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Morphological and molecular comparison of white truffle ectomycorrhizae
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In the present study, white truffle ectomycorrhizae (EM) collected in deciduous forests (*Populus*, *Quercus*, and *Fagus*) from Hungary were characterized by morphological-anatomical and molecular methods. Our investigations suggest that the EM of white truffles (e.g., *Tuber rapaedorum*, *Tuber puberulum*, *Tuber rufum*) are common and abundant members of the forest communities in the area. The ITS sequences of 14 EM specimens and 46 additional fruitbody sequences from the GenBank were clustered into four main groups in phylogenetic analyses. In the ITS-1 region, a characteristic indel pattern was found, which supports the clades. Although our analyses indicate definite genetic distance between the groups of the phylogenetic tree, these clades do not correspond to the traditional taxons identified by fruitbody characteristics. Comparison of the ectomycorrhizae shows that neither is mycorrhizal anatomy a good tool to separate the groups, because the characters (like the epidermoid or angular mantle structure, cell wall thickness, the shape and size of cystidia) are too variable and overlap between the clades. The interspecific similarity, observed both in ectomycorrhizal and fruitbody characters, strengthen the sensu lato morpho-species concept of this group. Our study, which combines comprehensive molecular and anatomical approach to characterize and identify ectomycorrhizae of white truffles from natural samples, stress out the need of the taxonomical revision of this group.

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Tuber, White truffle, Ectomycorrhiza, ITS, Phylogenetic analysis, Morphology

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