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1 **First report of *Erysiphe corylacearum*, agent of powdery mildew, on hazelnut (*Corylus avellana*)**
2 **in Romania**

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4 Rosati M.¹, Bogoescu M.², Spadaro D.^{1†}

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6 ¹ Dept. Agricultural, Forestry and Food Sciences (DISAFA) – University of Torino, 10095 Grugliasco
7 (TO), Italy

8 ² Academy of Agricultural and Forestry Sciences "Gheorghe Ionescu-Sisesti", 011464 Bucharest,
9 Romania

10 † Corresponding author: Davide Spadaro, davide.spadaro@unito.it

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14 Romania has an increasing area dedicated to hazelnut (*Corylus avellana* L.), covering 890 hectares
15 in 2019. During October 2020, powdery mildew symptoms were observed on the upper side of leaves
16 of hazelnut ‘Tonda di Giffoni’ in two commercial orchards in Dudeștii Vechi, Romania (Fig. 1). The
17 disease was present on 70% of the trees, with at least 5 leaves per tree showing powdery
18 mildew. Micromorphological examination revealed amphigenous, hyaline, branched, septate
19 mycelial patches of 2.3 to 3.6 μm in diameter. Conidiophores measured 24-60 \times 5-6 (average: 45 \times
20 6) μm and consisted of erect, cylindrical to flexuous foot cells, followed by 1-2 shorter cells. Ellipsoid,
21 ovoid to doliform conidia were produced singly and they measured 19-35 \times 16-24 (average: 28 \times 19)
22 μm . Chasmothecia were spherical, 75 to 107 (average: 88) μm in diameter. Nine to thirteen straight,
23 sometimes flexuous, appendages measured 54 to 92 (average: 66) μm in length and they had five
24 times dichotomous branched apices with curved tips (Fig. 2). Each chasmothecium contained three
25 to five ellipsoid, ovoid to subglobose asci measuring 41-58 \times 29-55 μm (average 52 \times 43) μm . The
26 asci contained four to eight ascospores measuring 13-24 \times 11-15 (average 18 \times 14) μm .
27 Morphological identification was confirmed by sequencing the ITS-region of rDNA using two
28 isolates from leaves, stored as frozen mycelium at -20°C. PCR was performed with Erysiphales-
29 specific primer pair PMITS1/PMITS2 (Cunnington et al. 2003). The obtained sequences were
30 deposited in GenBank (Accession n° MW423075, MW423076). Blast analysis of both sequences
31 showed 100% identity to ITS rDNA sequences of *Erysiphe corylacearum* from Azerbaijan (Abasova
32 et al. 2018; Accession n° LC270863), Turkey (Sezer et al. 2017; KY082910), Switzerland (Beenken

33 et al. 2020; MN82272), Iran (Arzanlou et al. 2018; MH047243), Italy (Mezzalama et al. 2020;
34 MW045425) and 99% identity from Georgia (Meparishvili et al. 2019; MK157199). The sequences
35 showed a low similarity (83%) to *Phyllactinia guttata* (Accession n° AB080558) (Fig. 3).
36 Pathogenicity was verified on one-year-old plants of *C. avellana* ‘Tonda di Giffoni’, which were
37 artificially inoculated with a conidial suspension from infected leaves (n = 25). Inoculated plants were
38 incubated at 20 to 28°C and 70 to 80% relative humidity. White mycelium appeared on the upper
39 surface of the leaves at 8 to 10 days after inoculation. No symptoms were found on control plants
40 sprayed with sterile water. The fungus present on inoculated leaves was morphologically identical to
41 the original isolates from field diseased plants. *E. corylacearum* is native to East Asia and was
42 previously reported in Japan on wild species of *Corylus* (Takamatsu et al. 2015; Accession n°
43 LC009928). The pathogen most likely spread into Europe from east to west of Europe (Heluta et al.
44 2019), through the Caucasus, starting from Turkey, Azerbaijan, Georgia, and Iran. *P. guttata* was
45 considered the only causal agent of powdery mildew on hazelnut in most countries, including
46 Romania (Brown 1995). Differently from *P. guttata*, which generally develops a mycelium on the
47 underside of leaves, *E. corylacearum* grows with a white mycelium on the upper side of the leaves.
48 Recently, *E. corylacearum* on *C. avellana* was reported also in Ukraine (Heluta et al. 2019), from
49 which it could have moved to Romania. Crop protection strategy on hazelnut should be revised
50 according to the new pathogen occurrence.

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65 **Supplementary material**

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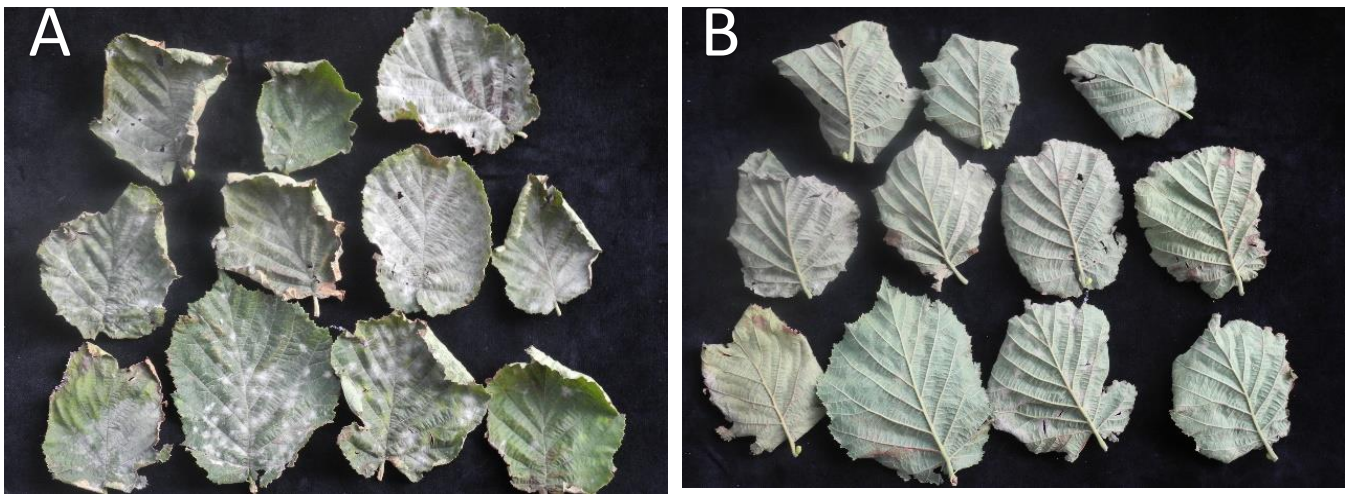


Figure 1: Symptoms of *Erysiphe corylacearum* on top (A) and bottom (B) side of leaves of *Corylus avellana*.



Figure 2: Chasmothecia with flexuous appendages.

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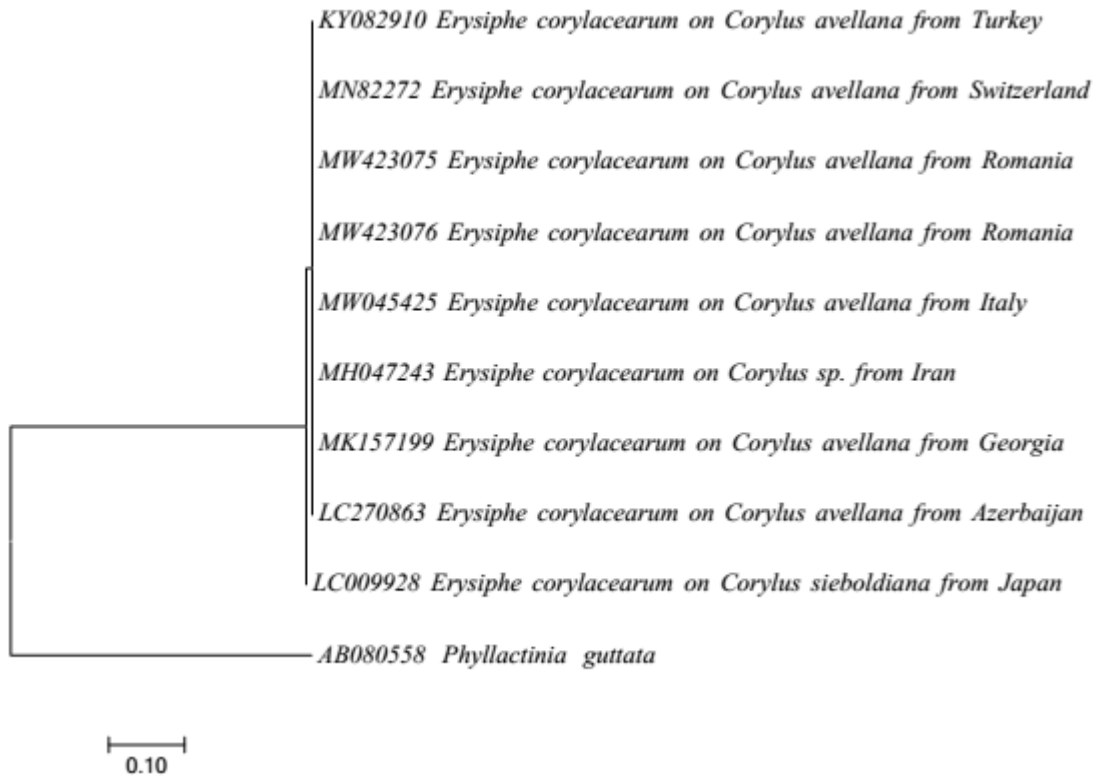


Figure 3: Phylogenetic tree based on maximum-likelihood analysis with MEGA 7 v.7.0.26 recovered from ITS sequences. Sample names include GenBank accession numbers, host plant and origin.