

MORPHOLOGICAL AND MOLECULAR CHARACTERIZATION OF SOME MYCORRHIZAE ASSOCIATED WITH *TUBER MAGNATUM* PICO

BENUCCI G.M.N., RAGGI L., PINNA V., GORETTI D., FALCINELLI M., BENCIVENGA M., ALBERTINI E., DI MASSIMO G.

Departimento di Biologia Applicata, Università di Perugia, Borgo XX Giugno 74, 06121 Perugia

Tuber magnatum, ITS, mycorrhizal, Thelephoraceae, Pyronemataceae

Truffles are the edible fruiting bodies of a group of species of the *Tuber* genus belonging to the ipogeous *Ascomycetes* class. These truffles are all ectomycorrhizal and live in close association with tree roots. *Tuber magnatum* Pico, or White Truffle, is the most uncommon and expensive species within the genus *Tuber*; it grows in several Italian regions as well as it has also been found in Croatia, on the Istria peninsula. It usually grows in typical forestall habitats with peculiar ecological and pedological soil characteristics. The natural abundance of the wild form of this fungus is decreasing very fast and the cultivated truffle orchards are still unproductive. Indeed, truffle cultivation for this species must be considered in the experimental phase.

To better understand the complex relationship and interaction between *T. magnatum* and other fungi as well as forest ecosystems, the investigation of the fungal mycorrhizal community is fundamental. Therefore the main aim of this study was to investigate the ectomycorrhizal variability associated with host plants in typical *T. magnatum* production areas in central Italy by using both the morphological approach, traditionally used in mycorrhiza symbiosis studies and the molecular one.

Root samples from 19 *T. magnatum* harvesting sites and 9 from non productive sites were collected and morphologically characterized. Five frequent ectomycorrhizal forms in harvesting sites were described in detail based on standard morphological and anatomical characters. A molecular approach was then carried out with the aim of associating each mycorrhizal form to its relative taxa. Internal transcribed spacer (ITS) of the 25S rDNA was PCR-amplified and sequenced. Similarities with known sequences were searched in the National Center for Biotechnology Information (NCBI) database using BLASTN application. The nucleotide sequences were also used for multiple sequence alignment. Four of the five micorrhizal type showed to belong to the *Thelephoraceae* family while the fifth one belongs to the *Pyronemataceae* family.