Diseases Caused by Fungi and Fungus-Like Organisms

Blue Mold Rot Caused by *Penicillium expansum* on *Polygonatum odoratum* var. *pluriflorum*

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Polygonatum odoratum var. *pluriflorum*, called “Dunggulle,” is cultivated in East Asia to obtain rhizomes. In Korea and China, these rhizomes are used in traditional teas, health beverages, and herbal medicines (Zhao and Li 2015). In 2019, Dunggulle was cultivated on 47 hectares, with an annual output of 120 metric tons in Korea. In November 2020, Dunggulle rhizomes with symptoms of blue mold rot were observed at a Dunggulle farm storage (36°06′01″N, 127°29′20″E) in Geumsan, Korea, where the temperature ranged from 9 to 13°C, with an average humidity of 70%. The disease incidence was 2 to 3% out of 200 rhizomes across all markets surveyed. The disease begins with a greenish blue mold covering the rhizome surface (30 to 60%), followed by rhizome rot with a dark brown color as the disease progresses. Leading edges of the rotten rhizome pieces were sterilized with 1% NaOCl and 70% ethanol and placed on MEA (malt extract agar) with penicillin G and streptomycin (both 50 µg/ml). After 7 days of incubation at 25°C, greenish-blue colonies appeared, from which a monospore was isolated. A representative isolated strain was deposited in the Korean Agricultural Culture Collection (KACC, Wanju, Korea) with acc. no. KACC 49832. The strain grew slowly on MEA at 25°C (8 to 18 mm in diameter after 7 days), producing

greenish blue conidia. The conidiophores were hyaline and mostly terverticillate; the branches were appressed against the main axis; the stipes were smooth-walled; and the metulae were cylindrical, 10 to 13 × 2.7 to 3.2 µm, with 6 to 10 flask-shaped phialides, measured 9 to 12 × 2.7 to 3.1 µm. The conidia were globose or subglobose and 2.8 to 4.1 µm in diameter. These morphological characteristics fit well with the description of *Penicillium expansum* (Frisvad and Samson 2004). Genomic DNA was extracted from the mycelia of the KACC 49832 MEA plate. ITS rDNA, beta-tubulin (*BenA*), and calmodulin (*CaM*) gene regions were sequenced for identification (Houbraken et al. 2020), and the resulting sequences were deposited in GenBank (acc. nos. MZ189258, MZ226688, and MZ226689, respectively). Comparison with the GenBank sequences revealed that the Korean isolate was highly similar to *P. expansum* (ITS rDNA 99.8%, *BenA* 98.6%, and *CaM* 97.8%). Phylogenetic results based on a maximum-likelihood analysis revealed that KACC 49832 was grouped with *P. expansum*. To demonstrate pathogenicity, 10 µl of conidial suspension (1.3×10^5 conidia/ml) was dropped on the surface of three Dunggulle rhizomes scratched with a syringe needle. For the control, sterile water was applied on three control rhizomes. All rhizomes were surface-sterilized as described above before being sprayed and dried. All inoculated and control rhizomes were kept in an incubator at 25°C and 90 to 95% relative humidity. After a week, the inoculated points showed symptoms similar to those of the initial infection, whereas controls remained symptomless. The reisolated fungus matched KACC 49832 based on morphological and sequence analyses, thereby fulfilling Koch's postulates. The experiment was performed three times. To our knowledge, this is the first report of *P. expansum* as a Dunggulle rhizome pathogen in Korea. As this pathogen is known to produce patulin, a carcinogenic fungal metabolite, further studies on the mycotoxicity of the infected rhizomes are required. This report might help manage the storage conditions of Dunggulle rhizomes to prevent blue mold rot.

References:

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