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ABSTRACT BOOK

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555A A quest for microbial indicators of the Tuber melanosporum production using an environmental genomics approach

Alessandra Pontiroli*[1], Hervé Sanguin[1], Marc Ducousso[1], Antoine Galiana[1], Christine Leroux[1], Odile Domergue[2], Daniel Mousain[3], Robin Duponnois[4], Yves Prin[1], Ezékiel Baudoin[4]
[1]LSTM-CIRAD, France, [2]LSTM-INRA, France, [3]Société d'Horticulture et d'Histoire Naturelle de l'Hérault/INRA, France, [4]LSTM-IRD, France

The «brûlé» - the area where the truffles tend to grow to a mature stage- is commonly characterized by a drastic drop in the plant diversity and biomass around those trees, which have been mycorrhized by Tuber melanosporum. Despite its presence, which indicates the development as well as the activity of the mycelium network of this symbiont, the «brûlé» is not systematically associated with the production of ascocarps. To date, understanding how truffle producing ecosystems function has been a puzzling task for researchers, particularly when attempting to explain what elements are involved in the spatio-temporal dynamics of the colonization process, in the intensity of the «brûlés» and in what influences the yield. In the frame of the ANR SYSTRUF project (2010-2014), and within a partnership with the professional bodies (FFT, CETEF) and some volunteer truffle growers, we have aimed to identify which bacterial and mycorrhizal (Glomeromycetes) markers are intrinsically associated with the productive status of the «brûlés», in relation to the non-producing «brûlés» and to the «brûlés» -deprived oaks. Two "natural"-spontaneous and slightly managed-truffle orchards (truffières) and two "planted" ones were sampled during November 2010 in the Languedoc-Roussillon region (at the ascocarp maturation stage). These truffières are composed of the evergreen holm oak (Quercus ilex) and are managed without mechanical soil laboring; in addition, they possess a spontaneous plant cover, which is kept to a minimal extent by the owners. Soil and root samples from plant species persisting on the «brûlé» have been collected around the oak trees (classified as: with a producing «brûlé», with a non-producing «brûlé», and «brûlé»-deprived ones) in order to (1) determine by pyrosequencing the genetic diversity of the total soil bacterial community (16S rDNA gene) and of the arbuscular mycorrhizae (18S rDNA gene) associated to the oak companion plants, and to (2) potentially identify specific taxa linked to the producing status of the «brûlé», at the level of a single truffière or along the four sampling sites. Eventually, the approach of relating sequence data with the producing status and the floral diversity of the studied ecosystems opens up new avenues for the study of the interaction networks established between Tuber melanosporum and certain components of the microbial and floral compartments, characterizing the truffières managed with low anthropic input.

556A Description of a new AMF strain from Ecuador, a potential epitype for Rhizophagus invermaius (Glomus invermaium)

Valentine Potten*[1], Carolina Senés Guerrero[2], Gloria Torres Cortés[2], Arthur Schüßler[2], Christopher Walker[3], Stephan Declerck[1], Sylvie Cranenbrouck[1]
[1]Université Catholique de Louvain-la-Neuve, Belgium, [2]Ludwig Maximilian University of Munich, Germany, [3]n/a, United Kingdom

Arbuscular mycorrhizal fungi (AMF) form symbiotic associations with plants. As far as is known, the symbiosis is obligate for the fungus and facilitates mineral nutrition, water uptake and improves resistance for the plant. These are the reasons why the AMF generate great interest in the research community. Until recently, the classification was mainly based on morphology. The development of various kinds of molecular analysis brought additional tools for species classification.

In this study, a new AMF strain (designated as Ecu 10.2), was isolated, cultivated and described with a combination of the traditional (morphological) and molecular methods.

Soil was collected in a potato field in Ecuador (province of Carchi, at 2837 m.a.s.l.) and used to initiate open trap cultures with Allium porrum in the greenhouse. Roots fragments were disinfected and used to initiate root organ cultures (ROC) with carrot and chicory. Spores and root fragments produced by these ROC cultures were used as inoculum to initiate half open arbuscular mycorrhizal cultures (HAMP) with potato plants and new pot cultures, in Sunbag with Plantago lanceolata. Spores, clusters of spores and roots were sampled from all cultures (pot, ROC and HAMP) for morphological observations and DNA extraction. PCR was performed on extracted DNA with primers covering the SSU-ITS-LSU (partial small subunit, internal transcribed spacer, and partial large subunit) rRNA gene region. Products were cloned and clones screened with the RFLP technique. Sequences were 1500-