Diseases Caused by Fungi and Fungus-Like Organisms

Fusarium fujikuroi Causing Fusarium Wilt of *Lactuca serriola* in Korea

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Lactuca serriola L. (syn. *L. scariola* L.) is an annual Asteraceae plant, native to Europe, and accidentally introduced to Korea in the late 1970s (Yim and Jeon 1981). The Korean Ministry of Environment designated this weed as a harmful plant that may disturb the balance of ecosystems (Kim et al. 2013). In July 2019, wilting symptoms of prickly lettuce were found along a roadside in Sangju (36°26'15" N, 128°07'35" E), Korea, with a disease incidence of 60%. Initial symptoms appeared as pale to dark brown lesions on the basal stem and leaves of the plant, and over time the lesions expanded to the upper parts of the plant, resulting in extensive rot. Ultimately, the plants wilted and died. Symptomatic vascular tissues (5 × 5 mm²) of two diseased plants were surface sterilized in 2% NaClO solution for 1 min, followed by 70% ethanol for 1 min, and rinsed two times in sterile distilled water. The pieces were placed on potato dextrose agar (PDA) and incubated at 25°C in the dark for 1 week. Each single-spore isolate was obtained from the hypha tip growing on PDA and examined for morphological and molecular analyses. A representative isolate has been deposited at the Korean Agricultural Culture Collection (KACC49588). Macroconidia were slender, straight, and measured 20.4 to 59.6 × 2.5 to 3.9 µm (*n* = 50), with three to five septa. Microconidia were clavate and measured 6.1 to 13 × 2.5 to 3.3 µm (*n* = 50). Chlamydospores were absent. The colonies developed white aerial mycelium and turned pale purple after a week on PDA. Both morphological and cultural characteristics of the Korean isolate were close to *Fusarium fujikuroi* (Leslie and Summerell 2006). Also, DNA sequence-based identification was carried out using

primer sets of ITS1-F/ITS4 for the internal transcribed spacer (ITS) rDNA region, Btu-F01/Btu-F-R01 for β-tubulin (TUB) gene (Watanabe et al. 2011), and EF-1/EF-2 for translation elongation factor 1-α (TEF) gene. The resulting sequences were deposited in GenBank with accession numbers of MT102938 for ITS, MT182734 for TUB, and MT625962 for TEF. On a BLASTn search, the Korean isolate revealed 100% sequence identity with the verified sequences of *F. fujikuroi* MF984413.1 for ITS, 99.79% (1 of 368 bp is different) with U34415.1 for TUB, and 99.85% (1 of 675 bp) with MN193860.1 for TEF. Pathogenicity was tested by dipping the roots of five healthy prickly lettuce seedlings in the spore suspension (1 × 10⁶ conidia/ml) for 1 h. Inoculated plants were transplanted into pots and maintained in a growth chamber at 90% relative humidity and 20°C. Five noninoculated plants served as controls. After 4 weeks, wilt symptoms accompanied by expanding brown spots were observed on the basal stem and leaves of all inoculated seedlings, whereas the control plants remained symptomless. The fungus present on the inoculated plants was identical to one of the original infections, fulfilling Koch's postulates. Based on the morphological characteristics, sequencing data, and pathogenicity test, the pathogen was identified as *F. fujikuroi*. Bakanae (foolish seedling) disease caused by *F. fujikuroi* is one of the most serious rice diseases in Asia, but also this pathogen has been recorded on *Lactuca sativa* in Thailand (Farr and Rossman 2020). To our knowledge, this is the first report of *F. fujikuroi* causing Fusarium wilt on *L. serriola* in Korea.

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