

According to modern taxonomic nomenclature lichens are not considered plants but are rather lichenized fungi that form obligatory symbiotic interactions – mainly with eukaryotic green algae or/and prokaryotic cyanobacteria. Contrary to the cryptogamic plants (vascular and mosses) inhabiting only sheltered and water abundant sites in Antarctica, lichens commonly thrive in areas exposed to the harshest polar conditions. Lichens significance is highlighted by their potential to colonize postglacial terrains, playing a major role in biogenic element turnover, diverse soil processes and rock substrate weathering. Recent investigations conclude that besides the main myco- and photobiont partners lichen thalli comprise a third integral partner in form of a diverse heterotrophic microbial community. Our main goal is to determine whether the non-photosynthetic prokaryotic part of the lichen microbiome is species-specific, is it dependent on the trophic status of the surrounding polar environment and also are the changes within this microbial community connected to lichen thalli age. Based on microscopic and metagenomic investigations of the Antarctic lichen material as well as bacterial strains isolated from it we want to shed a light on the functional role of this part of the long-lived lichen symbiotic assemblage exposed to the harsh Antarctic climate and potential pathogenic or competitor bacteria and fungi. The usage of modern epifluorescence microscopy techniques, next-generation DNA sequencing and appropriate cultivation methods will allow to broaden the knowledge on the lichen-hosted microbial communities and their functions. An important task will concern the formulation of new cultivation methods as well as the modifications of existing ones to improve the efficiency of isolate recovery. Physiological testing methods will further elucidate the isolates' potential for practical use. The chosen lichen species, not investigated so far in terms of their resident bacterial communities, are: a) growing in sites of high nutrient content (penguin nesting sites) *Ramalina terebrata* and *Caloplaca regalis*; b) growing in nutrient poor sites *Himantormia lugubris* and *Usnea aurantiaco-atra*; c) growing in sites of varying nutrient levels *Usnea antarctica*. The fact that this last species is also a common one in the region allows to investigate the thalli (and the associated microbiome) from the youngest to the oldest ones, occurring at different distances from the glacier foot. The reason for investigating lichen bacterial microbiomes is to broaden the scarce knowledge on the symbiotic microbes of Antarctic lichens, which are very common and important to this regions ecology. The aforementioned arguments as well as the lichen community biodiversity impoverishment threat due to global warming and air pollution fully justifies the time, place as well as the purpose of this projects objectives.