



Treasures of the forest : Towards understanding life history of *Tuber aestivum*

Virginie Molinier, Daniel D. Wipf, Claude Murat-Furminieux, R. Splivallo, S. Egli, M. Peter

► To cite this version:

Virginie Molinier, Daniel D. Wipf, Claude Murat-Furminieux, R. Splivallo, S. Egli, et al.. Treasures of the forest : Towards understanding life history of *Tuber aestivum*. 8. International Conference on Mycorrhiza (ICOM8), Aug 2015, Flagstaff, United States. , 216 p., 2015. hal-02740088

HAL Id: hal-02740088

<https://hal.inrae.fr/hal-02740088>

Submitted on 2 Jun 2020

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

MOLINIER, V.^{1,2}, D. Wipf², C. Murat^{3,4}, R. Splivallo^{5,6}, S. Egli¹ and M. Peter¹

¹Swiss Federal Institute for Forest Snow and Landscape Research (WSL), 8903 Birmensdorf, Switzerland, virginie.molinier@wsl.ch; ²Université de Bourgogne, UMR Agroecologie INRA /Agrosup/u. Bourgogne, Pole Interactions Plantes Microorganismes ERL 6300CNRS, BP 86510, 21065 Dijon Cedex, France; ³Université de Lorraine, UMR1136 Interactions Arbres-Microorganismes, F-54500 Vandoeuvre-les-Nancy, France; ⁴INRA, UMR1136 Interactions Arbres-Microorganismes, F-54280 Champenoux, France; ⁵Goethe University Frankfurt, Institute for Molecular Biosciences, 60438 Frankfurt am Main, Germany; ⁶Integrative Fungal Research Cluster (IPF), Georg-Voigt-Str. 14-16, 60325 Frankfurt am Main, Germany.

Abstract: *Tuber aestivum* (Vittad.) is an ectomycorrhizal fungus found throughout Europe. Whether natural populations consist of different genetic ecotypes and how the fungus completes its life cycle is still largely unknown. Genome sequencing and development of microsatellites markers allowed us to obtain a deep insight into its genetic structure. Here we present data from several hundreds of fruitbodies collected all over Europe as well as within single forest stands. At the European scale, our purpose was to identify possible genetic clusters. At smaller scales, our aims were to study temporal and spatial dynamics of genets, to assess the distribution of mating type strains of this heterothallic ascomycete and to understand how genetic structuring along with fruitbody maturation and geographical origin influence truffle aromas. In Europe, we could identify four genetic clusters suggesting the existence of different ecotypes of *T. aestivum*. With the exception of one cluster, which was exclusively present in South-Eastern France, Italy, and Spain, the other clusters did not show a clear geographical separation. A significant deficit of heterozygosity indicated population expansion in Europe. At smaller scales, genetic diversity was high and an important yearly turnover was found. The genet sizes were generally small but some could reach up to 150 m. Genetic differentiation could be detected between and within forest sites indicating the existence of ecotypes among which gene flow might be limited by biological or ecological barriers. Unlike to what has been observed for *T. melanosporum*, the mating type distribution was not clearly clustered. Finally, geographical origin or maturity only had minor effects on aroma profiles but genetic structuring had a pronounced influence on the concentrations of some odorants. Results presented give a pioneering vision about the genetic structure of *T. aestivum* which allows for a better understanding of the biology and life history of this natural forest resource.

Tuesday Banquet Lecture **International Culture Collection of Arbuscular Mycorrhizal Fungi (INVAM): A 25 year perspective**

MORTON, J.B.¹

¹West Virginia University, 1090 Agricultural Sciences Building, Morgantown, WV 26506-6108, USA, jbmorton@mail.wvu.edu.

Abstract: Considerable knowledge has been gained from the management of an International Culture Collection of Arbuscular Mycorrhizal Fungi (INVAM) for 25 years. Notable advances have been made through reliable maintenance of diverse fungal stocks and a wide range of collaborations. Sustainability of cultures has been achieved by making use of low host and ecological specificity and standardizing host plant (sudangrass) and a low nutrient sand soil mix, all grown for <5 months and then stored. Under these conditions, <8% of stocks have been lost and more than 70% have been productive for longer than 10-15 years. Inoculum potential assays have provided an indispensable tool to test quality of inoculants and other products, to screen stocks for soil or host compatibility, and to establish equivalent between stocks with disparate life history traits. Morphological studies have provided criteria for maintaining purity and quality of ca. 1,100 strains of 112 species representing all but two genera. Support from LSU and TUB2 sequences, as well as expressed protein profiles, is helping to clarify relationships at all scales. Intraspecific variation is especially important; 22 species are represented by >10 strains, six of which have >50 widely distributed strains. These stocks are clarifying species grouping and ranking criteria, biogeographic distribution, ranges of adaptation, and patterns of transmission by endosymbionts. Species are broadly classified as “r” versus “k” based on rate of mycorrhizal development and proportionality between colonization and sporulation to assist in germplasm choices. As a public resource, the number of annual users and stock usage has averaged 62 and 340, respectively. Future plans include transitioning to a new curator in 2017, investing in metagenomic analyses, expanding web-based approaches for education and training, and improving networking with other major collections to establish standard best practices.