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First Report of Powdery Mildew Caused by *Phyllactinia fraxini* on Chinese Fringe Tree in Korea

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During 2008 and 2009, a powdery mildew disease was observed on the leaf of a Chinese fringe tree (*Chionanthus retusus* Lind. & Paxt.) at the campus of Chonnam National University, Gwangju, Korea. Symptoms included white superficial mycelia and a large number of necrotic black spots on leaf (Fig. 1). Mature cleistothecia (chasmothecia) with penicillate cells have transparent tapering appendages with a bulbous base. The size of the cleistothecia ranged from 218.4–262.8 (av. 237.1) µm. Cleistothecia contained 10 to 15 appendages and formed a gelatinous mass of penicillate cells. The size of the tapering appendages and bulbous base were 137.0–268.1 (av. 191.6) × 4.6–7.8 (av. 6.2) µm and 25.1–34.4 (av. 31.0) µm in diameter, respectively. 18S rDNA sequence analysis by BLASTN search indicated that our EML-PHYL1 (GenBank accession no. HM560023) isolate was closest to a *Phyllactinia* species, *P. fraxini* (GenBank accession no. AB080549) with 99% identity value, comprising of a Fraxini clade (Fig. 2). *P. fraxini* has been found on 67 hosts containing *Alnus* spp., *Bauhinia* spp., *Chionanthus virginicus*, *Fraxinus* spp., *Magnolia* spp. and *Syringa* spp. (Farr and Rossman, 2010; Takamatsu et al., 2008). In Korea, the species was reported to cause powdery mildews only on *Fraxinus mandshurica*, *F. rhynchophylla* and *Magnolia kobus*. The species was also reported to cause powdery mildews on a *Chionanthus* species, *C. virginicus* in Germany and Poland (Farr and Rossman, 2010). To our knowledge, this is the first report of powdery mildew caused by *P. fraxini* on *C. retusus* in Korea as well as the world.

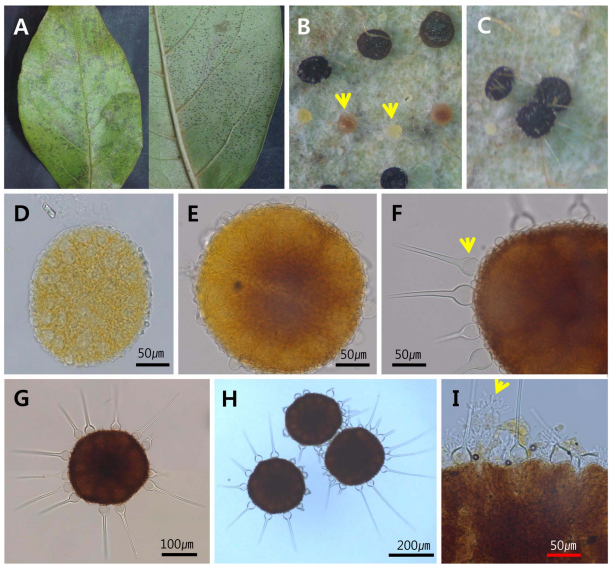

Fig. 1. Leaf powdery mildew caused by *Phyllactinia fraxini* on *Chionanthus retusus* and the morphology of the causal pathogen [A: powdery mildew symptom (left: necrotic symptom on abaxial leaf surface; right: adaxial leaf surface covered with a number of black chasmothecia), B: young cleistothecia (yellow arrows) and early mature cleistothecia (50X), C: mature cleistothecia with clear appendages (50X), D: young cleistothecium without appendages (100X), E: early maturing cleisthothecium forming bulbous base, F-H: mature cleistothecia having clear tapering appendages (yellow arrow) with a bulbous base (F: 100X; G-H: 50X), and I: penicillate cells (yellow arrow) on cleistothecium].

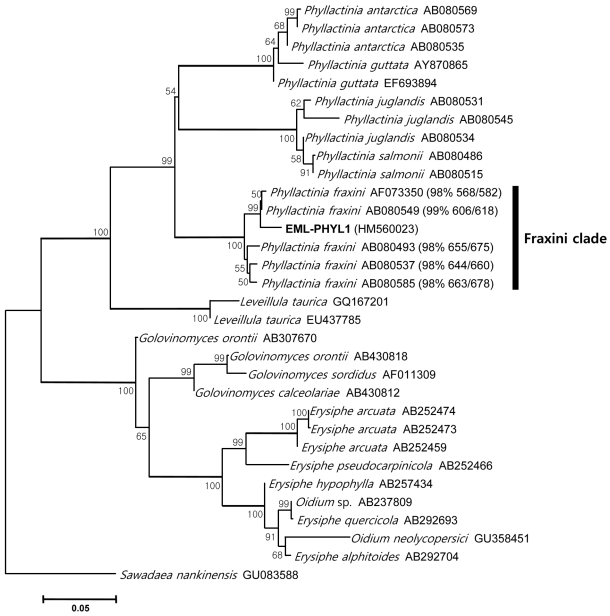

Fig. 2. NJ tree of alignment of the partial sequence of the ITS region showing an evolutionary relationship between EML-PHYL1 and 31 taxa retrieved from GenBank. *Sawadaea nankinensis* GU083588 was used as an outgroup. The % sequence identity (the number of matches/the complete alignment length) values in the parentheses were obtained via NCBI BLASTN searching of each isolate. *P. fraxini* bootstrap values were shown above branches supported by more than 50% from 1,000 replications.

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