

Disease Report Open Access

## Anthracnose Caused by *Colletotrichum gloeosporioides* on Sweet Crabapple in Korea

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Sweet crabapple [*Malus coronaria* (L.) Mill.], native to China, is grown widely for its beautiful flowers and as a street or garden tree in Korea. Anthracnose was observed on fruit of the sweet crabapple collected at the campus of Gyeongsang National University at Jinju, Korea from July to August in 2010 (Fig. 1A and B). The causal fungus was isolated from diseased fruit, and a representative isolate was deposited in the Korean Agricultural Culture Collection (KACC 45482), National Academy of Agricultural Science, Suwon, Korea. Anthracnose is known from many rosaceous hosts worldwide, including *M. pumila* and *Pyrus serotina* (Farr and Rossman, 2010).

Here, the disease occurred relatively frequently on the fruit of sweet crabapple. The necrotic regions seen on the fruit were reddish brown and darkened as the spots expanded. Later, the lesions became dark brown and bristled acervuli were observed on the dark brown areas (Fig. 1C). The bristles measured 80–120  $\mu\text{m}$  and were septate (Fig. 1D). The fungus grown on potato dextrose agar (PDA) produced whitish mycelia initially, which became dark gray, and later salmon-colored conidial masses formed under artificial light (Fig. 1E). The optimal temperature for mycelia growth was 25°C. The conidia were cylindrical, ovoid, and measured 8–15  $\times$  3–7  $\mu\text{m}$  (Fig. 1F). The appressoria on water agar were one-celled, pale brown, thick-walled, ellipsoidal, or clavate, rarely irregular, and measured 6–8  $\times$  5–10  $\mu\text{m}$  (Fig. 1H). The measurements and taxonomic characters coincided with those of *Colletotrichum gloeosporioides* (Penz.) Penz. & Sacc. described by Sutton (1990). To fulfill Koch's postulates, fresh sweet crabapple fruits were

artificially inoculated with a conidial suspension ( $2 \times 10^4$  conidia/ml) of the pathogen obtained from PDA cultures. After incubation, the same fungal fruiting symptoms were reproduced, and the fungus was re-isolated based on these symptoms (Fig. 1I).

To confirm the identification of the causal fungus, an rDNA internal transcribed spacer (ITS) sequence was amplified according to the method of White et al. (1999) and sequenced. The resulting 574-bp sequence was deposited in GenBank (Accession No. HQ420815). Phylogenetic analysis was performed using MEGA4 with the neighbor-joining method and Tajima-Nei distance model. Comparison with ITS rDNA sequences showed high similarity with the sequences of *C. gloeosporioides* (GenBank Accession No. GU174549), which infects apple fruits (Fig. 2). Based on the mycological characteristics, molecular data, and pathogenicity to the host plant obtained in this study, the fungus was identified as *C. gloeosporioides*. To our knowledge, this is the first report of the presence of *C. gloeosporioides* on sweet crabapple in Korea. Although crabapple is not important economically in Korea, anthracnose pathogen in them could be a potential inoculum source causing heavy damage to apple tree or fruit.

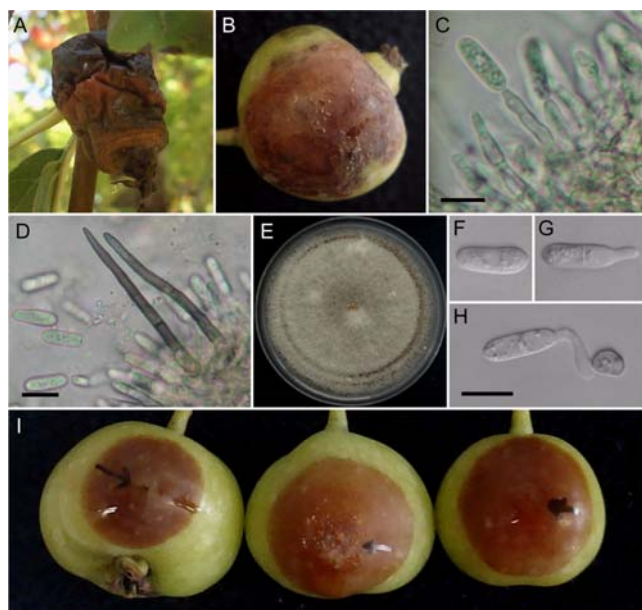


Fig. 1. Symptoms of anthracnose of *Colletotrichum gloeosporioides* and its morphological characteristics. A and B: Naturally infected fruit. C: Conidiogenous cells. D: Bristles on diseased fruit. E: Mycelial colony grown on PDA for 7 days. F: Ungerminated spore. G: Germ tube. H: Appressorium melanization. I: Symptoms after artificial inoculation. Bars = 10  $\mu\text{m}$ .

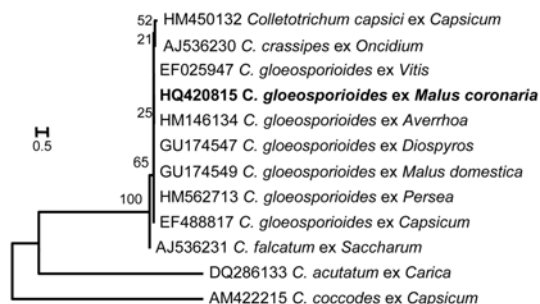


Fig. 2. Phylogenetic tree using ITS sequences showing the closest known relatives of *Colletotrichum gloeosporioides*, including anthracnose fungus infecting *Malus coronaria*. Numbers above the branches indicate the bootstrap values. Bars indicate number of nucleotide substitutions per site. Our isolate infecting sweet crabapple is shown in bold font.

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### References

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