

# First Report of Beech Leaf Disease, Caused by the Foliar Nematode, *Litylenchus crenatae mccannii*, on American Beech (*Fagus grandifolia*) in Connecticut

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First discovered in 2012 in Lake County, Ohio, beech leaf disease (BLD) has since spread to stands of American beech (*Fagus grandifolia* Ehrh.) across much of northern Ohio, western and northern Pennsylvania, New York, and Ontario, Canada ([Ewing et al. 2018](#)), and has also been found on European beech (*Fagus sylvatica* L.) in Ohio. The disease is characterized by dark interveinal banding of leaves appearing soon after spring flush, and in advanced stages results in canopy thinning, followed in some cases by tree mortality. Nematodes extracted from symptomatic leaves of American and European beech in North America were confirmed to be most similar to *Litylenchus crenata* Kanzaki (Tylenchomorpha: Anguinidae), a nematode associated with leaf gall symptoms on Japanese beech (*Fagus crenata*) ([Kanzaki et al. 2019](#)). However, because North American populations differ in morphology, host range, and ribosomal DNA marker from those in Japan, the North American nematodes associated with BLD have been designated subspecies *L. crenatae mccannii* ([Carta et al. 2020](#)). Inoculation of beech seedlings with freshly isolated *L. crenatae mccannii* nematodes resulted in BLD symptoms, confirming the nematode as a cause of BLD in North America ([Carta et al. 2020](#)). In the summer of 2019, BLD symptoms were found on American beech trees in Greenwich, Stamford, and New Canaan, Fairfield County, Connecticut. The disease was not observed beyond this area. Symptomatic leaf tissue contained females, males, and juveniles with morphometrics consistent with *L. crenatae mccannii* ([Carta et al. 2020](#)). Sequence of a 3.6-kb segment of the ribosomal DNA from an isolate from Bartlett Arboretum in Stamford was deposited in the GenBank database with accession number MT079193. A BLAST search returned a 100% match to similarly sized sequences encompassing partial 18S, partial 28S, and complete ITS and 5.8S sequences from North American *L. crenatae mccannii* strains 104H81 (GenBank MK292137) and 104H88 (GenBank MK292138) ([Carta et al. 2020](#)). Additionally, the BLAST search returned a 100% match to partial 28S (GenBank LC383725) and 99% matches to partial 18S (GenBank LC383723) and complete ITS and 5.8S (GenBank LC383724) sequences from *L. crenatae* ([Kanzaki et al. 2019](#)). This represents the first report of BLD in Connecticut and in New England. The American beech is an important and iconic tree of northern hardwood forests, serving as both habitat and food source for native wildlife. Given the rapid spread and mortality observed in Ohio, it is therefore important to document the occurrence and development of BLD as it spreads northward and eastward from southwestern Connecticut.