Diseases Caused by Fungi and Fungus-Like Organisms

First Report of *Erysiphe cruciferarum* Causing Powdery Mildew of *Alliaria petiolata* in Maryland

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Alliaria petiolata (Bieb.) Cavara & Grande (garlic mustard) is a biennial crucifer native to Europe and invasive in North America, where it outcompetes native plants in deciduous forests. In July 2021, powdery mildew was observed on *A. petiolata* in Frederick County, Maryland. Signs of the disease included white, tomentose mycelium producing abundant conidia. A majority of plants were affected, and severity ranged from the presence of small, discrete infections to complete colonization of leaves, stems, and ripening seed pods. Conidia from field collected leaves were transferred to disease-free *A. petiolata* for maintenance in a growth chamber at 20°C and 80% RH with a 24 h photoperiod. Fungal morphology was recorded 30 days after this transfer. Appressoria were irregularly lobed, and conidiophores were straight and composed of two to three cells. Cylindrical to oblong conidia were produced singly in pseudochains of two to six ($\bar{x}$ = 3), measured 39 to 64 × 18 to 29 ($\bar{x}$ = 52 × 24) μm, had a length to width ratio greater than two, and germinated at the ends. Fibrosin bodies were absent from conidia, and chasmothecia were not observed in the field or on inoculated plant material. Based on anamorphic characteristics, the pathogen was placed in the genus *Erysiphe* (Boesewinkel 1980). Species level identity was determined using DNA sequences. Conidia and mycelia were scraped from leaves and used for genomic DNA extraction with the Quick-DNA Fungal/Bacterial Miniprep Kit (Zymo Research, Irvine, CA). A portion of the internal transcribed spacer region of rDNA was amplified using the primers ITS5/ITS4 (White et al. 1990). Purified amplicons (PCR & DNA Cleanup Kit, New England Biolabs, Ipswich, MA) were sequenced at Eurofins Genomics (Louisville, KY). The resulting sequence was compared with those in

NCBI GenBank using the BLASTn algorithm (Altschul et al. 1990). The newly generated sequence (GenBank: OK157430) was identical (599/599 bp) to samples of *E. cruciferarum* from the United Kingdom (GenBank: KY660931.1, KY660879.1, KY660752.1). Because *E. cruciferarum* sensu lato is heterogeneous (Pastirčáková et al. 2016), additional sequence comparisons were made to the *E. cruciferarum* sensu stricto holotype (589/599 bp, GenBank: KU672364) and a vouchered *E. cruciferarum* s. lat. (596/599 bp, GenBank: LC009943). This supports identification of the pathogen as *E. cruciferarum* s. lat. and suggests the taxonomy of isolates from *A. petiolata* should be reassessed following any revision to *E. cruciferarum*. A modified Koch's postulates procedure was followed to confirm pathogenicity. Leaves colonized by *E. cruciferarum* were briefly pressed against the leaves of three disease-free plants grown from seed in a greenhouse. After 14 days, inoculated plants showed signs of powdery mildew similar to those observed in the field, and a control treatment using pathogen-free leaves resulted in no disease. This inoculation experiment was performed twice, and the identity of the pathogen was reconfirmed based on morphology. This is the first report of powdery mildew on *A. petiolata* in Maryland. *E. cruciferarum* s. lat. is widely distributed on other hosts and has been found on *A. petiolata* throughout Europe and in Ohio and Indiana (Blossey et al. 2001; Ciola and Cipollini 2011; Enright and Cipollini 2007; Farr and Rossman 2021). This pathogen has been proposed as a biological control agent (Cipollini and Enright 2009; Cipollini et al. 2020), and the presence of disease in Maryland suggests the local population of *A. petiolata* is susceptible to *E. cruciferarum* and the environment there is favorable to disease development.

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