

WORKSHOP 2

From data to discovery: overcoming analytical hurdles in lichen omics

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Data derived from omics methods such as [meta]genomics, [meta]transcriptomics, and metabolomics, are increasingly offering deepened insights into lichen symbioses. However, their multi-kingdom nature and status as non-model organisms, increases methodological complexity, and poses challenges in the interpretation of results derived from this type of data. Working with lichen omics data often requires the development of innovative strategies to tackle emerging issues, however the analytical challenges involved are rarely discussed in literature. This knowledge gap can lead to the duplication of efforts, and potentially slows down the adoption of best practices in this still emerging field. In the proposed workshop, we aim to bring together specialists working with various omics-scale data, focusing primarily on the methodological and analytical challenges they encounter in their research. Our goal is to foster an in-depth discussion about complexities and innovations involved in analyzing large-scale omics datasets, while also highlighting the considerable time investment necessary to process this data. By spotlighting what are typically "behind-the-scenes" aspects of lichen research —such as experimental design, analytical workflows, and data processing related to omics data— we aim to encourage knowledge exchange and facilitate the development of best practices specifically tailored to studying lichen symbioses.