Diseases Caused by Fungi and Fungus-Like Organisms

First Report of Postharvest Blue Mold Decay Caused by *Penicillium expansum* on Lemon (*Citrus limon*) Fruit in China

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Lemon (*Citrus limon*) is one of the most important commercial (both dried and fresh) citrus fruits in China. In the spring of 2019, postharvest blue mold decay was observed at an incidence of 3 to 5% on lemon fruit at the local markets in Beijing, China. Fruit lesions were circular, brown, soft, watery, and rapidly expanded at 25°C. To isolate the causal organism, small pieces (2 mm³) were cut from the lesions, surface sterilized for 1 min in 1.5% NaOCl, rinsed three times with sterilized water, dried with sterile filter paper, placed onto potato dextrose agar medium, and incubated at 25°C for 6 days. Eight morphologically similar single-colony fungal isolates were recovered from six lemon fruits. Colony surfaces were bluish-green on the upper surface and cream to yellow-brown on the reverse. Hyphae on colony margins were entirely subsurface and cream in color. Mycelium was highly branched, septate, and colorless, and conidiophores were 250 to 450 × 3.0 to 4.0 µm in size. Stipes of conidiophores were smooth-walled, bearing terminal penicilli, typically terverticillate or less commonly biverticillate, rami occurring singly, 16 to 23 × 3.0 to 4.0 µm, metulae in three to six, measuring 12 to 15 × 3.0 to 4.0 µm. Phialides were ampulliform to almost cylindrical, in verticils of five to eight, measuring 8 to 11 × 2.5 to 3.2 µm with collula. Conidia were

smooth-walled, ellipsoidal, measuring 3.0 to 3.5 × 2.5 to 3.0 µm. According to morphological characteristics, the fungus was identified as *Penicillium expansum* (Visagie et al. 2014). For molecular identification, genomic DNA of eight fungal isolates was extracted, and regions of the beta-tubulin (*TUB*) and calmodulin (*CAL*) genes and ITS region were amplified using Bt2a/Bt2b, CAL-228F/CAL-737, and ITS1/ITS4 primers, respectively. Obtained sequences of all isolates were identical to sequences of the representative isolate YC-IK12, which was submitted in GenBank. BLAST results of YC-IK12 sequences (ITS, MT856700; *TUB*, MT856958; *CAL*, MT856959) showed 98 to 100% similarity with *P. expansum* accessions (NR-077154, LN896428, JX141581). For pathogenicity tests, 10 µl of conidial suspension (1.0 × 10⁶ conidia/ml) from 7-day-old YC-IK12 culture was inoculated using a sterilized needle into the surface of each of five asymptomatic disinfected lemons. As a control, three lemons were inoculated using sterile distilled water. All inoculated lemons were placed in plastic containers and incubated at 25°C for 7 days. Decay lesions, identical to the original observations, developed on all inoculated lemons, whereas control lemons remained asymptomatic. Fungus reisolated from the inoculated lemon was identified as *P. expansum* on the basis morphology and Bt2a/Bt2b, CAL-228F/CAL-737, and ITS1/ITS4 sequences. Previously, *Penicillium* spp. including *P. expansum* have been reported as postharvest pathogens on various *Citrus* spp. (Louw and Korsten 2015). However, *P. digitatum* has been reported on lemons, and *P. expansum* has been reported on stored kiwifruit (*Actinidia arguta*), *Malus*, and *Pyrus* species in China (Tai 1979; Wang et al. 2015). To our knowledge, this is the first report of blue mold caused by *P. expansum* on lemons in China.

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