

## First report of powdery mildew on *Astragalus sinicus* (Chinese milk vetch) caused by *Erysiphe trifoliorum* in China

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*Astragalus sinicus* L., (Chinese milk vetch) is a traditional leguminous green manure that plays a significant role in maintaining paddy soil fertility to enhance yield and the quality of rice in China. It is also found in gardens, roadsides, farms, fields, riverbanks, open wastelands, and is often used as livestock feed. From February 2019 to 2021, severe powdery mildew infections were observed on hundreds of *A. sinicus* grown in gardens and at roadsides of Fuzhou city, China. The disease incidence was up to 100% on leaves and stems of *A. sinicus*. White superficial fungal colonies (circular to irregular patches) were present on both sides of the leaves. Hyphae were flexuous to straight, branched, 4 to 8  $\mu\text{m}$  in width, and septate. Hyphal appressoria were lobulate and solitary or in opposite pairs. Conidiophores were erect and straight, hyaline, and 60 to 120  $\times$  8 to 10  $\mu\text{m}$  (n=30). Foot cell was cylindrical, straight to slightly curved, 22 to 38  $\times$  8 to 10  $\mu\text{m}$ , followed by two to three shorter cells. Conidia were cylindrical-oval to doliiiform, 30 to 48  $\times$  13.5 to 24  $\mu\text{m}$  with a length/width ratio of 1.6 to 2.4 (n = 30), formed singly, and without fibrosin bodies. Conidial germ tubes were produced subterminal position. No chasmothecia were found in the collected samples. The morphological characteristics of asexual structures were consistent with the descriptions of *E. trifoliorum* (Wallr.) U. Braun in Braun and Cook (2012). To verify the identification of the pathogen, the ITS and the part of large subunit (LSU) rDNA gene of the isolates were amplified using ITS1/ITS4 and LSU1/ LSU2 primers (Scholin et al. 1994 and White et al. 1990, respectively) and sequences were deposited in GenBank (ITS: MZ021332, MZ021333; LSU: MZ021334, MZ021335). In BLASTn searches, the ITS and LSU sequences were 99 to 100% identical with those of *E. trifoliorum* parasitic on *Lathyrus magellanicus* (LC010015), *Medicago littoralis* (LC270860), *Melilotus officinalis* (LC009924) and *Trifolium* spp., (MN216308, KY660821), as well as *E. baeumleri* (Bradshaw et al. 2021) on *Vicia nigricans* (LC010014). Pathogenicity test was performed by gently pressing a diseased leaf onto 10 young leaves of three healthy potted plants, while three non-inoculated plants were used as controls. All plants were

maintained in a greenhouse at 20 to 25°C, without humidity control, and natural light. Symptoms developed 7 days after inoculation, whereas the control leaves remained symptomless. The morphology of the fungus on the inoculated leaves was identical to that observed on the originally diseased leaves. Powdery mildew on *A. sinicus* has been reported as *E. pisi* and *E. polygoni* from Korea and China (Shin, 2000; Tai 1979), respectively. Amano (1986) listed *E. pisi* and *Microsphaera astragali* (now *E. astragali*) on *A. sinicus* from China and Japan. To our knowledge, this is the first report of powdery mildew caused by *E. trifoliorum* on *A. sinicus* in China and in general. *E. astragali* is the most common and widespread powdery mildew species on *Astragalus* spp. (Braun and Cook 2012) and would be expected on *A. sinicus*, but this species is genetically clearly different from *E. trifoliorum* (Bradshaw et al. 2021). The *E. trifoliorum* complex (clade) is composed of several morphologically well-distinguishable species, besides *E. trifoliorum* also including *E. baeumleri* (on *Vicia* spp.), *E. hyperici* (on *Hypericum* spp.), and *E. euonymi* (on *Euonymus* spp.), but based on a combination of sequence plus host identity, the collection on *A. sinicus* can be assigned to *E. trifoliorum* (Bradshaw et al. 2021). The information in this study extended the host range of *E. trifoliorum* as well as future studies on *A. sinicus* in relation to powdery mildew outbreaks in China.

#### References:

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**Figure S1:** (A) Powdery mildew symptoms on *Astragalus sinicus* (Chinese milk vetch); (B) initial fungal colonies on the leaves; (C) conidiophores on the leaf; (D) shapes of conidiophores and conidia

**Figure S2:** Phylogenetic analysis of the genus *Erysiphe* inferred from ITS + 28S rRNA gene sequences constructed by Maximum likelihood (ML) method. Sequences obtained from isolates in this study were highlighted in blue font.

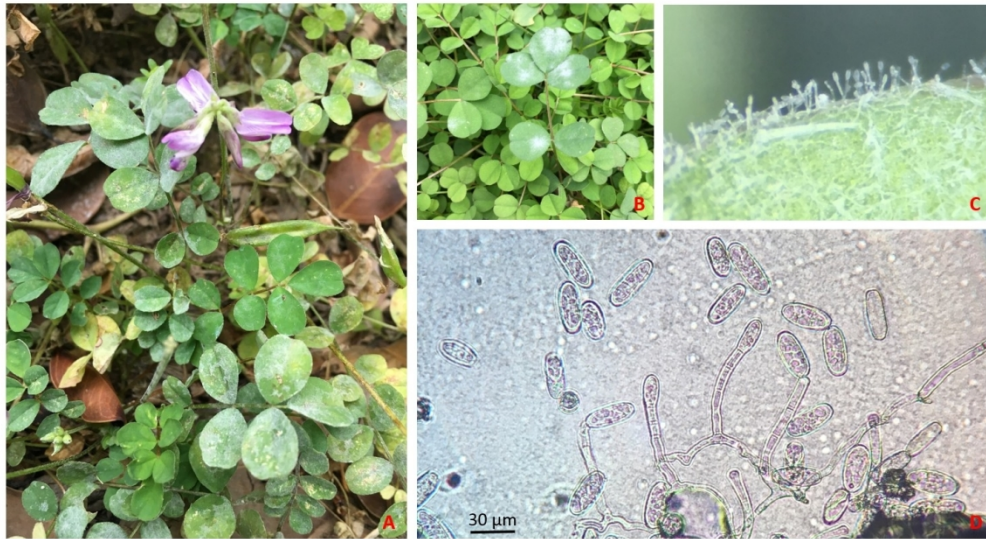
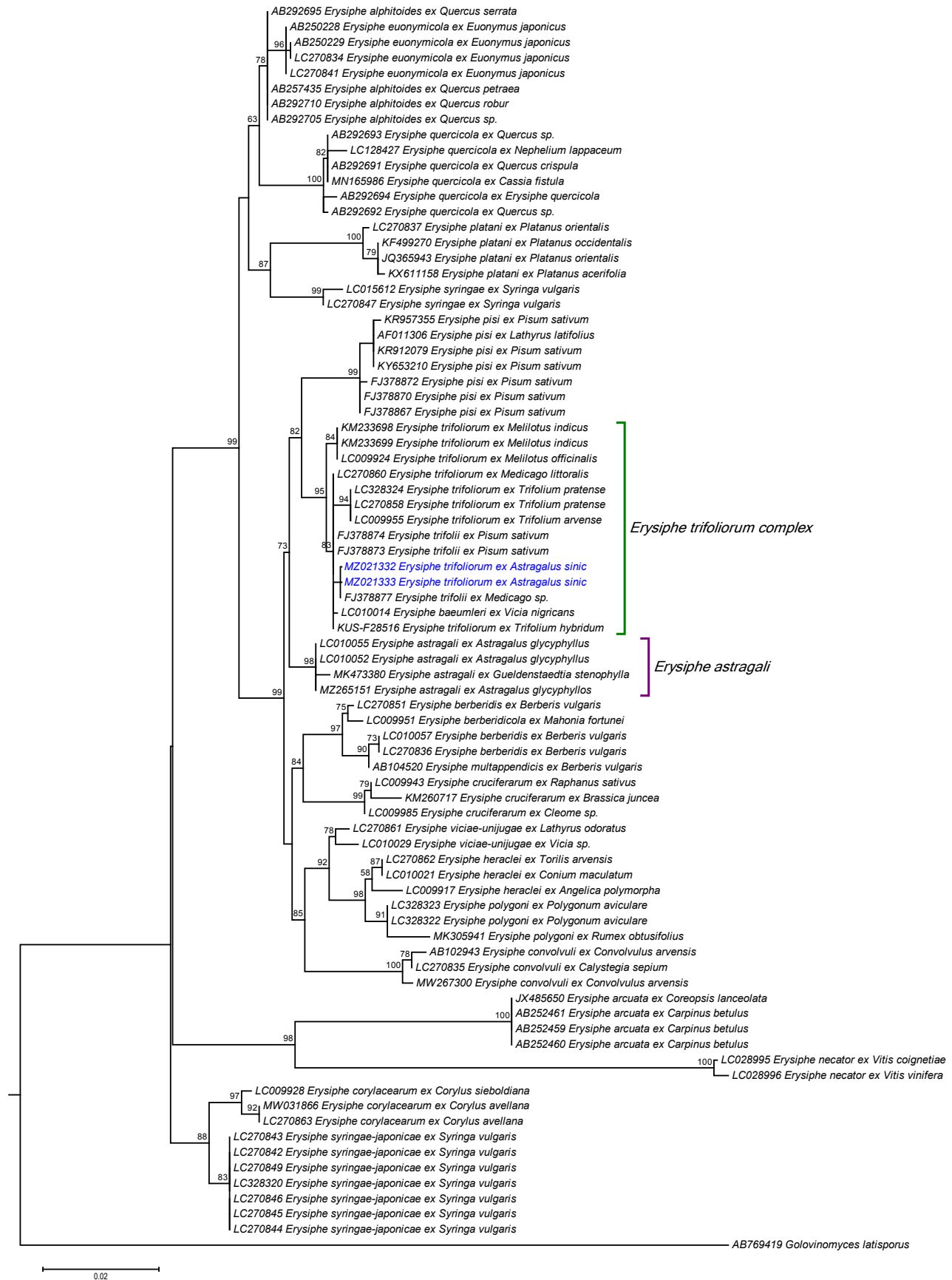


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395x218mm (96 x 96 DPI)



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