The lichen-associated bacterial microbiome in evolution and function: from deep phylogeny to meta-omics insights

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Bacteria are essential yet often overlooked components of lichen symbioses. Lichen thalli provide stable microhabitats for complex bacterial communities that are phylogenetically diverse and functionally versatile. These bacterial partners engage in a variety of interactions with the fungal and algal symbionts, contributing to nutrient cycling, secondary metabolite production, stress resilience, and protection against pathogens. Recent advances in meta-omics and phylogenetic profiling have revealed unexpected bacterial lineages, possible co-evolutionary patterns, and the presence of functional gene clusters with ecological and biotechnological relevance. This symposium focuses on the bacterial dimension of the lichen microbiome, inviting contributions that explore its composition, functional roles, and evolutionary dynamics. We particularly welcome studies employing metagenomics, metatranscriptomics, metabolomics, and single-cell approaches to dissect the roles of bacteria in lichen symbiosis and ecosystem function. Integrative frameworks that link microbial ecology, host biology, and evolutionary theory are especially encouraged, as they are key to unravelling the hidden diversity and functional significance of lichen-associated bacteria.