



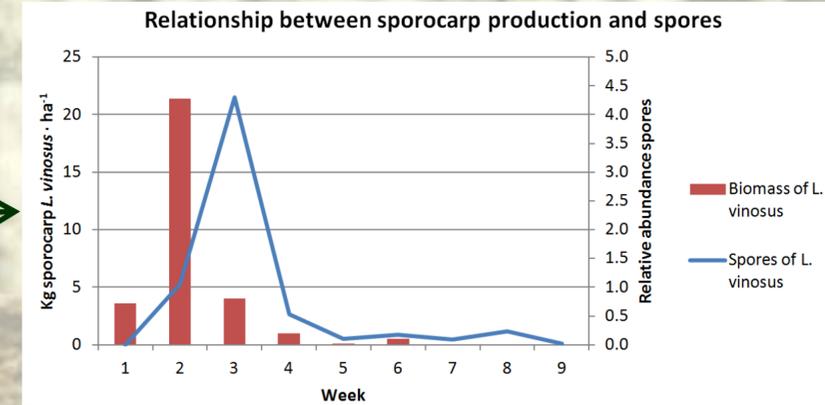
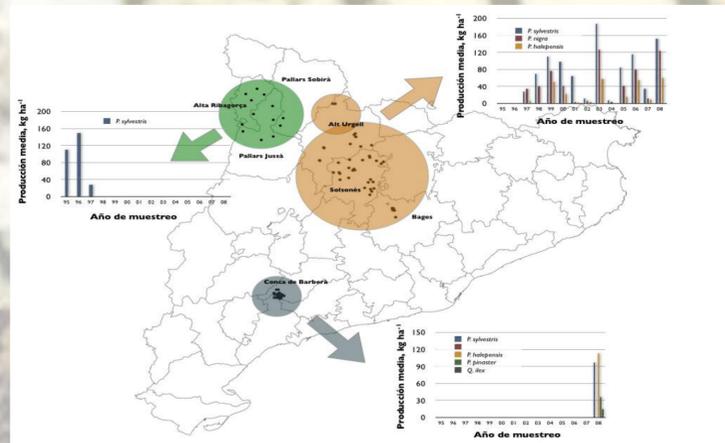
INTRODUCTION

➤ Non-wood forest products (NWFPs) are gaining importance and very often represent a higher income than the timber itself in many forest ecosystems. An important step in managing a resource is the knowledge of its production in quantifiable terms. However, some NWFPs such as mushrooms are difficult to quantify and predict. One approach to estimate the potential mushroom production would be through monitoring of productions during different years (Martínez de Aragón et al., 2007). Unfortunately, the mushroom samplings are generally time consuming and need important resources in human and economical terms.

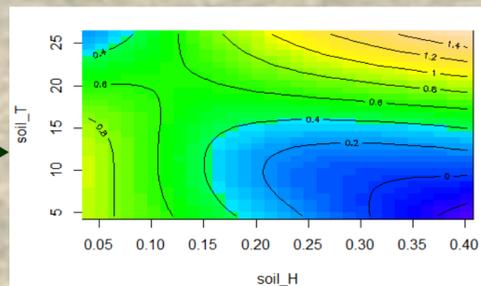
PHYLOSOPHY, OBJECTIVES and MAIN RESULTS

➤ The aim of the STSM was to use molecular and bioinformatic tools to study the fungal communities. A **Multidisciplinary (From Forestry to Microbiology)** approach based on a **Multi-scale (From Macro to Micro)** view of this complex system would allow the understanding of each **Multi-level (From the Spores to the Fungal Mycelia)** component and their interactions. At long term, we aim in studying the red arrow interactions (**A, B, C**)

1.- Aboveground productions: A dataset of mushroom productions is available in Catalonia for the last 8-20 years, based on more than 100 plots, covering the most abundant forest ecosystems in the region (Fig 1a, 1b, 1c), in which mushrooms are collected during autumn season every week



3.- Data from soil mycelia: More than 2000 soil samples have been collected from the permanent plots, to study both the fungal community and the biomass of specific ectomycorrhizal species. We have identified more than 500 fungal species



STSM TOPIC: Bioinformatic tools to study soil fungal communities

- 1. Species-specific analysis:** DNA from soils and spore trap samples were extracted and quantified using Real-Time PCR. A specie-specific TaqMan probe was designed to quantify *Lactarius vinosus*
- 2. Community analysis:** A total of 500 soil samples and more than 100 spore trap samples were sequenced using PacBio RS X platform (1 million sequences) and illumina MiSeq (15 millions sequences)
- 3. Bioinformatic analysis:** We used the SCATA pipeline for quality control, filtering and clustering the DNA sequences
- 4.- Species identification:** Species were identified using UNITE. We confirm the taxonomical identity by building phylogenetic trees

4.- Data from mycorrhizas: Mycorrhizas has been also taken in the study plots. Mycorrhizas are being identified and characterized



CONCLUSIONS

- Spore traps coupled with qPCR may be used to quantify productions of specific taxa
- Next generation sequencing provided a full range of fungal species living in soil
- Fungal community in the studied soils is dominated by ectomycorrhizal species

Bibliography

Martínez de Aragón, J., J. A. Bonet, C. R. Fischer, and C. Colinas. 2007. Productivity of ectomycorrhizal and selected edible saprotrophic fungi in pine forests of the pre-Pyrenees mountains, Spain: Predictive equations for forest management of mycological resources. *Forest Ecology and Management* 252: 239–256.

Acknowledgments

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AND



NEXT STEPS

- The relationship sporocarp-soil mycelia-spores at community level
- Spatial patterns of spore dispersal and fungal mycelia
- Improvement of detection tools (Soil samples, Spore trap type...)