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DISEASE NOTES

Cercospora Leaf Spot Caused by *Cercospora armoraciae* on Watercress in California

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ABSTRACT

Watercress (*Nasturtium officinale* R. Br.) is a semiaquatic plant in the Brassicaceae that is grown as a fresh-market, specialty leafy green, minor crop commodity. The 2014 watercress crop in Santa Clara Co. was 4.9 ha and the size of grower operations ranged from 0.04 to 1.5 ha. In July 2014, commercially grown greenhouse watercress plantings in this county exhibited symptoms of a foliar disease. Leaf spots were circular to oval or irregular in shape, whitish to tan, and observable on both adaxial and abaxial leaf surfaces. Sparse fungal sporulation was observed on both leaf surfaces. Spots ranged from 3 to 15 mm in diameter and were observed on both new and old foliage. Leaf spots sometimes coalesced and resulted in a blight-like symptom. In some greenhouses, the disease incidence reached 80%. Because diseased leaves are unmarketable and it was not feasible to sort healthy from diseased leaves, greenhouses with high disease incidence resulted in complete crop loss. For isolations, symptomatic leaves were soaked in 0.1% NaOCl for 1 min. Tissues from the leaf spot margins were placed onto malt extract agar (MEA) amended with tetracycline (0.1 g/liter). Isolations resulted in the recovery of one dominant type of fungus. On synthetic nutrient-poor agar plates, isolates (CPC 25340 [= CBS 140181], and CPC 25341 to 25346) formed fasciculate, brown conidiophores that gave rise to conidia that were hyaline, straight to slightly curved, cylindrical to cylindro-obclavate, with slight obconically truncate bases and obtuse apices. Conidia measured 20 to 150 × 2.5 to 6.0 μm and were 3- to 17-septate. DNA sequencing of the seven isolates (CPC 25340 to 25346) was conducted for the following genes: internal transcribed spacer (ITS) ribosomal DNA (GenBank Accession Nos. KT193770 to KT193776, respectively), actin (KT193777 to KT193782, respectively), calmodulin (KT193783 to KT193789, respectively), and histone H3 (KT193790 to KT193796, respectively). In comparison with published sequences (Groenewald et al. 2013), the watercress isolates were 99 to 100% identical to GenBank sequences for all loci evaluated for *Cercospora armoraciae* Sacc. Based on morphological characteristics and DNA sequence data, the isolates were identified as *C. armoraciae* (Groenewald et al. 2013). To test pathogenicity, six characterized isolates (CPC 25340 to 25345) were grown on MEA. Spore suspensions (1 × 10⁵ conidia/ml) were prepared for each isolate and sprayed, using a hand-held mister, onto leaves of 4-month-old potted watercress plants; plants were incubated

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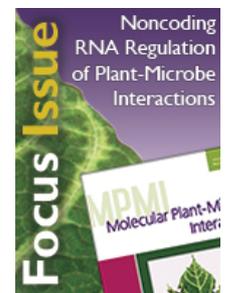
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under enclosed, clear humidomes maintaining 100% relative humidity and daytime temperatures of 26 to 28°C. After 8 days, white to tan spots developed on inoculated plants and appeared identical to spots observed in the greenhouse. Isolation from inoculated plants resulted in the recovery of fungi that were morphologically identical to the original isolates. Control watercress plants were sprayed with water and incubated in the same way as the other plants, but did not develop leaf spots. The experiment was repeated and the results were the same. To our knowledge, this is the first documentation of *Cercospora* leaf spot on watercress in California and characterization of the causal pathogen, *C. armoraciae*. Previous reports in the United States linked this disease to *C. nasturtii* Pass., which is now regarded as a synonym of *C. armoraciae*. This watercress pathogen has been reported (frequently as *C. nasturtii*) from Africa, Asia, New Caledonia, New Zealand, South America, and several other states in the United States (Farr and Rossman 2015).

References:

Section:

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