



11-15 August 2024

PROCEEDINGS



International
Mycological
Association



of *Sphagnum*'s microbiome remains less characterized. Here, we examined fungal communities in *Sphagnum* and two co-occurring moss genera (*Pleurozium*, *Aulacomnium*) from four Alaskan sites. We characterized fungal communities from living and senescing tissues with Illumina ITS1 nrDNA amplicon sequencing, and examined connections between fungi and moss metabolites using liquid chromatography-tandem mass spectrometry on the same tissues. In total, we detected 399 metabolites and 1,768 fungal OTUs from 53 samples. Although all moss genera harbored similar fungal and metabolite classes, both metabolite and fungal species richness and composition differed among sites, moss genera, and tissue type. In both *Sphagnum* and *Pleurozium*, total fungal richness decreased with tissue age, while total metabolite richness increased. In senescing *Sphagnum*, total metabolite richness was negatively correlated with total fungal richness as well as richness of Ascomycota, suggesting that other factors impact fungal richness. Our on-going analyses will identify metabolites that are negatively correlated with the abundance of fungal OTU, potentially inhibiting fungal growth and thereby decreasing decomposition.

SHIFT 02-049 / #1744

FUNDIVE: MONITORING AND MAPPING FUNGAL DIVERSITY FOR NATURE CONSERVATION

POSTER ON BOARDS - SHIFT 02: ENVIRONMENT, ECOLOGY AND INTERACTIONS

Jorinde Nuytinck¹, Jean-Michel Bellanger², Balint Dima³, Ursula Eberhardt⁴, Vasco Fachada^{5,6}, Danny Haelewaters⁷, María Martín⁸, Viktor Papp⁹, Julia Pawlowska¹⁰, Lukas Pícek¹¹, Kadri Põldmaa¹², Andrea Rinaldi¹³, Holger Thüs⁴, Carlos Vila-Viçosa¹⁴, Alfredo Vizzini¹⁵, Georgios Zervakis¹⁶, Jacob Heilmann-Clausen¹⁷

¹Understanding Evolution, Naturalis Biodiversity Center, Leiden, Netherlands, ²CEFE, CNRS, Univ Montpellier, EPHE, IRD, INSERM, Montpellier, France, ³Department Of Plant Anatomy, Institute Of Biology, Eötvös Loránd University, Budapest, Hungary, ⁴Botany Department, State Museum of Natural History Stuttgart, Stuttgart, Germany, ⁵BIOPOLIS Program in Genomics, Biodiversity and Land Planning, CIBIO, University of Porto, Vairão, Portugal, ⁶Faculty Of Medicine, University of Helsinki, Helsinki, Finland, ⁷Faculty Of Science, University of South Bohemia, Ceske Budejovice, Czech Republic, ⁸Department of Mycology, Real Jardín Botánico-CSIC, Madrid, Spain, ⁹Department Of Botany, Hungarian University of Agriculture and Life Sciences, Budapest, Hungary, ¹⁰Institute Of Evolutionary Biology, Biological And Chemical Research Centre, Faculty of Biology, University of Warsaw, Warsaw, Poland, ¹¹University of West Bohemia, Faculty of Applied Sciences, Pilsen, Czech Republic, ¹²Institute Of Ecology & Earth Sciences; Natural History Museum, University of Tartu, Tartu, Estonia, ¹³Department Of Biomedical Sciences, University of Cagliari, Cagliari, Italy, ¹⁴MHNC-UP - Museu de História Natural e da Ciência da Universidade do Porto - Herbário PO, Universidade do Porto, Porto, Portugal, ¹⁵Department Of Life Sciences And Systems Biology, University of Torino, Torino, Italy, ¹⁶Laboratory Of General And Agricultural Microbiology, Agricultural University of Athens, Athens, Greece, ¹⁷Globe Institute, University of Copenhagen, Copenhagen, Denmark

Abstract Body: 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' (<https://fun-dive.eu/>) 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 hypothesis 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.

SHIFT 02-050 / #2194

METABARCODING INSIGHTS INTO FUNGAL BIODIVERSITY IN MOUNTAIN WETLANDS OF SOUTH KOREA

POSTER ON BOARDS - SHIFT 02: ENVIRONMENT, ECOLOGY AND INTERACTIONS

Yehyeon Cha, Seung-Yoon Oh

Department Of Biology And Chemistry, Changwon National University, Changwon, Korea, Republic of

Abstract Body: Mountain wetlands are critical ecosystems that support high levels of biodiversity and serve as essential buffers against the impacts of global warming. These unique habitats provide refuge for a variety of species and help regulate local environments such as water cycle. While fungal diversity in other mountainous regions has been well-studied, mountain wetlands have not received as much attention. In this study, we used metabarcoding analysis to investigate the fungal diversity and community structure in a mountain wetland in South Korea. Our findings reveal that the fungal communities in the wetland are markedly different from those in the nearby mountain soil. The wetland exhibited distinct fungal community compositions, showing the unique ecological niches it supports. These differences highlight the importance of preserving mountain wetlands, as they harbour specialised fungal taxa that contribute to overall ecosystem stability and resilience. This result emphasises the need for targeted conservation efforts to protect these vital habitats among the growing challenges posed by climate change.