

HOW MICROBES SHAPE THE FOREFRONT OF RETREATING GLACIERS



Global warming has increased the rate of ice melting. Glacier retreat is a special case of ice melting which strongly impacts Arctic polar regions. When a glacier retreats, new, unstable ground is left over, without any vegetation coverage. A process of primary colonisation and subsequent species successions in the biotic community immediately takes place, with the establishment of a microbial community, mainly formed by phototrophic populations, followed by the introduction of pioneer plants and finally leading to a mature, stable biotic community. The initial steps of this process involve a gradual increase of the biodiversity of the microbial community, connected to the establishment of diverse key functions related to soil formation and structural stabilization and to the increase of nutrient content. The formation of microbial crusts and the appearance of nitrogen fixation and respiration activities are among these functions. When this delicate development is disturbed, soil formation and colonisation is impaired, possibly leading to erosion and environment degradation. Succession, the gradual process by which the species composition of a community changes over time, can be profitably studied in the foreground of a retreating glacier. Areas in the Arctic regions, presenting newly exposed soils after glacial retreat, are especially suitable for this kind of study since the processes occur rather slowly.



In cold, polar environments, cyanobacteria are found in great variety and are the dominant microorganisms in terms of biomass and productivity. There, they play a major role in nitrogen fixation, compensating for the lack of nitrogen in soil, and permit the subsequent colonisation by other microorganisms and higher plants. Cyanobacteria also fix carbon through photosynthesis and can grow in places otherwise characterised by very low nutrient concentrations. Cyanobacteria and heterotrophic bacteria can occur in consortia that are bound together by polysaccharides and bind soil particles thereby stabilising soils and facilitating the establishment of vegetation.

We study a phenomenon which, due to global warming, is presently more diffused and more evident than in the recent past. It is the formation of new soil, that takes place when the annual ice budget of a glacier is negative and the glacier front retreats. This gives the opportunity to study a relatively fast habitat evolution, driving adaptation and colonization by new species. In this frame we will address the structure of the microbial communities which are responsible for primary colonisation and initial successions of the foreland of receding glaciers and their functional role in the dramatic shift from ice to soil. Attention will also be placed on the diversity and composition of the polar ground microbial communities along a vertical profile from the ground surface to the active layer of permafrost, including soil microbial crusts, epiphytic microbial communities, the rhizosphere of pioneer plants, the microbial community of the active layer of permafrost. To achieve these goals we target Arctic regions, where all biological processes are slowed down and anthropogenic pressure is reduced or nearly absent.



The research is implemented through the application of up-to-date technologies that are fully mastered by the proponent team, including integration of bacteriological, morphological, and molecular approaches for the characterization of the microbial communities, metagenomics and metatranscriptomics, phenotypic arrays, in situ and ex situ activity measurements, soil micromorphology, soil biogeochemistry and mineralogy, and diffractometry.

A major innovation of the project is the extensive use of a state of the art molecular approach, including metagenome (environmental genome) analysis, complemented, as much as possible, with the isolation and study of "real" organisms. Culture independent methods have been used to study microbial community structure, but only a few addressed microbial successions. Molecular fingerprints can be obtained in a semi-automated way from DNA directly extracted from the environment; community components can be identified by gene cloning. Metagenomes can be readily sequenced with state of the art technology. Such an approach, that was not feasible or extremely expensive until the new generation of DNA sequencers has appeared, has recently yielded a broad insight of the microbial and functional diversity, providing access to the genetic information of uncultured soil microorganisms.

