Diseases Caused by Fungi and Fungus-Like Organisms

First Report of Sour Rot of Strawberry Caused by *Geotrichum candidum* in the United States

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Strawberry (*Fragaria × ananassa*) is an important crop in the United States, and Florida is the second major producer in the country. In January 2020, an unknown fruit rot was observed in two strawberry fields in Dover (seedling selection) and Plant City (cultivar Florida127), Florida. Disease incidence varied from less than 1% in one field to up to 15% in the second field during some harvests in which over-ripe fruit were present. Affected fruit had a water-soaked soft rot with a sour smell, and sometimes with white mycelium on the fruit surface. Direct isolation was performed from symptomatic fruit from each area by touching the surface of a lesion with a sterile needle and streaking the fungus over general isolation medium (Amiri et al. 2018). The fungus was incubated at 25°C and 12-h photoperiod for 5 days. Four single-spore isolates (20-46 and 20-47 from Plant City; 20-49 and 20-50 from Dover) obtained from different colonies were grown on potato dextrose agar (PDA). Colonies were white to cream, flat, with a powdery surface, and had a characteristic sour odor. Hyphae were hyaline, septate, growing in a dichotomous pattern and often disarticulating into arthroconidia, which were unicellular, spherical to cylindrical, measuring 4.8 to 9.5 × 3.5 to 5.6 µm ($n = 50$). Based on the morphological characteristics, the fungus was identified as *Geotrichum candidum* (De Hoog et al. 1986). To confirm the identity of the isolates, the ribosomal internal transcribed spacer (ITS-rDNA) and the translation elongation factor 1-alpha (TEF1-α) gene regions were amplified and sequenced using the primers ITS1/ITS4 (White et al. 1990) and EF1-728F/

EF1-1567R (Carbone and Kohn 1999), respectively. Consensus sequences were deposited in the GenBank (accession nos. MT353975 to MT353978 for ITS-rDNA, and MT346367 to MT346370 for TEF1-α). The BLASTn analysis revealed 99% identity with reference sequences of *G. candidum* for ITS-rDNA (KU373122) and TEF1-α (MK397513). Phylogenetic analysis, including ITS sequences of *G. candidum* and other spp., obtained from GenBank, was performed using maximum likelihood and Bayesian inference methods, implemented in MEGA-X and MrBayes, respectively. The isolates were grouped within the *G. candidum* clade. The pathogenicity of the fungus (isolate 20-46) was evaluated in ripe and green strawberry fruit (cultivar Florida127). Nonwounded and superficially wounded (with a sterilized needle) fruit were inoculated with 20 µl of a spore suspension (1×10^7 spore/ml), prepared by washing the surface of a 5-day-old colony on PDA, with sterile deionized water (SDW) plus 0.01% (v/v) Tween 20. Wounded and nonwounded control fruit were treated with SDW. Fruit were maintained in moist containers at 25°C. Each treatment consisted of 12 fruit (three replicates, each containing four fruit) and was evaluated daily for 10 days. Symptoms of sour rot were visible as soon as 48 h after inoculation, but only on ripe (100% incidence) and green (58% incidence) wounded fruit. Symptoms progressed to an intense water-soaking with the presence of a typical white mycelium on the surface. Control fruit remained symptomless. The fungus was successfully recovered from symptomatic fruit, fulfilling Koch's postulates. Although strawberry fruit rots caused by *G. candidum* have already been reported in Pakistan and China (Hussain et al. 2016; Ma et al. 2018), this is the first report of this species causing sour rot on strawberry in the United States. The disease may be a minor problem on damaged or over-ripe fruit, but further studies might be needed to determine its importance, distribution, and potential strategies for control.

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