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Genetic diversity and pathogenicity of *Diaporthe* spp. causing hazelnut defects of hazelnut nuts from Italy

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Abstract

The main hazelnut producing countries are Turkey, Italy, and the USA. In Italy, hazelnut is cultivated on over 80,000 ha, with a production of about 110,000 t. Hazelnut supply chain is increasingly affected by the phenomenon of rotten hazelnut, which includes a series of internal hazelnut defects such as browning and rot, which can be visible after cutting. In order to investigate and better understand the etiology of the hazelnut defects and the identification of the causal agents, surveys were conducted in 2020 in Piedmont, Northern Italy, historically area dedicated to hazelnut cultivation. A total of 383 fungal strains were isolated, from mouldy, necrotic or black rotted hazelnuts and 38.9% of the isolates were identified as *Diaporthe* spp. In particular, the incidence of *Diaporthe* spp. was much higher on mouldy hazelnuts (68.5%) than from hazelnuts showing black rots (14.8%) or necrotic spots (16.8%). A multi-locus phylogeny was established based on two genomic regions, ITS (ITS1/ITS4) and *tef-1α* (EF1-728F/EF1-986R) on 40 isolates of *Diaporthe* spp. Pathogenicity tests were performed on immature hazelnuts with the 40 isolates. Three nuts per isolate, and per three replicates, were surface disinfected with 1% NaClO. Nuts were wounded with a cork borer (5 mm diameter) and inoculated with mycelium plug cut from 7 days old PDA colony. Five species of *Diaporthe* were identified. Among the species identified, *D. eres* was the dominant one (75% of the isolates). Pathogenicity tests showed that the five species were pathogenic on hazelnut nuts, but *D. eres* was the most aggressive species. The present study improves our understanding of the epidemiology as well as the species associated with hazelnut defects and provides useful information for effective management of the disease.

Keywords: Hazelnut, phylogenesis, nut rot, *Diaporthe eres*, *Corylus avellane*