Diseases Caused by Fungi and Fungus-Like Organisms

First Report of *Gnomoniopsis idaeicola* Causing Cane Wilt and Canker in Commercial Blackberry Fields in Oregon

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Oregon is the leading producer of blackberries in the United States (USDA-NASS 2021). In November 2020, we visited a 7-year-old, 5.6-ha field of thornless trailing cultivar ‘Columbia Star’ in Marion County, Oregon, in response to grower reports of rapid plant death that they called “Blackberry Collapse.” The disease pattern in the field was semicircular patches of dead plants. We estimate that ca. 17% of the plants were killed. Symptoms included fewer, stunted primocanes, floricanes reddening, premature floricanes senescence, or elliptical or irregular brown to purple cane lesions often appearing near the base of necrotic petioles clasping the cane. Twenty-two cane lesions were collected, surface-disinfested, and placed on potato dextrose agar with streptomycin. In addition to common *Rubus* cane pathogens (*Kalmusia coniothyrium*, *Botrytis* spp., *Diaporthe* spp., and *Seimatosporium lichenicola*), *Gnomoniopsis idaeicola* was isolated from 23% of the samples. After isolation of *G. idaeicola* from ‘Columbia Star’, we also isolated the pathogen from symptomatic ‘Black Diamond’ blackberry in fields in Washington and Linn Counties in Oregon. *G. idaeicola* grew as white- to cream-colored circular colonies on the agar surface with sparse to dense aerial hyphae. Some isolates produced cream-colored exudate from irregular conidiomata. Conidia were single-celled, hyaline, oval to ellipsoid, and ranged from 4.9 to 6.9 µm long and 1.2 to 2.5 µm wide ($n = 100$). Perithecia and ascospores were not seen on canes or in culture; molecular methods were used to identify the fungus. Genomic DNA was extracted from nine isolates and β -tubulin, the ITS region, and *tef-1 α* were amplified using the primers and conditions described by Walker et al. (2010).

Amplicons were Sanger sequenced in both directions by the Core Facilities of the Center for Quantitative Life Sciences of Oregon State University, Corvallis, Oregon. Sequences were deposited in GenBank (β -tubulin OK539758 to OK539766; ITS OK348854 to OK348862; *tef-1 α* OK539767 to OK539775). The β -tubulin sequences (737 bp) were 100% identical to the sequence of *G. idaeicola* from *Rubus procerus*, Oregon (GU320783). The ITS sequences (518 bp) were 99.2 to 100% identical to *G. idaeicola* CBS125674^T (GU320796). The *tef-1 α* sequences (860 bp) were 99.9 to 100% identical to reference sequences of *G. idaeicola*. Phylogenetic analyses of concatenated sequences using Tamura-Nei neighbor-joining (Tamura et al. 2004) confirmed the identity. Pathogenicity of *G. idaeicola* isolates was tested in repeated experiments on four to five detached ‘Black Diamond’ primocanes and potted ‘Columbia Star’ plants with 4-mm hyphal plugs placed on fresh wounds and wrapped in Parafilm; controls were treated with sterile agar plugs (Ellis et al. 1984; Stevanović et al. 2019). After 14 days in each experiment, expanding necrotic lesions were observed on canes inoculated with *G. idaeicola* but not with sterile agar plugs. The ITS sequence of fungi isolated from lesions confirmed its identity as *G. idaeicola*, fulfilling Koch’s postulates. *G. idaeicola* was described as a new species by Walker et al. (2010) from perithecia collected from wild *Rubus* spp. in the Pacific Northwest. Despite its presence on native *Rubus*, *G. idaeicola* has not been reported in commercial blackberry fields in Oregon. Stevanović et al. (2019) identified *G. idaeicola* as an important pathogen causing canker, wilt, and death of blackberry in Serbia. Surveys of Oregon blackberry fields for *G. idaeicola* are ongoing, along with research on the epidemiology and management of this emerging pathogen.

References:

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