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NEW DISEASE REPORT

First identification of a '*Candidatus* Phytoplasma fragariae'-related strain infecting *Corylus avellana* in southern Switzerland

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Phytoplasmas are associated with serious diseases in a wide range of plants. Several studies have shown that woody species can be infected by a variety of phytoplasmas, including strains associated with economically significant diseases. Infected woody species are often difficult to detect due to their asymptomatic status or the expression of non-specific symptoms (Marcone *et al.*, 2023). Nevertheless, they can serve as inoculum for further spread of the disease to susceptible plants. *Corylus avellana* is of particular concern as it is widely spread in forests and shrublands and known to host phytoplasma strains associated with flavescence dorée (Casati *et al.*, 2017; Kogej Zwitter *et al.*, 2023). In Italy and Germany, hazelnut tree decline has been associated with infection by phytoplasmas from the group 16SrX whereas phytoplasmas from groups 16SrIII and 16SrI were found in diseased trees in USA and Poland, respectively (Mehle *et al.*, 2019).

In southern Switzerland, a survey of potential woody species acting as reservoirs of disease-inducing phytoplasmas was performed. Thirty-seven root samples of *C. avellana* were collected at random in March 2022 in the Canton of Ticino (southern Switzerland) from five different locations and the DNA extracted as previously described (Oggier *et al.*, 2023). Two hazel trees were found to be positive to phytoplasmas based on a generic detection using a quantitative PCR method adapted from Hodgetts *et al.* (2009). Subsequent nested PCR amplifications of 16S rRNA and *tuf* genes were performed according to the EPPO standards (PM 7/133 and PM 7/129, respectively). The sequences from the samples were identical although the samples were collected from two locations about 50 km from each other. Analysis of the partial 16S rRNA fragment revealed 99.84% shared identity with the '*Candidatus* Phytoplasma fragariae' ('*Ca.* P. fragariae') reference strain (GenBank Accession No. DQ086423), a member of 16SrXII-E subgroup. Phylogenetic analysis of both partial 16S rRNA and *tuf* genes confirmed that the phytoplasma is related to '*Ca.* P. fragariae' (Fig. 1). These sequence data have been submitted to the GenBank database under accession numbers OR594267 (16S rRNA) and OR594268 (*tuf*), respectively. To our knowledge, this is the first evidence of a group 16SrXII phytoplasma infecting *C. avellana* in Switzerland. One of the two infected trees of this study later showed rapid decline and died in summer 2022.

Additional studies are required to assess if '*Ca.* P. fragariae' represents a threat to forest trees and hazelnut orchards and to identify potential insect vectors. Nevertheless, given its recent detection in Slovenian hazelnut orchards associated with severe symptoms and high mortality of infected trees (Mehle *et al.*, 2019), '*Ca.* P. fragariae' may become an economic problem for hazelnut production in Switzerland and elsewhere in Europe.

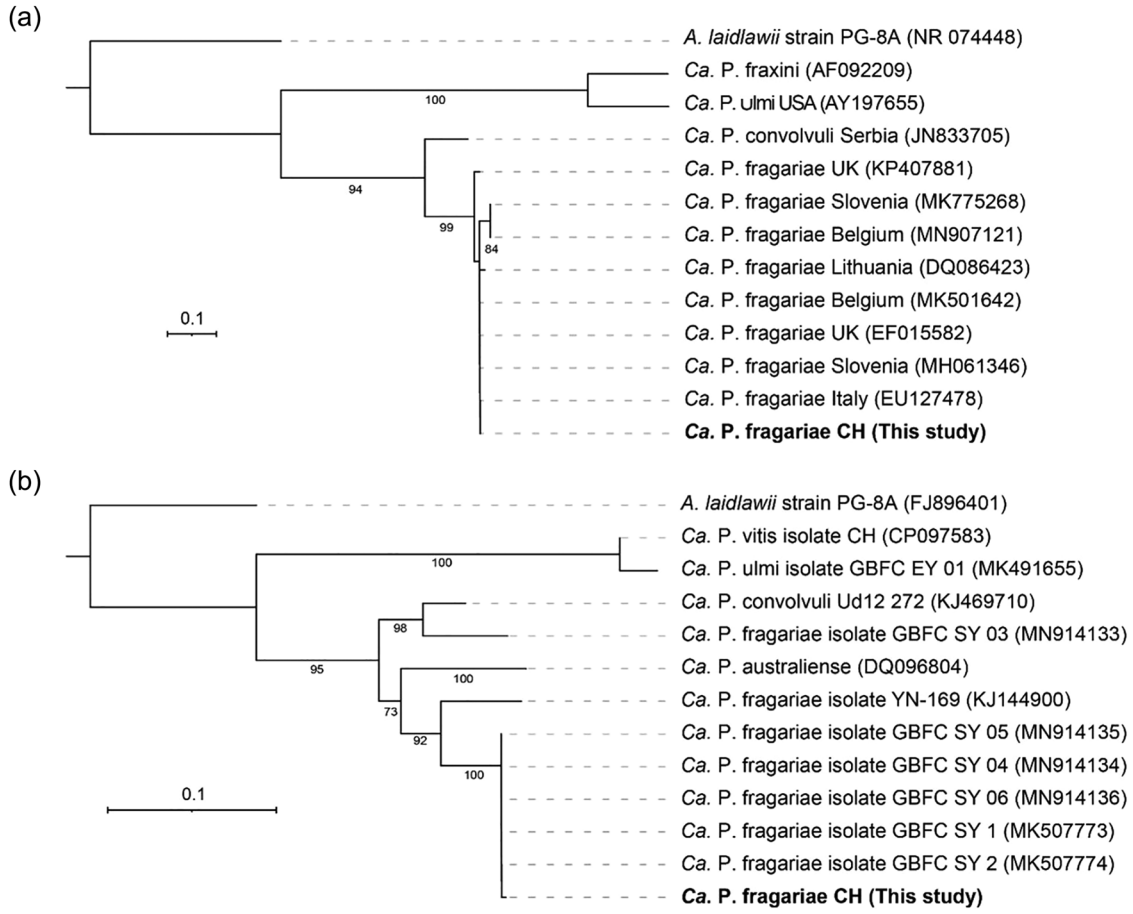

FIGURE 1 Phylogenetic analysis based on (a) 16S rRNA gene sequence (1165bp) and (b) *tuf* gene sequence (282bp) of *Corylus avellana* phytoplasma strain (in bold) with diverse phytoplasma strains. Phylogenetic trees were generated using MEGA software version 11.0.13 using the maximum likelihood method in a bootstrap test (500 replicates). Support values above 70% are labeled. The scale bar shows the number of substitutions per site. *Acholeplasma laidlawii* was used as the outgroup.

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