Disease Note

Diseases Caused by Fungi and Fungus-Like Organisms

First Report of Powdery Mildew Caused by *Erysiphe corylacearum* on Hazelnut in Bulgaria

D. V. Boneva,[1] S. G. Bobev,[1,†] and K. Van Poucke[2]

[1] Agricultural University, Plovdiv, Bulgaria
[2] Institute for Agricultural, Fisheries and Food Research, Plant Sciences Unit, Merelbeke, Belgium

Funding: Funding was provided by Agriculture University Plovdiv (Ph.D. program), Instituut voor Landbouw-, Visserij- en Voedingsonderzoek, Vlaamse Overheid (Belgium), and Erasmus+. Plant Dis. 107:4023, 2023; published online as https://doi.org/10.1094/PDIS-05-23-0840-PDN. Accepted for publication 21 August 2023.

In June 2020, during an observation of fruit-bearing hazelnut trees (*Corylus avellana* L., cv. Tonda Gentile) grown in a small private home garden in the region of Kavarna (northeastern Black Sea coast of Bulgaria), symptoms of powdery mildew were observed on each of the 15 trees. Compared to the widely spread powdery mildew in Bulgaria caused by *Phyllactinia guttata* and known for its powdery patches and differing chasmothecia exclusively formed on the abaxial leaf surface, the newly observed disease was characterized by the presence of concomitant pathogen's structures on both the abaxial and adaxial surfaces of the leaves, varying from single pustules to 90% severity on certain leaves, as well as on the husks, which were 100% affected. On the white mycelium, cylindrical conidiophores and singly produced conidia (22 to 34 × 16 to 22 µm; n = 50) were found. Scattered or in groups, black spherical chasmothecia (diameter of 85 to 115 µm; n = 30), possessing 8 to 12 appendages with dichotomous branched apices, were also observed in the autumn. Chasmothecia contained 3 to 5 subglobose asci (45 to 60 × 34 to 62 µm; n = 30), and each ascus contained 8 hyaline and ellipsoid ascospores (15 to 22 × 9 to 16 µm; n = 50). From one field powdery mildew sample, DNA was extracted using the Nucleospin Plant II kit (Macherey-Nagel, Germany) and the rDNA internal transcribed spacer (ITS) region was amplified using the primers PMITS1 and PMITS2 (Cunnington et al. 2003). The amplicon was sequenced (Macrogen Europe, The Netherlands) and used in a BLAST analysis. This resulted in 100% homology with the ITS sequence of *Erysiphe corylacearum*. The obtained sequence was different from the ones of *E. pseudocorylacearum* (99.20% homology) and *E. coryli-americanae* (96.52% homology). The targeted sequence was submitted to GenBank (accession no. OQ860748). Based on the symptoms, morphological characteristics, and molecular identification, the pathogen was identified as *E. corylacearum*. Pathogenicity of the fungus was confirmed under lab conditions (natural day/light regime, 23 to 25°C) by shaking down conidia from naturally infected leaves on both sides of healthy leaves (2-year-old plantlets, cv. Tonda Gentile, three replicates) and incubating in a moist chamber (plastic bags) for the first 24 h. First, small fluffy white pustules appeared 6 to 7 days after inoculation; subsequently, the disease progressed, and the pathogen's conidiophores and conidia were morphologically identical to those first observed under natural infections in the private garden. The noninoculated control plantlets (grown under the same conditions in a separate room) remained symptomless during the entire 3-week testing period. To our knowledge, this is the first report of *E. corylacearum* on hazelnut in Bulgaria. In October 2021, the same disease was also found in a hazelnut orchard (1.2 ha) located in the region of Pazardzhik (central southern part of the country). Globally, this report indicates the disease's expansion in the Black Sea region since its first observation in Turkey in 2013 (Heluta et al. 2019; Meparishvili et al. 2019; Rosati et al. 2021; Sezer et al. 2017) and elsewhere in Europe as well (Beenken et al. 2020; Mezzalama et al. 2021; Voglmayr et al. 2020).

References:

Beenken, L., et al. 2020. New Dis. Rep. 41:11.
Cunnington, J. H., et al. 2003. Australas. Plant Pathol. 32:421.
Heluta, V. P., et al. 2019. Ukr. Bot. J. 76:252.
Meparishvili, G., et al. 2019. Plant Dis. 103:2952.
Mezzalama, M., et al. 2021. Plant Dis. 105:1565.
Rosati, M., et al. 2021. Plant Dis. 105:2728.
Sezer, A., et al. 2017. Phytoparasitica 45:577.
Voglmayr, H., et al. 2020. New Dis. Rep. 42:14.

The author(s) declare no conflict of interest.

e-Xtra

Keywords: etiology, fungi, pathogen detection, tree fruits

[†]Indicates the corresponding author.
S. G. Bobev; svetoslavbobev@abv.bg