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Morphological, physiological and molecular characterization of *Monostichella coryli*, the causal agent of hazelnut anthracnose

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During 2019 and 2020, repeated field surveys were carried out in hazelnut orchards located in the Viterbo province, in Lazio region (Italy). Dry rot of buds, desiccation of twigs, and necrosis of leaf lamina were diffusely observed on hazelnut trees, particularly on cv. Nocchione. As result of fungal isolation from symptomatic tissues, one morphotype was persistently obtained from the margin of lesions of collected samples. The analysis of morphological features of the fungus grown on malt extract agar (MEA), potato dextrose agar (PDA), corn meal agar (CMA) and oatmeal agar (OA), provided for the attribution to the species *Monostichella coryli*. This initial identification was molecularly confirmed by sequencing the partial large subunit rDNA, the internal transcribed spacer region and partial beta-tubulin region and blasting the sequences in the NCBI database. Pathogenicity tests proved that the fungus is able to multiply and systematically invade artificially inoculated hazelnut tissues and incite disease symptoms on both Nocchione and Tonda Gentile Romana cultivars. *In vitro* assays demonstrated that environmental conditions, such as temperature and relative humidity influence growth rate, sporulation and conidial germination and allowed the definition of mathematical functions describing optimal, suboptimal and critical condition for these biological facets. Findings in this study provide useful information for epidemiology studies on hazelnut anthracnose and will help to choose the appropriate control strategies for the management of the disease.

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