

Connecting above- and below-ground genetic diversity in ectomycorrhizal fungi

M. Garnier^{1*}, A. Champion¹, M. Heuertz¹, R. Gargiulo²

¹BIOGECO, National Research Institute for Agriculture, Food and the Environment (INRAE), University of Bordeaux, 69 Route d'Arcachon, 33612 Cestas Cedex, France, *martin.garnier@inrae.fr

²Royal Botanic Gardens, Kew, Richmond, TW9 3AB, UK

Keywords : ectomycorrhizal fungi, conservation genetics, SSRseq

Ectomycorrhizal fungi (EMF) form an ecologically important functional group due to their symbiosis with most European tree species. Their role in the nutrient and carbon cycles is essential for preserving forest health in the context of global environmental change. Nevertheless, little is known about the conservation genetics of EMF. This knowledge gap is mainly due to their dominant underground lifestyle and their complex life cycle, with both sexual and asexual reproduction, making it difficult to distinguish among individuals and populations. Population genetic studies of EMF mainly rely on genotyping easily sampled sporocarps, thus ignoring underground genetic diversity in mycelia. To comprehensively assess genetic diversity in an EMF population, it is necessary to sample both above- and below-ground compartments (i.e., sporocarps and mycelium or root tips).

In our project, we use sporocarps of two common European basidiomycete species (*Suillus bovinus* and *Amanita citrina*) harvested in France to develop new genetic markers with the sequence-based microsatellite genotyping (SSRseq) method. By targeting both repeated and flanking region sequences, this type of marker enhances polymorphism detection, primarily by reducing size homoplasy, and can be applied to environmental DNA, such as soil samples.

These new markers will be used in soil and root tip samples, collected from the same sites as sporocarps. We will assess (1) whether the SSRseq method allows re-detection of sporocarp genotypes in soil and root tip samples, (2) the correlation between genetic diversity metrics computed from above-ground samples and those from soil or root tips, and (3) the link between demographic parameters derived from sporocarps (e.g. the number of sporocarps) and genetic metrics. We are also interested in ascertaining which below-ground compartment, soil or root tips, contains the highest intraspecific genetic diversity.

Answering these questions will be crucial for developing appropriate tools for EMF conservation genetic assessments and for better understanding the link between sporocarps, soil, and root dynamics.