Comparative analysis of the bacterial community of the Patagonian lichen *Peltigera frigida* and its soil substrate

Diego Leiva$^{1,2}$, Fernando Fernández-Mendoza$^2$, José Acevedo$^1$, Margarita Carú$^1$, Martin Grube$^2$, and Julieta Orlando$^1$

$^1$Departamento de Ciencias Ecológicas, Facultad de Ciencias, Universidad de Chile, Santiago, Chile
$^2$Institute of Biology, University of Graz, Graz, Austria

The lichen microbiome includes a diverse community of organisms, spanning widely across the bacterial tree of life. Lichens have been proposed to form partially open symbiotic systems, in which some microorganisms may be transmitted along within lichen propagules, while others are acquired from the surrounding environmental community.

In this survey, we discuss the extent to which the lichen microbiome is connected to that of its immediate substrate. For this we sampled ten specimens of the Patagonian foliose cyanolichen *Peltigera frigida* and their underlying soil substrates in two forest sites of the Coyhaique National Reserve (Aysén Region, Chile). Using 16S metabarcoding with primers that exclude cyanobacteria, we identified a significant taxonomic divergence between the bacterial communities of lichens and substrates.

At the Phylum level, Proteobacteria (37% of relative abundance) are most abundant within lichens, while soil substrates are dominated by Acidobacteriota (39%). At the Genus level, some bacteria are significantly more abundant in lichens, such as *Sphingomonas* (8% in lichens vs 0.2% in substrates) or an unassigned genus of Chitinophagaceae (10% vs 2%). Conversely, genera like the unassigned acidobacterial genus SCN-69-37 (0.9% vs 12%) are more abundant in substrates.

Overall, our results are consistent with the idea that lichens shape their microbiome obtaining components from various sources, including reproductive propagules and the substrate on which they grow. Further experimental and ecological approaches are needed to assess the contribution of these microorganisms to the fitness of the symbiotic system.

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