Lichen metabarcoding for biodiversity assessment across environments

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Brief description of the societal challenge

Human activities including habitat degradation, pollution, and climate change are leading to an ongoing mass extinction event, resulting in a dramatic decline in global biodiversity across ecosystems. To mitigate the impacts of these stressors, an accurate understanding of community composition is essential, and this requires robust and efficient biomonitoring strategies and bioindicator species.

Current monitoring efforts mostly rely on traditional morphological methods and are constrained by limited infrastructure, high costs, and logistical challenges. Among bioindicator organisms, lichens are particularly interesting (Asplund & Wardle 2016, Thakur et al. 2014). They are successful colonizers of most terrestrial environments and play an important role in the mineral cycling patterns. Often overlooked, these slow growing organisms show a wide diversity of growth forms and have the capacity to absorb moistures, vital minerals, and gases from their environment (Thakur et al. 2014). They occur in various terrestrial ecosystems and are extremely sensitive to a range of anthropogenetic factors, displaying physiological variations depending on air quality, climate variation, and habitat conditions. They are perfect bioindicators to monitor long term accumulation of pollutants and contaminants and can be used as markers of air pollution on a regional scale.

However, traditional lichens monitoring relies on direct observation and a high level of taxonomic expertise, require intensive fieldwork efforts, and are associated with false negative detection. Nowadays, the use of molecular based detection methods such as environmental DNA (eDNA) metabarcoding is revolutionizing the field, with recent studies showing that eDNA analysis of swabs collected from trees can detect up to 50% of lichens missed in floristic surveys (Dreyling et al. 2024).

Recent expeditions were conducted in Svalbard and in New Caledonia, and lichen eDNA samples were collected in a broad range of habitats. Here, we aim to assess whether the lichen eDNA samples collected can serve as a proxy to monitor lichen biodiversity across environments (Fediajevaite et al. 2021).

Description of the interdisciplinary nature of the project

The use of molecular techniques such as eDNA based detection became a reliable and widely used tool in ecological studies (Thomsen and Willerslev 2015), allowing the detection of rare species (Mächler et al. 2014), alien species in the early stages of invasion (Sepulveda et al. 2020) and to distinguish between cryptic species. As this non-invasive monitoring technique is based on the detection and identification of DNA traces left by organisms, large areas can easily and cheaply be monitored in a relatively short time frame compared to the use of traditional

surveys. eDNA-based detection is therefore an optimal tool for quickly assessing the health and status of ecosystems.

Lichen eDNA samples consisting of swabs collected on rocks and trees have been previously collected in Svalbard and New Caledonia. The recruited student will be in charge to extract lichen eDNA in the modern lab facilities of the Natural History Museum of Oslo and perform PCR and electrophoresis before sending the library for sequencing. Bioinformatic analysis will be performed later and are out of scope of this current project.

The student will conduct the summer research project at the Natural History Museum with the EDGE research group. She/he will focus on molecular analyses in modern lab facilities and will have the opportunity to learn cutting edge monitoring techniques, as well as learn various laboratory protocols and skills (DNA extraction, PCR, electrophoresis, eDNA workflow).

References:

Asplund & Wardle 2016. How lichens impact on terrestrial community and ecosystem properties. Biological reviews.

Dreyling et al. 2024. Surveying lichen diversity in forests: A comparison of expert mapping and eDNA metabarcoding of bark surfaces. MycoKeys.

Fediajevaite et al. 2021. Meta-analysis shows that environmental DNA outperforms traditional surveys, but warrants better reporting standards. Ecology and Evolution.

Mächler, E., Deiner, K., Steinmann, P., & Altermatt, F. (2014). Utility of environmental DNA for monitoring rare and indicator macroinvertebrate species. Freshwater Science.

Sepulveda, A. J., Nelson, N. M., Jerde, C. L., & Luikart, G. (2020). Are Environmental DNA Methods Ready for Aquatic Invasive Species Management? Trends in Ecology & Evolution.

Thakur et al. 2024. Lichens as effective bioindicators for monitoring environmental changes: A comprehensive review. Total Environment Advances.

Thomsen, P. F., & Willerslev, E. (2015). Environmental DNA – An emerging tool in conservation for monitoring past and present biodiversity. Biological Conservation.