tested were similar to those observed in the field. No symptoms were observed on water-inoculated plants. Comparative repetitive sequence-based (rep)-PCR DNA analysis using the BOXA1R primer (3) resulted in a DNA banding pattern of each of the isolates from the South Carolina fields (23 isolates), as well as those reisolated from inoculated plants, that was identical to *P. syringae* pv. *alisalensis* BS91 and differed from the *P. syringae* pv. *maculicola* F18 strain. On the basis of the rep-PCR assays and the differential host range (1), the current disease outbreak on broccoli and cabbage in South Carolina is caused by the bacterium *P. syringae* pv. *alisalensis*. Broccoli is a relatively new, albeit rapidly expanding, production vegetable in South Carolina; this disease may represent a limiting factor to future production.

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*The *e*-Xtra logo stands for "electronic extra" and indicates this Disease Note online contains supplemental material not included in the print edition.

First Report of *Chalara fraxinea* on Common Ash in Italy. N. Ogris, T. Hauptman, and D. Jurc, Slovenian Forestry Institute, Večna pot 2, 1000 Ljubljana, Slovenia; and V. Floreancig, F. Marsich, and L. Montecchio, Università degli Studi di Padova, Dipartimento Territorio e Sistemi Agro-Forestali, viale dell'Università 16, I-35020 Legnaro, Italy. Plant Dis. 94:133, 2010; published online as doi:10.1094/PDIS-94-1-0133A. Accepted for publication 19 October 2009.

In many European countries, the anamorphic *Chalara fraxinea* Kowalski (teleomorph *Hymenoscyphus albidus* [Roberge ex Desm.] Phillips; 1–3) is responsible for a severe and rapidly spreading dieback of common ash (*Fraxinus excelsior* L.) since it was first reported in Poland. Recently, this disease was added to the EPPO Alert List and the NAPPO Phytosanitary Alert System. Symptomatic trees were observed in a 1.8-ha ash-maple forest in northeastern Italy (Fusine, UD; 46°30′N, 13°37′E; 782 m above sea level) along the Italo-Slovenian border in July 2009. Symptoms were found on approximately 10% of mature common ash and 70% of seedlings. Main symptoms were shoot, twig, and branch dieback, wilting, and bark cankers (1). Fungal fruiting bodies were not found on or near the canker surface. Furthermore, longitudinal and radial sections through the cankers revealed gray-to-brown xylem discoloration. One symptomatic 3-year-old plant was randomly selected and from the necrotic margin of one canker previously surface-sterilized with 3% sodium hypochlorite and rinsed, four 2-mm-wide chips were placed on malt extract agar (MEA) and incubated at 21 ± 1°C in the dark. Among a variety of microorganisms, after 19 days, slow-growing colonies (mean radius of 12 mm) appeared that were effuse, cottony, and often fulvous brown but sometimes dull white with occasional gray-to-dark gray patches. The purified isolate was then transferred to the same medium at 4 ± 1°C in the dark, and after 11 days, hyaline-to-dark gray phialides were observed producing numerous conidia in slimy droplets and sometimes in chains. Phialophores measured 8.6 to 21.0 (15.1) µm long (n = 20), 4.2 to 13.4 (8.8) × 3.6 to 5.5 (4.7) µm at the base, and 5.2 to 8.7 (6.5) × 2.5 to 3.1 (2.8) µm at the collarette; conidia measured 2.8 to 4.2 (3.4) × 1.9 to 2.5 (2.2) µm (n = 40); and first formed conidia measured 5.5 to 6.5 (5.9) × 1.8 to 2.5 (2.1) µm (n = 20). These morphological characteristics matched Kowalski's (1) description of *C. fraxinea*. In August of 2009, the fungal isolate was used to test pathogenicity with current year shoots of 25 6-year-old (150 to 210 cm high) asymptomatic common ash trees under quarantine conditions (Slovenian Forestry Institute's experimental plots). For every plant, the bark of the main shoot (10 to 13 mm in diameter) was wounded with a 6-mm-diameter cork borer. Twenty saplings were inoculated with one 6-mm-diameter mycelial plug obtained from the margin of a 26-day-old culture (MEA), while five saplings were inoculated with sterile MEA plugs. All wounds were sealed with Parafilm and aluminum foil. After 28 days, all plants inoculated with the *C. fraxinea* showed bark lesions (2 to 39 mm long, mean 7 mm) and wood discoloration (6 to 85 mm long, mean 22 mm) from which the pathogen was reisolated. These symptoms were absent from controls and the pathogen was never reisolated. To our knowledge, this is the first report of *C. fraxinea* in Italy. Investigations on its presence in all *Fraxinus* species naturally growing in the investigated area and in the nearest regions are in progress. The obtained isolate is preserved in both Padova and Ljubljana herbaria as CFIT01.

References: (1) T. Kowalski. For. Pathol. 36:264, 2006. (2) T. Kowalski and O. Holdenrieder. For. Pathol. 39:1, 2009. (3) T. Kowalski and O. Holdenrieder. For. Pathol. 39:304, 2009.

e-Xtra*

First Report of the Sting Nematode *Belonolaimus longicaudatus* on Soybean in Delaware. Z. A. Handoo and A. M. Skantar, Nematology Laboratory, USDA-ARS, Beltsville Agricultural Research Center, Beltsville, MD 20705; and R. P. Mulrooney, Department of Plant and Soil Sciences, University of Delaware, Newark 19716. Plant Dis. 94:133, 2010; published online as doi:10.1094/PDIS-94-1-0133B. Accepted for publication 31 October 2009.

In late July of 2005, several, large, irregular areas of severely chlorotic, stunted, and dead soybean plants were observed in two fields of soybean (*Glycine max*), 8.05 km apart, in sandy soil (94% sand, 2% silt, and 4% clay) in southwestern Sussex County, DE. The grower also had observed stunted corn the previous year in the same areas and thought the fields had a fertility problem. The morphology of adults and molecular analyses of the juveniles isolated from soil samples established the identity of the species as the sting nematode, *Belonolaimus longicaudatus* (1–4). The population density was 216 nematodes per 250 cm^3 of soil. Morphological characters used for identification included female body, stylet and tail length, shape of head, stylet knobs, tail and tail terminus, number of lines in the lateral field, and vulva percentage in relation to body length. The male characters critical for identification were the following: body, stylet, spicule, and gubernaculum length; shape of head and stylet knobs; and number of lines in the lateral field. Measurements of females (n = 5) included body length (range = 2,035 to 2,120 µm, mean = 2,073.7, standard deviation [SD] = 37.0), stylet (117.0 to 127.5, 123.4, 4.5), V% (48.4 to 52.3, 50.6, 1.5), and tail (109 to 140, 120, 14.2). The lateral field had one incisure. Shape of head, stylet knobs, and tail were also consistent with *B. longicaudatus*. Males (n = 4) were characterized by the body length (range = 1,500 to 2,070 µm, mean = 1,753.3, SD = 290.2), stylet (117.0 to 127.5, 121.5, 5.4), spicules (41 to 50, 47, 5.2), and gubernaculum (17.0 to 18.5, 17.8, 0.8). Molecular diagnosis as *B. longicaudatus* was confirmed by sequencing two ribosomal DNA markers from three juveniles. Sequence of the internal transcribed spacer region ITS1 and 2 (GenBank Accession No. GQ896549) from this population was 99% identical to Florida isolate BlCi6 (DQ672368), and the 28S large ribosomal subunit D2-D3 expansion region (GQ896548) was 99% identical to Florida isolate BlCi4 (DQ672344). A high degree of similarity (>98%) was also shared by several other *B. longicaudatus* sequences (1). This detection represents a new state record in Delaware for *B. longicaudatus*. Since this detection in 2005, there have been no new reports of other observations of sting nematode or spread from these two fields tilled by the same farm operator in Delaware. Elsewhere, *B. longicaudatus* is known to occur in subtropical regions of the lower coastal plain, from Virginia to Florida and along the Gulf Coast into Texas. On the east coast, USDA Nematode Collection records document this nematode from Florida, Georgia, New Jersey, and South Carolina. Within Delaware, another sting nematode species, *Belonolaimus maritimus*, was detected on American beachgrass (*Ammophila breviligulata*) and bitter panicgrass (*Panicum amarum* var. *amarulum*) from Fenwick Island, near the Maryland border. Sting nematodes have also been reported in Burlington County, NJ.

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(*Disease Notes* continued on next page)