

Disease Note

Diseases Caused by Nematodes

First Report of Beech Leaf Disease, Caused by *Litylenchus crenatae mccannii*, on American Beech (*Fagus grandifolia*) in Virginia

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Beech leaf disease (BLD) was first reported in 2012 in Lake County, Ohio, on American beech trees (*Fagus grandifolia* Ehrh.). Since then, it spread across the Northeastern United States and has been reported from Ohio, Pennsylvania, New York, New Jersey, Connecticut, Rhode Island, Maine, West Virginia, and Ontario, Canada (Carta et al. 2020; Marra and LaMondia 2020; Reed et al. 2020). The symptoms of BLD are characterized by dark interveinal banding of leaves appearing soon after spring flush that become chlorotic and necrotic through autumn, resulting in canopy thinning in advanced stages, followed in some young trees by death. The North American nematode subspecies *Litylenchus crenatae mccannii* has similar morphological characteristics to a subspecies of *Litylenchus crenatae* (Kanzaki et al. 2019) reported on *F. crenata* from Japan. However, that beech species has not shown BLD symptoms or yielded any *L. crenatae mccannii* in North America. There are several morphological differences between the two

nematode subspecies. The North American subspecies has a shorter postuterine sac and narrower body width in mature females, shorter tail in immature females, longer tail in mature females, and longer stylet in males when compared with the Japanese subspecies (Carta et al. 2020). BLD symptoms were found on American beech trees in Prince William Forest Park, Prince William County, Virginia, in June 2021. The affected leaves contained females, males, and juveniles with morphometrics consistent with *L. crenatae mccannii* (Carta et al. 2020). The crude genomic DNA from a live single *Litylenchus* was prepared with freeze-thaw lysis (Carta and Li 2019). ITS PCR was performed using the procedures and primer set, ITS-CL-F2 and 28S-CL-R, described in a previous study (Carta and Li 2020). The visualization, cleanup, and direct DNA sequencing of the PCR products were performed using the procedures described in previous studies (Carta and Li 2018, 2019). Sequences were the same as in a previous study (Carta et al. 2020) and were submitted to GenBank as accessions MZ611855 and MZ611856. This represents the first report of BLD in Virginia. It is also approximately 300 miles south of the 2020 detection of BLD from New Cumberland, West Virginia, and represents the southernmost detection of the disease and nematode in North America.

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