Disease Notes

Diseases Caused by Fungi and Fungus-Like Organisms

First Report of *Neofusicoccum parvum* Causing Dieback and Canker Disease on Hemp in the United States

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Hemp (*Cannabis sativa* L.) had been grown as a fiber crop in the United States for over 300 years prior to it being banned as schedule 1 drug in 1970 (Small et al. 2002). After the farm bill legislation in 2018, hemp was reintroduced as a crop into Arkansas, where approximately 700 ha were grown in 2019. In July, on a single farm in Searcy Co., AR, 1- to 2-month-old hemp plants (cultivars: Trump and Cherry Wine) were observed with leaf discoloration and curling, and branch dieback with distinct lesion margins on the stem. The dieback was predominantly on the main terminal. Approximately 10% of the plants were observed with dieback symptoms. The infected branches and the whole plants with terminal infections often would die, significantly impacting yield. Small pieces from symptomatic stems and leaves of the field samples were surface sterilized in 10% bleach for 1 min, washed in sterile deionized water three times, and then placed on water agar (WA). After 3 days, mycelia growing out from both leaf and stem tissue was transferred onto potato dextrose agar (PDA) to recover pure cultures. Seventeen isolates recovered from eight separate plants had an identical colony morphology. Seven-day-old colonies developed gray aerial mycelia but no conidia. However, pycnidia, containing a large number of both septate and nonseptate conidia, were found on the WA surface after 7 days, or on symptomatic plant tissue incubated in a moist chamber for 48 h. The average size of conidia ($n = 20$) was 22.9 ± 1.6 μm long by 12.8 ± 1.1 μm wide. DNA was extracted from mycelia of two isolates (ON1 and ON4A1) (Feng et al. 2014) and used to amplify the internal transcribed spacer region (ITS) with ITS1/ITS4 primers or the β -tubulin gene using tub 2F/2R primers (Hirsch et al. 2000; White et al. 1990). Polymerase chain reaction products were sequenced after cleaning. The BLAST search against GenBank indicated that the sequences of ITS and β -tubulin

fragments of the isolates ON1 and ON4A1 (GenBank accession nos. MT093349, MT093350, and MT141110) matched *Neofusicoccum parvum* with 99 to 100% identity. Multiple pathogenicity tests were conducted. In the first test, stems (approximately 0.5 to 1 cm in diameter) of three cultivars (Cherry Blossom, Berry Blossom, and Cherry Wine) were wounded with toothpicks, inoculated with PDA plugs colonized by *N. parvum* (isolate ON4A1), and then wrapped with Parafilm. Plants inoculated with uncolonized PDA plugs were used as controls. Approximately 50 days after inoculation, plants started to show symptoms of branch dieback and canker at the inoculation point, whereas the control plants showed no symptoms. The inoculation resulted in 50 to 100% branch mortality after 4 months. In a second test, two isolates (ON1 and ON4A1) were used to inoculate smaller stems (approximately 0.2 to 0.3 cm in diameter) of the cultivar Cherry Blossom after wounding similar to the previous test. The inoculated stems showed canker symptoms and wilting of the leaves distal to the point of inoculation within 2 to 3 weeks. Within 5 weeks, almost all tissue distal to the point of inoculation had died. *N. parvum* was recovered from multiple symptomatic inoculated stems, confirming that *N. parvum* was the causal agent. *N. parvum* has been reported to cause dieback and canker disease on a wide range of plants, including grape (Galarneau et al. 2019), cacao (Puig et al. 2019), and strawberry (Oliveira et al. 2019) in the United States and hemp in Italy (Alberti et al. 2018). However, this is the first report of *N. parvum* causing dieback and canker disease on hemp in the United States.

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