

Abstract Book





37th **SIL** 2024
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SS27 - Advancing and implementing environmental DNA and RNA methods for assessing, monitoring and managing freshwater ecosystems

1498

Having IMPACT on monitoring aquatic parasite diversity – presenting a new pipeline evaluating eDNA as an integrative tool for studying parasites

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Parasites are usually presented as biological villains due to threats posed to human health and wildlife conservation. However, most metazoan parasites have no zoonotic potential and are instead known to be crucial organisms that contribute to the health and functioning of ecosystems and make up an overwhelming proportion of current biodiversity. Nonetheless, parasites remain the most neglected components of biodiversity monitoring and management strategies, and have only recently begun to be considered in conservation discussions. Monitoring of parasite biodiversity is hampered by inefficient tools for detecting parasites, with current methods involving the sacrifice of many hosts to quantify parasite biodiversity, and still, parasites occurring in low prevalence may be difficult to detect. Thus, for ethical reasons and amid a potential 6th mass species extinction, it is necessary to develop less invasive and non-lethal monitoring methods. Environmental DNA (eDNA) offers a potential solution, particularly for studying aquatic parasites by allowing them to be monitored in environmental matrices without the need to sacrifice hosts. Recent literature reviews show that eDNA has proven useful in the detection of single parasite species. However, very few studies targeted multiple parasite species within and across defined parasite groups at once. Given that eDNA is increasingly used in aquatic biodiversity monitoring worldwide, it offers a great opportunity for obtaining parasite diversity data in existing monitoring programs. Here, we present a methodological pipeline for the simultaneous detection of multiple fish parasite groups using eDNA that will be tested within the framework of the newly acquired project IMPACT.

1645

Application of eDNA metabarcoding to phytoplankton research in freshwater and saline lakes

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Freshwater lakes have been heavily altered by multiple stressors for decades, including a wide range of harmful human activities. Similarly, it is estimated that most of continental saline lakes will have undergone changes in their functioning by 2025. In the European Water Framework Directive (WFD), the ecological status assessment of lakes is based on the survey of key communities (i.e., Biological Quality Elements, BQEs). Due to its ecological features, phytoplankton is one of the key BQEs required by the WFD. In current assessments, phytoplankton is studied using a standardised microscopy approach. The advent of methods based on molecular techniques (e.g., eDNA metabarcoding) provides an alternative to overcome issues associated with microscopy-based assessment. The aim of our study was to compare phytoplankton data obtained by microscopy approach with eDNA metabarcoding based on the 23S RNA marker gene. Water was sampled in eight sites: four sites in Savsko lake (urban freshwater lake) and four sites in Plava Banja (saline clay pit pond) during spring, summer, and autumn 2023. The water quality analyses showed that nutrient concentrations (especially total nitrogen), chlorophyll a and conductivity were several times lower in the freshwater lake than in the saline lake. The very high total dissolved mineral content in Plava Banja had a substantial impact on the phytoplankton composition. The results of lake species inventories obtained using both approaches will be presented. Particular attention will be paid to the level of congruence between the floristic lists. This study is a part of the EU funded BIOLAWEB project.