

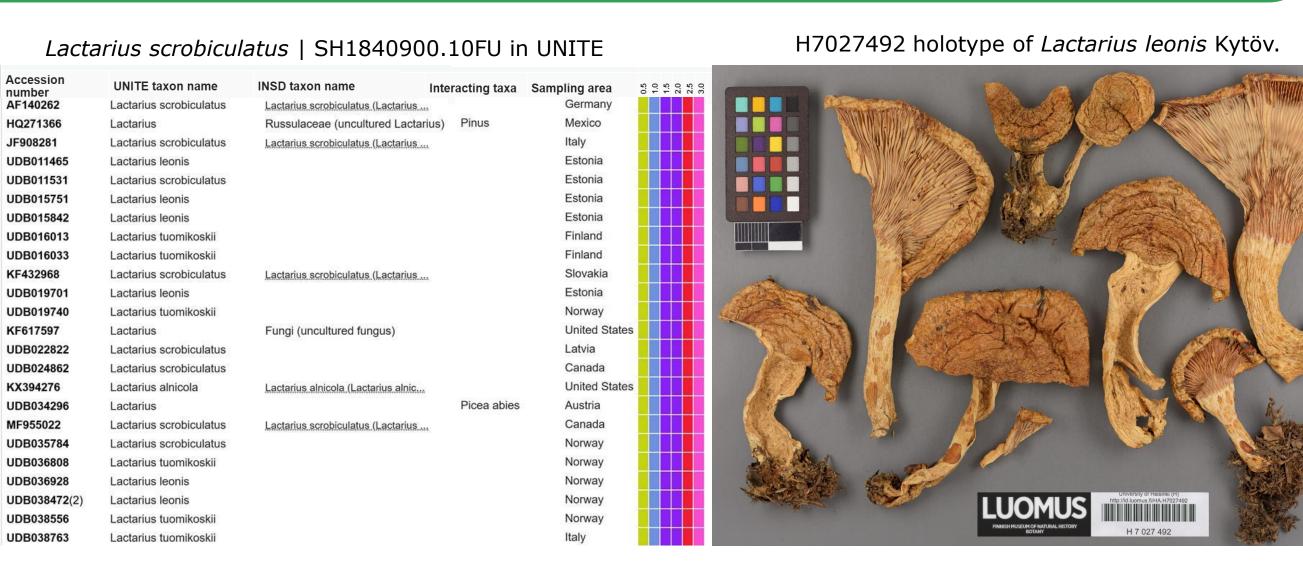
Monitoring and mapping fungal diversity for nature conservation

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Fungi are increasingly appreciated as networkers, recyclers and symbionts in natural ecosystems, and as crucial active agents for sustainable society transformation and innovation. New technologies including machine-learning tools and molecular methods allow steps towards automated identification of fungi, exploration of environmental fungal DNA from various substrates, and deeper insights into fungal biodiversity patterns and ecosystem functioning. Citizen science has emerged as a highly engaging approach to data collection involving a rich community of mycologists from a wide range of professional backgrounds with and without institutional backup. Fungi have also entered the global conservation agenda, with 625 species assessed for the IUCN Red List. Despite obvious synergetic potentials, these methodological approaches have largely been developed in parallel tracks. They often rely on different species concepts, mostly either morphology or DNA-based. In many cases, neither of these are unambiguously linked to biologically well-defined species with a scientific binomial, hindering comparisons of species lists across datasets. The goal of the pan-European project 'FunDive' is to bridge this gap and provide a knowledge platform allowing the inclusion of fungi in biodiversity conservation and monitoring in an integrative manner. The project aims to: (1) align scientific binomials of fungi with molecular species hypotheses by sequencing of type specimens preserved in European fungaria, (2) apply and improve AI tools for fungal monitoring, (3) involve citizen scientists in biodiversity discovery and monitoring, (4) sample fungal communities by eDNA, and (5) analyze fungal biodiversity patterns in time and space.









AI tools for fungal monitoring

- Develop AI-based identification tools
- Re-train AI-models

unite

community

GBIF

Global Biodiversity

Information Facility

- Add metadata on fungal records
- Species recognition in open-species-set scenario

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Empower and involve citizen scientists

- campaigns
- Molecular field laboratories
- Explore motivation factors of citizen scientists
- (Haelewaters et al.) for more information

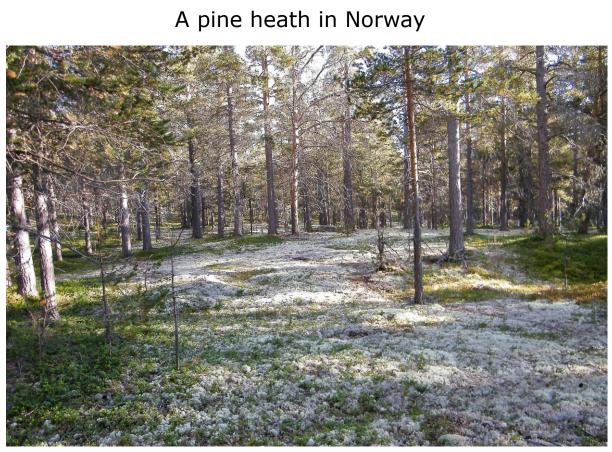
Citizen science sampling

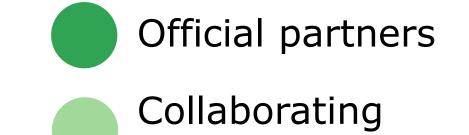
- Epitypification mission
- See also poster #990

Fine-tune environmental **DNA-based sampling**

- Capture fungal diversity in pine forests
- Sample different substrate types
- Compare short- and long-read sequencing pipelines
- Fungal alpha diversity, uniquity, and phylogenetic diversity across European pine forests







partners

Mycological societies involved



DNA barcoding and annotation

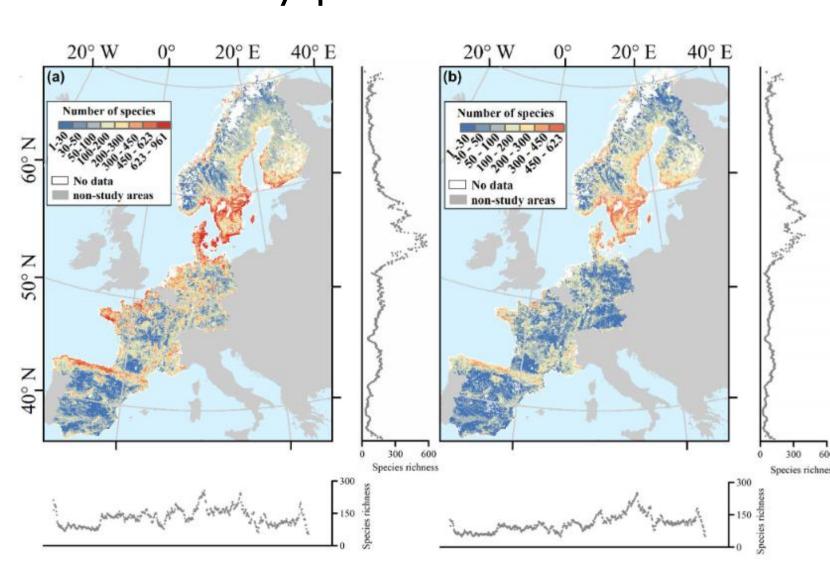
- Sequence type specimens
- Develop molecular protocols
- Select species for epitypification
- Improve linking scientific names to UNITE Species Hypotheses based on DNA barcodes

The fungarium in Leiden, the Netherlands



Investigate biodiversity patterns

- Handle sampling bias in citizen science
- Compare eDNA and citizen science sporocarp data
- Evaluate existing conservation measures for threatened macrofungi
- Analyze environmental factors to explain temporal and spatial biodiversity patterns



The distribution of the predicted number of species of two different functional groups of macrofungi, (a) saprotrophic fungi and (b) ectomycorrhizal fungi. From Yu H, Wang T, Skidmore A, Heurich M, Bässler C (2021) The critical role of tree species and human disturbance in determining the macrofungal diversity in Europe. Global Ecol. Biogeogr. 30: 2084-2100.







