — *Erysiphaceae*, *Helotiales*, *Leotiomycetes*.

Mycelium on leaves, epiphytic, amphigenous, producing dense, white patches mostly on the upper leaf surfaces. *Hyphae* hyaline, thin-walled, 3–6 µm wide; *hyphal appressoria* mostly simple, nipple-shaped or knob-like, and rarely slightly lobed. *Conidiophores* erect, consisting of a *foot-cell*, straight or occasionally slightly curved-sinuous at the base, 35–48 × 5–7 µm, basal septum at the branching point, followed by (0–)1–2 cells up to the same length as the foot-cell. *Conidia* produced singly, mostly cylindrical or ellipsoid-cylindrical, and occasionally doliiform, 27–43 × 10–14 µm. *Germ tubes* terminal or subterminal, 1.2–3(–5) times longer than conidia (*longitubus* pattern when 5× longer), terminating in simple, often swollen, or rarely lobed appressoria. *Sexual morph* not observed.

Typus. Australia, Queensland, Toowoomba, -27.607396, 151.931924, on leaves of *Medicago polymorpha* (*Fabaceae*), 8 Aug. 2019, *L. Kiss* (holotype BRIP 70957; ITS and LSU sequences GenBank MT160214 and MT248412, MycoBank MB834939).

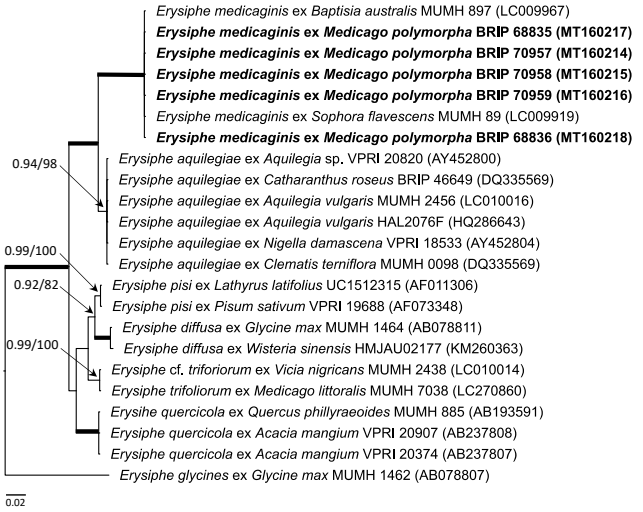
Additional material examined. Australia, Queensland, Tipton, -27.4403, 151.2465, on leaves of *M. polymorpha*, 19 Oct. 2017, *J.D.W. Dearnaley*, BRIP 68835; ITS sequence GenBank MT160217; Toowoomba, -27.5813, 151.9730, on leaves of *M. polymorpha*, 21 June 2018, *S. Takamatsu*, BRIP 68836; ITS sequence GenBank MT160218; Toowoomba, -27.534456, 151.928203, on leaves of *M. polymorpha*, 30 May 2019, *L. Kelly*, BRIP 70958; ITS and LSU sequences GenBank MT160215 and MT248413; Toowoomba, -27.556519, 151.932673, on leaves of *M. polymorpha*, 27 June 2019, *L. Kelly*, BRIP 70959; ITS and LSU sequences GenBank MT160216 and MT248414.

Notes — *Erysiphe* contains approximately 450 species of powdery mildew (Braun & Cook 2012), including many common, widespread, plurivorous taxa (Takamatsu et al. 2015). Some are taxonomically unresolved species complexes that are difficult to distinguish morphologically. These have similar or identical ITS sequences, and overlapping, or little-known, host ranges. An example is *E. aquilegiae* (Jankovics et al. 2008, Kovacs et al. 2011, Takamatsu et al. 2015). Powdery mildews with ITS sequences that were identical or highly similar to *E. aquilegiae* were recorded on diverse host plants in different parts of the world (Takamatsu et al. 2015), including Australia (Cunnington et al. 2004, Southwell et al. 2018), and belonged to the *E. aquilegiae* clade as defined by Takamatsu et al. (2015).

Phylogenetically, *E. medicaginis* belongs to a well-defined lineage that is sister to the *E. aquilegiae* clade. Morphologically, it differs from *E. aquilegiae*, and also from the asexual morphs of other taxa that had ITS sequences identical, or highly similar, to *E. aquilegiae*, by having mostly simple, and not lobed or multi-lobed hyphal appressoria.

The closest hits using the ITS sequence of *E. medicaginis* were two powdery mildew specimens from Japan, MUMH897 and MUMH89, collected from fabaceous hosts, *Baptisia australis* and *Sophora flavescens*, respectively. Their ITS sequences (GenBank LC009967 and LC009919) were identical to the five *E. medicaginis* specimens. These two specimens from Japan were recognised as representing a distinct lineage, sister to the *E. aquilegiae* clade, without being identified at the species level (Takamatsu et al. 2015).

Erysiphe medicaginis is commonly found on *M. polymorpha* in Queensland, Australia. Its host plant is a common weed globally, therefore it is likely that *E. medicaginis* is also widespread on *M. polymorpha* in different parts of the world, and likely on other fabaceous hosts, as indicated by the two specimens from Japan.



The majority rule consensus phylogram inferred from the internal transcribed spacer sequences of the nuclear ribosomal DNA and the intervening 5.8S nrDNA region using Bayesian Inference. The analysis was performed using MrBayes v. 3.2.4 (Ronquist et al. 2012) based on the GTR+G nucleotide substitution model selected using PAUP v. 4.0b10 (Swofford 2003) and MrModeltest v. 2.3. (Nylander 2009). A second measure of branch support was estimated through Maximum Likelihood analysis of the same alignment using RAxML v. 8 (Stamatakis 2014) in Geneious Prime (Biomatters Ltd.) based on the GTR substitution model with gamma-distribution rate variation. The tip labels in **bold** represent specimens sequenced in the current study. GenBank accession numbers are indicated in parentheses. Posterior Probability (PP) values > 0.90 and Bootstrap support (BS) values > 80 % are shown at the branches. Thickened lines indicate nodes with PP and BS values of 1.0 and 100 %, respectively. The tree is rooted to *Erysiphe glycines* MUMH 1462. The scale bar represents nucleotide substitutions per site.

Colour illustrations. *Medicago polymorpha* with powdery mildew-infected older leaves in a weedy area in Tipton, Queensland, Australia. Conidiophores; a non-germinating and a germinated conidium; and simple, nipple-shaped and knob-like hyphal appressoria of *Erysiphe medicaginis*. Micrographs were taken following rehydration of the powdery mildew mycelium by boiling small pieces of infected plant tissues in lactic acid. Scale bars = 10 µm (conidiophores, conidia), 5 µm (hyphal appressoria)

Levente Kiss, Niloofar Vaghefi & John D.W. Dearnaley, Centre for Crop Health, University of Southern Queensland, Toowoomba 4350, Queensland, Australia; e-mail: Levente.Kiss@usq.edu.au, Niloofar.Vaghefi@usq.edu.au & John.Dearnaley@usq.edu.au
Lisa Kelly, Department of Agriculture and Fisheries, Queensland Government, Toowoomba 4350, Queensland, Australia; e-mail: Lisa.Kelly@daf.qld.gov.au
Kaylene Bransgrove, Queensland Plant Pathology Herbarium, Department of Agriculture and Fisheries, Dutton Park, Queensland, Australia; e-mail: Kaylene.Bransgrove@daf.qld.gov.au