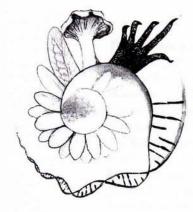
Javols Aural





CENTRO LINCEO INTERDISCIPLINARE



## Molecular Biodiversity and DNA Barcode

Accademia Nazionale dei Lincei Rome, 17-19 May, 2007

Final programme - Abstracts book

## DNA barcoding in truffles: from taxonomy to an oligonucleotide barcode

Claude Murat\* [1], Elisa Zampieri [1], Khalid El Karkouri [2], Yongjin Wang [4], Sylvain Jeandroz [4], François Le Tacon [4], Paola Bonfante [1]

[11] Dipartimento di Biologia Vegetale dell'Università di Torino and Istituto per la Protezione delle Piante del CNR, Sezione di Torino ~ Turin, Italy - [21] Unité des Rickettsies, CNRS UMR 6020, IFR-48, Faculté de Médecine, Université de la Méditerranée ~ Marseille, France - [4] INRA and Université Henri Poincaré-Nancy 1, Unité mixte de recherches 1136, Interactions arbres micro-organismes ~ Nancy, France

Truffles are fungi which accomplish their life cycle living in symbiosis with the roots of some plants. Some truffles have a remarkable commercial value, like Tuber melanosporum from Perigord and T. magnatum from Alba: due to its taste and fragrance, T. magnatum is one of the most expensive delicacies of the market (300-400 /100g -winter 2006). The name "truffle" is a broad term that comprises species of the genus Tuber belonging to the Ascomycota, order Pezizales and family Tuberaceae. The Index Fungorum recognizes 227 species, subspecies and varieties of truffles, however the Tuber classification based on the morphological features of ascomata and spores has led to many controversy. Currently, only 70-75 species have been validated in the world, 32 out of them in Europe. In the frame of a long-standing project, we investigated the phylogeny of the truffle species with a particular interest on Chinese species and set up an oligonucleotide DNA barcoding for their identification.

In the first part of the project we investigated the phylogeny of Tuber sp by sequencing several genes such as internal transcribed spacer (ITS) of the rDNA repeat, beta-tubulin, elongation factor 1 alfa, protein kinase C. Our analysis of a total of 32 species coming from Europe, Asia and North-America allowed us to identify 8 groups of species. Using the molecular clock theory we estimated the common ancestor for truffle around 250-300 Mya.

In a second step, we identified several species-specific oligonucleotides (or motifs), located within the ITS. The barcodes has been developed for five Tuber spp. (T. magnatum, T. melanosporum, T. aestivum, T. indicum and T. mesentericum) on the bases of 526 ITS sequences available in GeneBank and allowed a reliable in silico identification of these Tuber spp. The last step of the project involves the development of a phyloarray, which is currently under construction. Thanks to this array, where species-specific motifs are spotted, multiple Tuber species will be detected at the same time. This new identification tool will allow to identify truffles in complex matrix such as mycorrhizal roots and soil.