

# Disease Note

## Diseases Caused by Fungi and Fungus-Like Organisms

### First Report of Powdery Mildew of *Quercus guyavifolia* (Fagaceae) Caused by *Erysiphe quercicola*

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Oaks are the most abundant trees in naturally regenerated forests in China and play a crucial role in preventing soil erosion and maintaining ecological stability (Du et al. 2022). *Quercus guyavifolia* H. Léveillé (family Fagaceae, subgenus *Cerris*, section *Ilex*) is endemic in China and distributed in the southeastern boundary of the Qinghai-Tibet Plateau, with elevations from 2,000 to 4,500 m a.s.l. (Denk et al. 2018; Sun et al. 2016). Powdery mildew is a prevalent disease of oaks with up to 60% of foliage infection, which can induce leaf necrosis or deformation and might contribute to oak decline (Marçais and Desprez-Loustau 2014). In September 2023, we found leaves of *Q. guyavifolia* near Yunnan Baima Snow Mountain covered with white fungal colonies. Diseased *Q. guyavifolia* plants were transplanted into a greenhouse at Yunnan University for pathogenicity tests. Conidia from diseased plants were blown into 20 healthy *Q. guyavifolia* seedlings by a cold air blower, and five noninoculated healthy seedlings were used as a control. The inoculated seedlings developed powdery mildew symptoms within 10 days on both sides of the leaves. Trypan blue staining was used to identify the pathogen that infects *Q. guyavifolia* (Xiao et al. 2017). Microscopic examination revealed abundant conidia and extensive branched

hyphae on leaves, similar to the characteristics of powdery mildew fungi. The mean length and width of conidia were  $29.06 \pm 3.96 \times 9.52 \pm 1.36 \mu\text{m}$  ( $n = 50$ ). We collected fungi (YNBAIMAXS01) and extracted genomic DNA from five diseased plants (from the same location) using the CTAB method. We amplified and sequenced the *ITS* (Gardes and Bruns 1993), *MS294*, and *MS447* (two nuclear protein-encoding genes; Feau et al. 2011; GenBank accession nos. PP079015, PP083693, and PP083694). BLAST analysis revealed 100% identity of the above three sequences with the *ITS* of the *Erysiphe quercicola* isolate DACA010 (GenBank accession no. MT569439), *MS294* of the *E. quercicola* isolate GEM09\_11\_FRTB1 (GenBank accession no. KY348509), and *MS447* of the *E. quercicola* isolate A111.5 (GenBank accession no. KY466619). Therefore, the isolate YNBAIMAXS01 was identified as *E. quercicola* based on its morphological and molecular characteristics. Sequences from the above three regions of YNBAIMAXS01 and five *Erysiphe* species were used to construct a maximum likelihood (ML) tree. In addition, we constructed a ML tree using only the *ITS* region of YNBAIMAXS01 and eight *Erysiphe* species from GenBank to better distinguish *E. quercicola* from these species. Both trees were constructed using MEGA X with K2 + G as the best model. The ML trees confirmed that the powdery mildew fungus isolated from *Q. guyavifolia* is closely related to *E. alphitoides*. To date, 34 powdery mildew species belonging to the genus *Erysiphe* have been found to be affecting *Quercus* spp., and nine oak species can be infected by *E. quercicola* (<https://fungi.ars.usda.gov/>). To our knowledge, this is the first report of powdery mildew caused by *E. quercicola* on *Q. guyavifolia*; thus, the development of disease control and management strategies is urgently needed.

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