Diseases Caused by Fungi and Fungus-Like Organisms

First Report of *Sarocladium kiliense* Causing Brown Rot of *Hypsizygus marmoreus* in China

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Hypsizygus marmoreus (Peck) H.E. Bigelow is one of the most popular and widely cultivated edible mushrooms worldwide. In June 2021, an epidemic of *H. marmoreus* fruiting bodies infected with brown rot occurred at a cultivation facility in Yan'an, Shaanxi province, China, which resulted in a 90% economic loss. The fruiting body surface was covered with white-to-gray velvet-like mycelia, which gradually spread to the pileus, eventually covering the whole fruiting body. Brown rot, which is the most important factor limiting *H. marmoreus* fruiting body yield and quality, is responsible for severe economic losses in northern Shaanxi province. To identify the causal agent of this disease, small pieces of diseased tissue were collected from fruiting bodies, disinfected with 70% ethanol, and rinsed three times with sterile distilled water. They were then placed on potato dextrose agar (PDA) medium in plates and incubated at 26°C. The colonies on the PDA medium after a 14-day incubation at 26°C were 40 to 45 mm in diameter, orange-white on the surface, pale orange on the underside, slightly wrinkled or cerebriform, and glabrous or fasciculate. Vegetative hyphae were septate, hyaline, smooth, and thin walled. The unicellular conidia were cylindrical with rounded ends (3.5 to 4.0 × 1.0 to 1.5 µm; *n* = 30). The cultural and morphological characteristics

of the representative isolate MG1 were consistent with those of *Sarocladium kiliense* (Grütz) Summerbell (Giraldo et al. 2015). For molecular identification, DNA was extracted from MG1. The internal transcribed spacer (ITS) region, a gene encoding the second largest RNA polymerase II subunit (*RPB2*), a β -tubulin gene (*TUB2*), and an actin gene (*ACT*) were amplified by PCR using primers ITS1/ITS4, fRPB2-5F/fRPB2-7cR, Bt2a/Bt2b, and ACT-512F/ACT-783R, respectively. The resulting ITS (MZ818340), *RPB2* (MZ833454), *TUB2* (MZ833455), and *ACT* (MZ833456) sequences from MG1 were 99.82, 99.19, 99.69, and 99.22% identical to the corresponding sequences in *S. kiliense* isolate CBS 400.52 (ITS: KM231849, *RPB2*: KM232425, *TUB2*: KC479789, and *ACT*: KM231258). On the basis of the morphological and molecular features, MG1 was identified as *S. kiliense* (Giraldo et al. 2015; Lombard et al. 2015; Summerbell et al. 2011). Pathogenicity tests, which were repeated three times, were conducted using conidial suspensions (approximately 1×10^5 spores/ml) prepared in sterile distilled water. The surfaces of 30 healthy *H. marmoreus* fruiting bodies maintained in a plastic box were sprayed with the MG1 conidial suspensions. Control *H. marmoreus* fruiting bodies were sprayed with sterile distilled water. The inoculated fruiting bodies were maintained in darkness at 25°C and 95% relative humidity. The disease symptoms that developed in 3 days included the presence of gray mycelia on the fruiting body surface. Additionally, *S. kiliense* was reisolated from symptomatic pilei at 6 days postinoculation. Disease symptoms were undetectable on the negative control. To the best of our knowledge, this is the first report of *H. marmoreus* infected with brown rot caused by *S. kiliense* in China.

References:

- Giraldo, A., et al. 2015. 34:10.
- Lombard, L., et al. 2015. Stud. Mycol. 80:189.
- Summerbell, R. C., et al. 2011. Stud. Mycol. 68:139.

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