Disease Notes

Diseases Caused by Fungi and Fungus-Like Organisms

First Report of Canker and Branch Dieback of Sweet Cherry Trees Caused by *Calosphaeria pulchella* in Chile

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In Chile, the 2019 to 2020 sweet cherry season yielded 228,548 t produced on 38,392 ha and an average annual crop value about US$1.6 billion (http://www.iqonsulting.com/yb/). Between autumn 2019 and summer 2020, branch and limb dieback symptoms were observed in two 12-year-old sweet cherry (*Prunus avium* L.) orchards located in the O'Higgins region (Chile Central Valley). Furthermore, other symptoms such as wilting leaves, cankers, bark cracking, emission of gum exudates, and internal wood necrosis were detected on trees of 'Bing', 'Santina', and 'Sweetheart' cultivars (Cainelli et al. 2017). Wood fragments from symptomatic branches were surface sterilized with 95% ethanol, flamed, and placed onto potato dextrose agar amended with 0.5 g/liter of streptomycin sulfate (Berbegal et al. 2014). After 7 days of incubation at 25°C, pink to red colonies with white margins were isolated. Each isolate was characterized by having hyaline and oblong-ellipsoidal conidia of 5.76 ± 0.88 × 1.76 ± 0.36 µm (n = 100) (Trouillas et al. 2012). According to these morphological features, the fungus was identified as *Calosphaeria pulchella* (Pers.: Fr.) J. Schröt (anamorph *Calosphaeriophora pulchella* Réblová, L. Mostert, W. Gams & Crous) (Réblová et al. 2004). The internal transcribed spacer (ITS) region of the rDNA sequence comparison using BLAST analysis revealed a 99.48% identity and 100% query coverage between *C. pulchella* sequence HM237297 and the Chilean isolates. Moreover, the Chilean isolates were confirmed by means of phylogenetic analysis using ITS sequences of *C. pulchella* available in the GenBank database. The maximum-parsimony phylogenetic tree supported the cluster analysis of the Chilean *C. pulchella* isolates with those obtained in other regions of the world with a bootstrap value of 95% (Berbegal et al. 2014; Trouillas et al. 2012). The Chilean ITS sequences were deposited into GenBank (MT378444 to MT378447). Two-year-old sweet cherry trees (cv. Bing) were inoculated with the Chilean isolates. Six trees were used as replicates. To accomplish this goal, two punctures of 5-mm diameter were made in two branches per tree with a cork borer, and a plug of mycelium from 7-day-old colonies was laid on the wound mycelium side down. Six trees were inoculated with sterile agar plugs. Every puncture was sealed with petroleum jelly and wrapped with Parafilm. Four months after inoculation, the vascular streaking developing from the inoculated wounds was measured. The average lesion lengths on inoculated and noninoculated shoots were 43.79 and 21.79 mm, respectively, which were significantly different according Fisher's LSD test ($P < 0.05$). *C. pulchella* was recovered from all the inoculated branches. No fungus was isolated from the controls, confirming Koch's postulates (Trouillas et al. 2012). To our knowledge this is the first report of *C. pulchella* causing canker and branch dieback in sweet cherry trees in Chile. This new disease represents a serious threat to the Chilean cherry industry, and further research on disease control is needed.

References:

Berbegal, M., et al. 2014. Plant Dis. 98:1008.
Cainelli, C., et al. 2017. IOBC WPRS Bull. 123:195-197.
Réblová, M., et al. 2004. Stud. Mycol. 50:533-550.
Trouillas, F. P., et al. 2012. Plant Dis. 96:648.

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