



**Project acronym:** MICASA

**Project title:** Exploring the influence of different stressors on the composition of microbial communities associated to *Silene acaulis* in Greenland

**Project leader:** Laura Bertini, University of Tuscia, Italy

**Discipline:** Earth Sciences & Environment: Ecosystems & Biodiversity

**Station(s):** Greenland Institute of Natural Resources (GINR) (Greenland/Denmark), Arctic Station (Greenland/Denmark)

In extreme environmental conditions, such as those experienced in the Arctic, the symbiotic relationships between plants and their microbiota hold a pivotal role in ecosystem functioning. Plants represent a unique ecological niche for diverse communities of mutualistic microorganisms, providing photosynthetically fixed carbon and low molecular weight root exudates that are used as energy sources by soil microorganisms, whose community composition is in turn shaped by their ability to metabolize different compounds and resist different antimicrobial metabolites present in the exudates. On the other hand, plant-associated microorganisms can strongly influence plant growth and health. Despite that, the drivers of diversity and composition of root-associated microbial communities in Arctic environments are still barely known. In this regard, the main ground-breaking objective of the project MICASA is to compare the composition of microbial communities associated with *Silene acaulis* plants collected in two localities of South-West Greenland, Kobbefjord and Disko Island, in order to assess the impact of different environmental conditions on plant physiology and associated microbiota diversity. Hitherto, only one published paper assessed the diversity of endophytic fungi associated with the leaves and stems of *S. acaulis* plants collected at Ny-Ålesund (Svalbard, Norway) (Zhang T, Yao YF. PLoS One, 2015, 10(6):e0130051), while no studies on the microbial community associated with the roots of this species have been conducted in Greenland so far. The analysis of microbiota will be carried out using combined culture-independent and culturomics approaches which will allow achieving both a fine characterization of the plant-associated microbial community at the

taxonomic level and isolated strains of representative members of the communities, to be tested for their resistance and production of cold-adapted molecules of biotechnological interest. In addition, the gene expression of molecular biomarkers of specific pathways (photosynthesis, photorespiration, oxidative metabolism, reproduction) will be characterized in the plants collected in the two different localities, in order to disclose the molecular basis of plant adaptation to different climatic conditions. Additionally, data generated within this project will give insights into future climate change scenarios and make speculation on the future spread of this vascular plant. Finally, the comparison of the composition of the microbial communities associated with *S. acaulis* and those associated with its Antarctic homolog *Colobanthus quitensis* will provide unprecedented information on the role of plant microbiota in the resistance to environmental stressors and adaptation to extreme environments.