



First report of *Erysiphe corylacearum* on *Corylus avellana* and *C. colurna* in Austria

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In September 2020, prominent powdery mildew disease symptoms were seen on leaves of *Corylus avellana* (hazelnut) and *C. colurna* (Turkish hazelnut) at several localities in eastern and southern Austria (Burgenland, Carinthia, Lower Austria, Styria, Vienna). The symptoms differed from those previously observed (caused by *Phyllactinia guttata*) by mycelia on the upper leaf surface and by smaller chasmothecia with branched appendices. The disease was observed on *Corylus* spp. growing in mixed deciduous forests, hedges as well as city gardens and parks.

Disease symptoms started as small spots of white, amphigenous surface mycelium, that radially enlarged to form effuse patches reaching up to 2 cm in diameter, eventually becoming confluent and then covering the entire leaf surface (Figs. 1-2). Infections on the lower leaf surface caused chlorotic spots on the upside (Fig. 1). Upon severe infection, leaves were distorted (Figs. 1-2). On surface mycelium, ellipsoid to doliform conidia (27-36 × 18-23 µm) were produced singly on conidiophores (Fig. 3). In addition, dark brown chasmothecia, 70-120 µm in diameter were abundantly produced (Fig. 4), which had up to 15, 60-90 µm long, stiff, hyaline appendages with repeatedly dichotomously branched tips. They contained 2-6 broadly ellipsoid, mostly (3-)7-8 spored asci of 51-70 × 38-57 µm, with hyaline ascospores 19-28 × 13-18 µm (Fig. 5). Based on these characters, the powdery mildew was identified as *Erysiphe corylacearum* (Braun & Cook, 2012).

To confirm the morphological identification, the ITS-LSU of sample WU 43287 (Lower Austria, Gießhübl, host: *Corylus avellana*) was sequenced. DNA was extracted from chasmothecia using the innuPREP DNA Micro Kit (Analytik Jena, Germany) according to the manufacturer's instructions, with a lysis time of 16 hours. The ITS-partial LSU was amplified as a single stretch with primers V9G and LR5 and sequenced according to Voglmayr *et al.* (2019). The obtained sequence was deposited in GenBank (Accession No. MW031866), and representative voucher specimens were deposited in the fungarium of the University of Vienna (WU 43287, WU 43421, WU 43423, WU 43424, WU 43514, WU 43515, WU 43520, WU 43525). A nBLAST analysis revealed 99-100% identity to sequences of *E. corylacearum*, with 100% identity to sequences from Azerbaijan (LC270863), Iran (MF668615, MH047243), Japan (MT095104), Switzerland (MN822721-MN822723) and Turkey (KY082910), confirming the species identification.

Native to East Asia and probably North America, *E. corylacearum* was first

observed in Turkey in 2013 and has since rapidly extended its distribution range to West Asia as well as Eastern and Central Europe (Beenken *et al.*, 2020; Heluta & Fokshei, 2020). *Erysiphe corylacearum* has been reported as a severe invasive alien pathogen, causing significant yield losses in hazelnut orchards in Turkey, Iran and Georgia (Arzanlou *et al.*, 2018; Meparishvili *et al.*, 2019).

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Figure 1



Figure 2

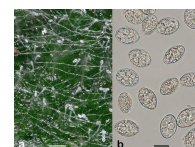


Figure 3

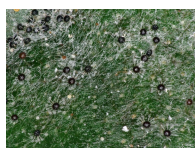


Figure 4



Figure 5

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