Alternaria tenuissima Causing Fruit Scab Disease on Actinidia chinensis in Anhui Province, China

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Chinese gooseberry (Actinidia chinensis Planch) is an economically and nutritionally important fruit widely cultivated in mountainous areas of Anhui, Zhejiang, Fujian, Hubei, Hunan, Sichuan, Guizhou and Shanxi Province in China. During 2018-2019, a fruit scab disease was identified on the Chinese cultivar Hongyang (A. chinensis var. rufopulpa) in Hefei city, Anhui Province. Irregular, cracked scabs 1 to 5 cm in diameter appeared on approximately 80% of kiwifruits at the survey site. The disease symptoms began as small, pale brown spots on fruits in late May. The spots multiplied and coalesced to form large brown, cracked scabs on immature fruits under high humidity (RH > 90%). The flesh beneath the hardened scab was undamaged, and green in color.

To understand the cause of this disease, fifteen symptomatic kiwifruits were cut into small segments and surface sterilized in 70% ethanol for 30 s, 0.1% HgCl for 30 s, and then washed with deionized water. Pieces of scab tissues were then incubated on potato dextrose agar (PDA) at 28°C in the dark. After three days, four fungal isolates were obtained from the fruit scab tissues by single-spore isolation. Pure cultures formed olive-colored mycelia with a light-colored, taupe-white center. Conidiophores were
short, pale brown, septate, arising singly, and measured 21.6 to 58.7 × 2.8 to 4.3 μm (n = 48). Conidia were multisepate, pale brown, obclavate or obpyriform, with zero to three longitudinal septa and one to four transverse septa, measuring 13.4 to 24.3 × 4.2 to 12.1 μm (n = 48). The pathogen was preliminary identified as *Alternaria tenuissima* based on morphological characterization (Simmons 2007). To confirm the identification, the internal transcribed spacer (ITS) region of rDNA was amplified with primers ITS4 / ITS5 (Guo et al. 2012), and the resulting sequence was deposited in GenBank (Accession No. MN396735). A BLASTN search showed 99.6% similarity with *A. tenuissima* (MG214860 and five other accessions; Query Cover, 100%; E-value, 0) and *A. alternata* (KU324787, Query Cover, 100%; E-value, 0). The ITS sequence did not distinguish *A. tenuissima* from the *A. alternata* complex. Therefore, a partial region of the histone 3 (*H3*) gene was amplified with primers H3-1a / H3-1b (Glass et al. 1995), and the resulting sequence (Accession No. MN395834) showed 99.8% similarity with *A. tenuissima* (MF070841 and 66 other accessions) in the NCBI database. Therefore, this pathogen was identified as *A. tenuissima* on the basis of morphology and similarity of the *H3* gene. To test pathogenicity of the four isolates, 5 ml of conidial suspensions (1 × 10⁶ conidia/ml) of each isolate was sprayed on ten healthy young fruits of *A. chinensis* var. *rufopulpa*. Equal amount of control fruits were inoculated with sterile water. All inoculated fruits were maintained in a moist chamber (RH > 90%) at 26°C for two weeks. Brown scabs consistent with those observed in the field formed on 60% of the inoculated fruits after 10 days, whereas the controls were asymptomatic. *A. tenuissima* was reisolated from the diseased fruits, fulfilling Koch’s
postulates. The pathogenicity experiment was repeated three times with the same results. 

*A. tenuissima* is a known pathogen in China, causing brown leaf spot on kiwifruit (Li et al. 2019). To our knowledge, however, this is the first time *A. tenuissima* has been shown to cause scabs on the fruit of *A. chinensis* in Anhui Province, China. This new disease seriously affects the quality and yield of *A. chinensis*, thus effective control strategies are urgently needed.

References:


Fruit Scab of Kiwifruit caused by *Alternaria tenuissima*.